

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96453

TO: Michael Pak
Location: cm1/10e18/10d19
Art Unit: 1646
Friday, June 20, 2003
Case Serial Number: 825147

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Pak,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:31 ; Search time 26 Seconds
(without alignments)
1044.514 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHHGEGEGGAAGLVKVS.....SICKAGESTDALSLPHVLLK 923

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database :

Issued Patents -AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1792.5	37.9	722	4	US-09-105-058C-23 Sequence 23, Appl
2	1789.5	37.8	930	4	US-09-177-650-96 Sequence 96, Appl
3	1788.5	37.8	871	4	US-09-105-058C-20 Sequence 20, Appl
4	1784	37.7	872	4	US-09-177-650-2 Sequence 2, Appl
5	1761	37.2	757	4	US-09-177-650-89 Sequence 89, Appl
6	1620.5	34.2	872	4	US-09-177-650-7 Sequence 7, Appl
7	1603.5	33.9	854	4	US-09-105-058C-27 Sequence 27, Appl
8	1570.5	33.2	870	4	US-09-177-650-91 Sequence 91, Appl
9	1207.5	25.5	300	4	US-09-105-058C-4 Sequence 4, Appl
10	1207.5	25.5	300	4	US-09-105-058C-6 Sequence 6, Appl
11	1188	25.1	807	4	US-09-177-650-3 Sequence 3, Appl
12	1102	23.3	676	4	US-09-135-021-2 Sequence 2, Appl
13	1102	23.3	676	4	US-09-135-020-2 Sequence 2, Appl
14	1102	23.3	676	4	US-09-135-010A-2 Sequence 2, Appl
15	1102	23.3	676	4	US-09-444-871-2 Sequence 2, Appl
16	1102	23.3	676	4	US-09-634-920-2 Sequence 2, Appl
17	1102	23.3	676	4	US-09-597-735-2 Sequence 2, Appl
18	1102	23.3	676	4	US-09-444-295-2 Sequence 2, Appl
19	1102	23.3	676	4	US-09-597-732-2 Sequence 2, Appl
20	1100.5	23.3	605	4	US-09-105-058C-24 Sequence 24, Appl
21	1092.5	23.1	677	4	US-09-177-650-4 Sequence 4, Appl
22	1091.5	23.1	581	4	US-09-135-021-80 Sequence 80, Appl
23	1091.5	23.1	581	4	US-09-135-010A-116 Sequence 116, App
24	1091.5	23.1	581	4	US-09-597-735-116 Sequence 116, App
25	1091.5	23.1	581	4	US-09-597-732-116 Sequence 116, App
26	1085	22.9	310	4	US-09-105-058C-18 Sequence 18, Appl
27	1081.5	22.9	570	4	US-09-135-020-114 Sequence 114, Appl

28	1081.5	22.9	570	4	US-09-135-010A-114 Sequence 114, App
29	1081.5	22.9	570	4	US-09-444-871-114 Sequence 114, App
30	1081.5	22.9	570	4	US-09-597-735-114 Sequence 114, App
31	1081.5	22.9	570	4	US-09-444-295-114 Sequence 114, App
32	1081.5	22.9	570	4	US-09-597-732-114 Sequence 114, App
33	993.5	21.0	245	4	US-09-105-058C-8 Sequence 8, Appl
34	957	20.2	298	4	US-09-105-058C-2 Sequence 2, Appl
35	905.5	19.1	430	4	US-09-105-058C-21 Sequence 21, Appl
36	898.5	19.0	376	4	US-09-135-020-113 Sequence 113, App
37	898.5	19.0	376	4	US-09-135-010A-113 Sequence 113, App
38	898.5	19.0	376	4	US-09-444-871-113 Sequence 113, App
39	898.5	19.0	376	4	US-09-597-735-113 Sequence 113, App
40	898.5	19.0	376	4	US-09-444-295-113 Sequence 113, App
41	898.5	19.0	376	4	US-09-597-732-113 Sequence 113, App
42	485.5	10.3	137	4	US-09-135-020-109 Sequence 109, App
43	485.5	10.3	137	4	US-09-135-010A-109 Sequence 109, App
44	485.5	10.3	137	4	US-09-444-871-109 Sequence 109, App
45	485.5	10.3	137	4	US-09-597-735-109 Sequence 109, App
46	485.5	10.3	137	4	US-09-444-295-109 Sequence 109, App
47	485.5	10.3	137	4	US-09-597-732-109 Sequence 109, App
48	250	5.3	539	1	US-08-464-340A-13 Sequence 13, Appl
49	245	5.2	646	4	US-09-336-643A-10 Sequence 10, Appl
50	243	5.1	601	4	US-09-336-643A-4 Sequence 4, Appl
51	234	4.9	283	4	US-09-135-021-6 Sequence 6, Appl
52	232.5	4.9	655	4	US-09-142-791A-4 Sequence 4, Appl
53	232.5	4.9	655	4	US-09-178-109-2 Sequence 2, Appl
54	232	4.9	528	2	US-08-527-152-2 Sequence 2, Appl
55	229	4.8	636	4	US-09-142-791A-2 Sequence 2, Appl
56	229	4.8	636	4	US-09-142-791A-6 Sequence 6, Appl
57	229	4.8	636	4	US-09-178-109-4 Sequence 4, Appl
58	224	4.7	477	4	US-09-336-643A-18 Sequence 18, Appl
59	223	4.7	499	4	US-09-336-643A-8 Sequence 8, Appl
60	209.5	4.4	532	1	US-08-288-405A-10 Sequence 10, Appl
61	206.5	4.4	494	1	US-08-464-340A-4 Sequence 4, Appl
62	206.5	4.4	494	5	PCT-US94-08449A-4 Sequence 4, Appl
63	204.5	4.3	490	4	US-09-336-643A-6 Sequence 6, Appl
64	199.5	4.2	513	1	US-08-464-340A-2 Sequence 2, Appl
65	199.5	4.2	513	5	PCT-US94-08449A-2 Sequence 2, Appl
66	174	3.7	61	4	US-09-135-020-108 Sequence 108, App
67	174	3.7	61	4	US-09-135-010A-108 Sequence 108, App
68	174	3.7	61	4	US-09-444-871-108 Sequence 108, App
69	174	3.7	61	4	US-09-597-735-108 Sequence 108, App
70	174	3.7	61	4	US-09-444-295-108 Sequence 108, App
71	174	3.7	61	4	US-09-597-732-108 Sequence 108, App
72	155.5	3.3	731	4	US-09-115-446-2 Sequence 2, Appl
73	153	3.2	120	4	US-09-105-058C-28 Sequence 28, Appl
74	142	3.0	2137	4	US-09-134-001C-4463 Sequence 4463, Ap
75	141	3.0	2161	1	US-07-745-206A-2 Sequence 2, Appl
76	141	3.0	2161	1	US-08-455-543A-49 Sequence 49, Appl
77	141	3.0	2161	2	US-08-223-305C-49 Sequence 2, Appl
78	141	3.0	2161	2	US-08-311-363-2 Sequence 2, Appl
79	141	3.0	2516	3	US-08-374-077C-2 Sequence 2, Appl
80	141	3.0	2516	4	US-08-895-590-2 Sequence 2, Appl
81	141	3.0	2516	4	US-09-539-879A-2 Sequence 2, Appl
82	137.5	2.9	2353	4	US-08-984-709A-50 Sequence 50, Appl
83	137	2.9	2353	1	US-08-455-543A-51 Sequence 51, Appl
84	137	2.9	2161	1	US-08-223-305C-51 Sequence 51, Appl
85	135	2.9	90	4	US-09-384-302A-17 Sequence 17, Appl
86	133	2.8	67	4	US-09-243-675-5 Sequence 5, Appl
87	133	2.8	67	4	US-09-243-675-6 Sequence 6, Appl
88	133	2.8	1835	4	US-09-404-650-5 Sequence 5, Appl
89	133	2.8	2336	4	US-09-268-163-10 Sequence 10, Appl
90	130	2.7	58	4	US-09-135-020-112 Sequence 112, App
91	130	2.7	58	4	US-09-135-010A-112 Sequence 112, App
92	130	2.7	58	4	US-09-444-871-112 Sequence 112, App
93	130	2.7	58	4	US-09-597-735-112 Sequence 112, App
94	130	2.7	58	4	US-09-444-295-112 Sequence 112, App
95	130	2.7	58	4	US-09-597-732-112 Sequence 112, App
96	129.5	2.7	75	4	US-09-105-058C-10 Sequence 10, Appl
97	129	2.7	2337	3	US-08-713-118-2 Sequence 2, Appl
98	129	2.7	2337	4	US-09-452-007-2 Sequence 2, Appl
99	127.5	2.7	3443	2	US-08-416-603-2 Sequence 2, Appl
100	127	2.7	67	4	US-09-243-675-7 Sequence 7, Appl

101	127	2.7	67	4	US-09-243-675-8	Sequence 8, Appl 1
102	126.5	2.7	1872	6	5386025-6	Patent No. 5386025
103	126	2.7	68	4	US-09-243-675-3	Sequence 1, Appl 1
104	126	2.7	75	4	US-09-243-675-1	Sequence 3, Appl 1
105	126	2.7	510	2	US-09-021-323-1	Sequence 1, Appl 1
106	126	2.7	1873	1	US-08-336-257A-7	Sequence 7, Appl 1
107	126	2.7	2265	2	US-08-149-097D-36	Sequence 36, Appl 1
108	126	2.7	2509	2	US-08-149-097D-35	Sequence 35, Appl 1
109	125.5	2.7	897	3	US-08-975-703-6	Sequence 6, Appl 1
110	125.5	2.7	1284	4	US-09-343-494-9	Sequence 9, Appl 1
111	125.5	2.7	2756	1	US-08-375-709-11	Sequence 11, Appl 1
112	125.5	2.7	2756	1	US-08-752-929-11	Sequence 11, Appl 1
113	125.5	2.7	2756	1	US-09-090-793-7	Sequence 7, Appl 1
114	125.5	2.7	2756	1	US-09-243-675-4	Sequence 4, Appl 1
115	125.5	2.6	67	4	US-08-455-543A-47	Sequence 47, Appl 1
116	125	2.6	2339	2	US-08-223-305C-47	Sequence 47, Appl 1
117	125	2.6	2339	2	US-09-268-163-6	Sequence 6, Appl 1
118	125	2.6	2343	4	US-09-268-163-4	Sequence 4, Appl 1
119	125	2.6	703	4	US-08-910-925-4	Sequence 4, Appl 1
120	124	2.6	1984	3	US-08-836-325-10	Sequence 10, Appl 1
121	123.5	2.6	2175	4	US-09-404-650-2	Sequence 2, Appl 1
122	122.5	2.6	2188	4	US-09-404-650-4	Sequence 4, Appl 1
123	122.5	2.6	3969	4	US-08-061-376-5	Sequence 5, Appl 1
124	122	2.6	2237	1	US-08-455-543A-48	Sequence 48, Appl 1
125	121.5	2.6	2237	2	US-08-223-305C-48	Sequence 48, Appl 1
126	121.5	2.6	1873	1	US-09-268-163-8	Sequence 8, Appl 1
127	121.5	2.6	1873	1	US-08-435-675B-4	Sequence 4, Appl 1
128	120.5	2.5	68	4	US-09-243-675-2	Sequence 2, Appl 1
129	120	2.5	921	1	US-08-188-582-2	Sequence 2, Appl 1
130	119.5	2.5	921	1	US-08-646-715-2	Sequence 2, Appl 1
131	119.5	2.5	1159	2	US-09-351-215-13	Sequence 13, Appl 1
132	119.5	2.5	1159	4	US-09-226-012-2	Sequence 2, Appl 1
133	119.5	2.5	1159	4	US-09-226-012-2	Sequence 2, Appl 1
134	119.5	2.5	1159	4	US-09-226-012-2	Sequence 2, Appl 1
135	119.5	2.5	1159	4	US-09-226-012-2	Sequence 2, Appl 1
136	118.5	2.5	1618	1	US-07-853-913-4	Sequence 4, Appl 1
137	116	2.5	1315	3	US-08-899-595-3	Sequence 3, Appl 1
138	116	2.5	1315	3	US-08-899-595-3	Sequence 3, Appl 1
139	116	2.5	1989	3	US-08-836-325-12	Sequence 12, Appl 1
140	116	2.5	2273	4	US-09-426-998-5	Sequence 5, Appl 1
141	115	2.4	1170	4	US-09-749-588-2	Sequence 2, Appl 1
142	114.5	2.4	586	4	US-09-643-597-152	Sequence 152, App
143	114.5	2.4	1248	2	US-09-080-897-2	Sequence 2, Appl 1
144	114.5	2.4	1248	4	US-09-323-735-2	Sequence 2, Appl 1
145	113.5	2.4	823	1	US-07-745-206A-15	Sequence 15, Appl 1
146	113.5	2.4	823	1	US-08-311-363-15	Sequence 15, Appl 1
147	113.5	2.4	1754	1	US-07-745-206A-13	Sequence 13, Appl 1
148	113.5	2.4	1754	2	US-08-311-363-13	Sequence 13, Appl 1
149	112	2.4	907	3	US-08-938-830-26	Sequence 26, Appl 1
150	112	2.4	907	3	US-09-020-222-26	Sequence 26, Appl 1

ALIGNMENTS

RESULT 1
US-09-105-058C-23
Sequence 23, Application US/09105058C
GENERAL INFORMATION:
APPLICANT: Blauer, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauser, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 722
TYPE: PRT
ORGANISM: mouse
US-09-105-058C-23

Query Match
Best Local Similarity 37.9%; Score 1792.5; DB 4; Length 722;
Best Similarity 53.4%; Pred. No. 8.8e-151;
Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;

QY	21	GAAGAAAGGRLGSGMKGVSRRGRVRLNSAAGDGLLGTAAATGCGGCGRLRESR	80
DB	9	GYPGTSGEKKLVGFVGLDPGA-----PDSTDGALLIGSEAPK---RGSVLSKPT	59
QY	81	GKOGAMRLSLGKPLSTYSSOSCRNRVYRQNTLYNLERPRGNAFYHAFVLLFGC	140
DB	60	GGAGA-----GKF-----PKRNATYRKLQNTLYNLERPRGNAFYHAFVLLFVSC	106
QY	141	LILSVSTPEHTKLASSCLLLEFWIIVFGLFTRIRWSAGCCCRYGMRGLRFARK	200
DB	107	LVLVSSTLKEKESGALYILEITVIVFGEYFVIRMAAGCCCRYRGNRGLRFARK	166
QY	201	PCFVIDTIVLIIASIAVVAKTGNIIFATSLRSLRFLQILMVRMDRGSTMKLGSVY	260
DB	167	PCFVIDIMVLIIASIAVVAKTGNIIFATSLRSLRFLQILMVRMDRGSTMKLGSVY	226
QY	261	ANSKELITAMYGFLVIFSSFLVYLYVEKDANKFEFSTYADALMWTITLTITGYGDKTPL	320
DB	227	ANSKELITAMYGFLVIFSSFLVYLYVEKDANKFEFSTYADALMWTITLTITGYGDKTPO	286
QY	321	TWNGRLSLGFGALGTSFPLPAGLIGSGFALKVQEOHROKHFEKRRRPAANLQCVRS	380
DB	287	TWNGRLSLGFGALGTSFPLPAGLIGSGFALKVQEOHROKHFEKRRRPAANLQCVRS	346
QY	381	VAAD-----EKSVSIAATWK--PHLKALHTC-----SPT	406
DB	347	YATNLSRTLDHSTWQYERTVTVPMYRLPIPLNGLELRLNLSKSGLFRKEPOPEP	405
QY	407	NOKLSKEVRYRASPFQSTKRSQASVGD--RNSPSTIDTAEGSPYKQKMSFENDRTF	464
DB	406	SKQVSLKDRV--FSSPRGMAGKGSPOAQTVRRSPADQSLDPSKPKKMSFENDRT	464
QY	465	RSRLRKSQPKVIDADTALGTDVYDEKGCODVSEDTPLPKYTRIRIRIMKEFVA	524
DB	465	RSRLRKSQPKVIDADTALGTDVYDEKGCODVSEDTPLPKYTRIRIRIMKEFVA	523
QY	525	KRKEETLRPYDVYKDYIEQYSAGHLMCLRIKSLQTRVDDIILGQITSDKRSREKITA	584
DB	524	KRKEETLRPYDVYKDYIEQYSAGHLMCLRIKSLQTRVDDIILGQITSDKRSREKITA	582
QY	585	HTTDDLSMLGKRVYKQVQSTIESKLDLDDIYQVLRKGSASALASALASALASALAS	642
DB	583	TELPEDPSMGRGKRVYKQVQSTIESKLDLDDIYQVLRKGSASALASALASALASALAS	629
QY	643	-----DQTSQSPVDSKDLGSAQNSGC-----LSRSTANISRGQITLTPNEFSQOT	692
DB	630	YFGAKEPEPAPRYHSDERD---HADKHCIIKIYRSTSS-----TGOR	671
QY	693	FYALSPTMHSQATQVAPISQS 712	
DB	672	NYAAPPAI--PPAQCPPTS 689	

RESULT 2
US-09-177-650-96
Sequence 96, Application US/09177650
GENERAL INFORMATION:
APPLICANT: Iepert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole

```

; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 96
; LENGTH: 930
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-177-650-96

Query Match      37.8%; Score 1789.5; DB 4; Length 930;
Best Local Similarity 43.9%; Pred. No. 2,5e-150;
Matches 433; Conservative 109; Mismatches 246; Indels 199; Gaps 26;

QY 21 GAAAAAGGRLSGMDVSGRGVLLNSAARGDGLLCTRAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLKVGFVGLDPA-----PDSTRGALLIAGSEAPK--RGSILSKPRA 59
QY 81 GKOGARMSLLGKPLSTYSOSCRNVRKYRYONYLYNLEBRGNAFYHAFFLLVFCG 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLFNLYNLEBRGNAFYHAFFLLVFCG 106
QY 141 LILSVFTIPHTKLASSCLLLEFVMIYVGLFELIRIWSAGCCCRYGWGRLEFARK 200
DB 107 LVLVSFTIKYKESSEKALYILETVIVGVFVIRMAAGCCCRYGWGRLEFARK 166
QY 201 PCYVIDIVLSTAVVSAKTOGNEFATSLRFLQILIRVMDRGTGKLLGSVY 260
DB 167 PCYVIDIVLSTAVVSAKTOGNEFATSLRFLQILIRVMDRGTGKLLGSVY 226
QY 261 AHSKELTAWYIGLVLFSSFLVYLVKEDANKERSTYADALMWGTLITTTGYGDKTFL 320
DB 227 AHSKELTAWYIGLVLFSSFLVYLVKEDANKERSTYADALMWGTLITTTGYGDKTFL 286
QY 321 TWLGRLLSAGPALLGISFPALPAGILGSGFALKVOEHQKHFEKRRNPAANLIQCVMS 380
DB 287 TWNGRLLAATFTLLIGVSEFALPAGILGSGFALKVOEHQKHFEKRRNPAANLIQCVMS 346
QY 381 YAAD-----EKSVSIATWK-----PHIKALHT----- 402
DB 347 YATNLSTRDLHSTWQYERTVIVPMYSSOTQYTGASRLPLPNOLELLNLKSKSLAR 406
QY 403 -----CSP-----TNOKLSFKERVRMASPRGOSIKSROASVGD--RR 437
DB 407 KDPPEPSPKSGPCRGPLCGCCPGRSSOKVSLKDRV--FSSPRGVAANKGKSPQACTVRR 465
QY 438 SPSPDITAEAGSPYKQKSMFNDTRFRPSLLKSSQPRVIDADPALTDDVYDEKGCQ 497
DB 466 SPSPDITAEAGSPYKQKSMFNDTRFRPSLLKSSQPRVIDADPALTDDVYDEKGCQ 524
QY 498 CDVASEDTPLPLKTVIRAIRIMKFPVAKRKFEKTELRYVYKDYIEOYSGHDLMLRIKS 557
DB 525 CEFTYEDITPLKTVIRAIRIMKFPVAKRKFEKTELRYVYKDYIEOYSGHDLMLRIKS 584
QY 558 LQTRVQDILGKQGITSDKRSREKITAHEHTTDLMSLGRVAVYKVOVOSTESKLDCLDI 617
DB 585 LQTRVQDILGKQGITSDKRSREKITAHEHTTDLMSLGRVAVYKVOVOSTESKLDCLDI 643
QY 618 YQOYVIRKSASALALASFOIPEFC-----EFTSOYQSPVDSKDLGSGNOSGCLS 668
DB 644 YMO-----RMG-----IPTEYAVFGAKEPEAPYHSPEDSRE--HYDRGCIV 687
QY 669 RSTANIRGLOFILTLPNEFSAQTFYALSPTHSQATQVPISSDSASAVATNTIANQIN 728
DB 668 KIVRSSSSSG----- 700
QY 729 TAPKPAAPTTLQIPPEL-----PAIKHLPPETLH-----PNPAGLOESISDVTTCL 775

```

```

DB 701 FSAAPPAAP--PYQCPSTMSWQSHPRGCHTSPVGDHSLVRIAPPAAHERSLSATYGGN 759
QY 776 VASKENVQVQASULTK--DRSMKSPFMGETLISVCPMPKDKGLSKLVONLIRSEEL 833
DB 760 RASMEFLROEDTFCRCPEENLNDSD-----DTSISIPSVHEELERSFSGFSISQENL 814
QY 834 NIGLGSSESGSGSQDYFPKWRRESKLFITDEEV-----EETEDTFDAAPQ 882
DB 815 DALNSCYAAYAPAKAPRYIABESD-----IDSCLCTCGPPRPSATGRCPPGDVGMWAPG 871
QY 883 PAREAAFASDSLRTGRSSSQSITCKAG 909
DB 872 PGSEAAALG-----QWTRPRPSARCLRG 894

RESULT 3
US-09-105-058C-20
; Sequence 20, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blannet, Michael A.
; APPLICANT: Dwojletzky, Steven
; APPLICANT: Gribkoft, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 871
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-105-058C-20

Query Match      37.8%; Score 1788.5; DB 4; Length 871;
Best Local Similarity 46.8%; Pred. No. 2.8e-150;
Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAAAGGRLSGMDVSGRGVLLNSAARGDGLLCTRAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLKVGFVGLDPA-----PDSTRGALLIAGSEAPK--RGSILSKPRA 59
QY 81 GKOGARMSLLGKPLSTYSOSCRNVRKYRYONYLYNLEBRGNAFYHAFFLLVFCG 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLFNLYNLEBRGNAFYHAFFLLVFCG 106
QY 141 LILSVFTIPHTKLASSCLLLEFVMIYVGLFELIRIWSAGCCCRYGWGRLEFARK 200
DB 107 LVLVSFTIKYKESSEKALYILETVIVGVFVIRMAAGCCCRYGWGRLEFARK 166
QY 201 PCYVIDIVLSTAVVSAKTOGNEFATSLRFLQILIRVMDRGTGKLLGSVY 260
DB 167 PCYVIDIVLSTAVVSAKTOGNEFATSLRFLQILIRVMDRGTGKLLGSVY 226
QY 261 AHSKELTAWYIGLVLFSSFLVYLVKEDANKERSTYADALMWGTLITTTGYGDKTFL 320
DB 227 AHSKELTAWYIGLVLFSSFLVYLVKEDANKERSTYADALMWGTLITTTGYGDKTFL 286
QY 321 TWLGRLLSAGPALLGISFPALPAGILGSGFALKVOEHQKHFEKRRNPAANLIQCVMS 380
DB 287 TWNGRLLAATFTLLIGVSEFALPAGILGSGFALKVOEHQKHFEKRRNPAANLIQCVMS 346
QY 381 YAAD-----EKSVSIATWK-----PHIKALHT----- 402
DB 347 YATNLSTRDLHSTWQYERTVIVPMYSSOTQYTGASRLPLPNOLELLNLKSKSLAR 406

```

QY 403 -----CSP--TNOKLSEKERYMASPRGOSIKSROASVGD--RR 437
 DB 407 KDPPEPSPKSGPCRGPLCGCCPGRSSQKVSLLKDRV-FSSPRGVAAGKSGSPAQOYRR 465
 QY 438 SPSDITAGSPTKQKSMSEFNDRTFRPSRLKSSOPKPYIDADTALGTDVYDEKCO 497
 DB 466 SPSADQSLDSSPKVKPSWSEFDRSRARQAFRIKGAASRO--NSEASLPGEDIYDCKSCP 523
 QY 498 CDVSVEDLTPPLKTVIRAIRIMKFKRKFKETLRPYDVKDYEIOYSAGHLDMLCRKS 557
 DB 524 CEFTYEDLTPGLKVSIRAVCMRFLVSKRKFKESLRYDMVDYEOYSAGHLDMLSRKS 583
 QY 558 LQTRVDQILGQOITSDDKSREKITAHEHTDLSMLGRVYKVEKQOYSIESKLDCLDI 617
 DB 584 LOSRVDQIVGRPAITD-KDRTKGPAAELPEDEPSMMGRGLGKVEKQYLSMEKKLDPLVNI 642
 QY 618 YOOVLKSGSASALALASFOIPPEEC-----EOTSQSPYDSKDLSSAONSGCLS 668
 DB 643 YMO--RMG-----IPPTETAYFGAKEPEAPPHSPDSRE--HYDRHGCIY 686
 QY 669 RSTSANISRGLOFILTPNEFSQOTFYALSPTHMSQATQVPISSO-----DGSAAVAT 720
 DB 687 KIVRSSSSSTG-----QKNFSAP--AAP-----VQCPSTSMQOSHPRQCHGTSVPV 732
 QY 721 NTINQINTAPKPAAPTTLOI-----PP-----PLPAI 748
 DB 733 GDHGLVIRIPPPAHRSLSAYGCGNRASMEFLROEDTPCGRPEGLRDSOTISIPSV 792
 QY 749 KHLPRPETHNPAGLOESISDVTTCVASKENYQVAOS 787
 DB 793 DH-----EELERSFSGF--SISO-----SKENLDALNS 818

RESULT 4
 US-09-177-650-2
 ; Sequence 2, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: LePERT, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177,650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 872
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-177-650-2

Query Match 37.7%; Score 1784; DB 4; Length 872;
 Best Local Similarity 46.8%; Pred. No. 7e-150;
 Matches 411; Conservative 92; Mismatches 196; Indels 180; Gaps 25;
 QY 21 GAAAAAAGGCRLOSCKMDESRRRVLNSAAAGDGLLLCTRAATLGGGGGGLRESRR 80
 DB 9 GYVPGSGEKKLVGVGLPGA-----PDSTRDGLALLIGSEAPK--RGSILSKPRA 59
 QY 81 GKGAGRSLLGKPLSTYSSOSCRNVKRYRQONTLYNLEPRGMAFYTHAVFLLPFCG 140
 DB 60 GGGGA-----GKP-----PKNARYKLLQNLNLYNLEPRGMAFYTHAVFLLPFCG 106
 QY 141 LILSVSTPEHKLASSCLLIEFVMIIVGLEFIIRISWAGCCCRYGRLFAFK 200
 DB 107 LVLSVSTIEKEKSSGALYILEITVIVGVEFVRAIMAGCCCRYKGMGRKLFARK 166

QY 201 PCGVIDITVILASIAVSATQGNIFATSAIRSLRFLDILKRVNDRRGCTKLLGSVY 260
 DB 167 PCGVIDITVILASIAVLAASQGNVFAISALRSRLFLDILKRVNDRRGCTKLLGSVY 226
 QY 261 AHSKELITANYIGFLVYIFSSFLVYVEKDNKESTYADALMWGTTTLTGTGDKPPL 320
 DB 227 AHSKELITANYIGFLCILASFLVYIAEKGNDFDYADALMWGLITLTGTGDKTPQ 286
 QY 321 TWIGRLISAGFALLGISFFALLPAGILSGFALKVOEQHQRKHFEKRRNPANLIGQWRS 380
 DB 287 TWNGRLIAAFTLLIGVSFFALLPAGILSGFALKVOEQHQRKHFEKRRNPAGLIGSAMRF 346
 QY 381 YAAD-----EKVSITATWK-----PLKLAHT-----402
 DB 347 YATNLSRTDLHSTWQYERTVYPMYSSQOTQYASRLIPLNDELRLNKSGLAFR 406
 QY 403 -----CSP--TNOKLSEKERYMASPRGOSIKSROASVGD--RR 437
 DB 407 KDPPEPSPKSGPCRGPLCGCCPGRSSQKVSLLKDRV-FSSPRGVAAGKSGSPAQOYRR 465
 QY 438 SPSDITAGSPTKQKSMSEFNDRTFRPSRLKSSOPKPYIDADTALGTDVYDEKCO 497
 DB 466 SPSADQSLDSSPKVKPSWSEFDRSRARQAFRIKGAASRONSE-EASLPGEDIYDCKSCP 524
 QY 498 CDVSVEDLTPPLKTVIRAIRIMKFKRKFKETLRPYDVKDYEIOYSAGHLDMLCRKS 557
 DB 525 CEFTYEDLTPGLKVSIRAVCMRFLVSKRKFKESLRYDMVDYEOYSAGHLDMLSRKS 584
 QY 558 LQTRVDQILGQOITSDDKSREKITAHEHTDLSMLGRVYKVEKQOYSIESKLDCLDI 617
 DB 585 LOSRVDQIVGRPAITD-KDRTKGPAAELPEDEPSMMGRGLGKVEKQYLSMEKKLDPLVNI 643
 QY 618 YOOVLKSGSASALALASFOIPPEEC-----EOTSQSPYDSKDLSSAONSGCLS 668
 DB 644 YMO--RMG-----IPPTETAYFGAKEPEAPPHSPDSRE--HYDRHGCIY 687
 QY 669 RSTSANISRGLOFILTPNEFSQOTFYALSPTHMSQATQVPISSO-----DGSAAVAT 720
 DB 688 KIVRSSSSSTG-----QKNFSAP--AAP-----VQCPSTSMQOSHPRQCHGTSVPV 733
 QY 721 NTINQINTAPKPAAPTTLOI-----PP-----PLPAI 748
 DB 734 GDHGLVIRIPPPAHRSLSAYGCGNRASMEFLROEDTPCGRPEGLRDSOTISIPSV 793
 QY 749 KHLPRPETHNPAGLOESISDVTTCVASKENYQVAOS 787
 DB 794 DH-----EELERSFSGF--SISO-----SKENLDALNS 819

RESULT 5
 US-09-177-650-89
 ; Sequence 89, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: LePERT, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177,650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 89
 ; LENGTH: 757
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-177-650-89

Query Match 37.2%; Score 1761; DB 4; Length 757;

Best Local Similarity 51.8%; Pred. No. 6.2e-148; Mismatches 395; Conservative 77; Indels 90; Gaps 18;

```

21 GAAAAAGGRLGSGKDVESGRVNLNSAARGDILLGTATATGCGGGLREERR 80
9 GAYPGISGEKXKLVGVGLDPR-----XPSITDGLLLTAGSAPK---RGXLSKRT 59
81 GKQAGAMSLGKPLSTSSQSCRNVKRVONYLVNLEPRGMATYAAFPVLLVFGC 140
60 GGAGX-----GKPKX-----RMAFYRLONFLYVNLPRGXAIFYHAYVFLVYFSC 106
141 LILSVSTIPEHKLASSCLLLEFVIYVGLFEIIRIMSGCCCRGMRGRLRFARK 200
107 LVLSVSTIKEYKSSGALYILEYIVYFVYVIMAGCCCRGMRGRLRFARK 166
201 PFCVIDIYLIASIAVAVSAKTOGNIFATSALRSRLFLQILRMVMDRGTWKLGSVY 260
167 PFCVIDIMVLASIAVLAAGSQGNVFSALRSRLFLQILRMVMDRGTWKLGSVY 226
261 ASKELITANYIGFLVILFESSFLVYLVKDKANKEFSTYADALMGTITLTIGYDKTPL 320
227 ASKELITANYIGFLCLILASFLVYLAKEGENDHEDYADALMGLITLTIGYDKTPO 286
321 TWIGRLISAGFALLIGISFFALPAGILGSGFALKVOEHRKHFEKRRNPAANLIQVRS 380
287 TWIGRLIAATFTLIGVFFALPAGILGSGFALKVOEHRKHFEKRRNPAANLIQVRS 346
381 YAADEKSVSI-ATWK-----PHLKAHLTCSPTNOK--LSFK 413
347 YATNLSTDLSTHSTWQYEXTVYVPMYSSQITQYTGASRLIPPLNOLELRLNLSKSGLEFR 406
414 ERRR---MASPROSISKROASVD--RRSPSTDLTAGESTPKYQKMSFNDRTRFRL 468
407 KEPQPEPSPRGAAAGKSPQAQIVRSPSADQSLDPSKYPKSWSFGSRSTRQAF 466
469 RLKSOQRPYIADATGALGTDDVYDEKGCQCDVSEDLTPPLKTVIRAIRIMFHAARKRF 528
467 RIGGAAROMSEERSLGEDVEDENKSCNCFYEDLPLGLKXIRAVCKMFLYLSKRF 526
529 KETLRPYDKVAVIEQYSAGHILMLCRKISLQTRVDQILGKQITSKRSREKITAHEHTT 588
527 KESLRPYDKVAVIEQYSAGHILMLCRKISLQTRVDQILGKQITSKRSREKITAHEHTT 585
589 DDLMLGRVAVKVEQVOSIESKLDCLDIYQOVLKKSASALALSFOIPRECQTSY 648
586 EDPBMGRGLKVEQVLSMERKLDLVISYQ--RMGIQPAETEAFFGAK--EPEAPPY 641
649 QSPVDSKDLGSAQNSGC---LSRSTANISRGLOFILTPNEFSAQTFYALSPTMHSQAT 705
642 HSPEDSRD---HAKHGCIITIVSTSS-----TGQRNAAAPPA----- 677
706 QVPISQSDGSAVAATNTIANQINTAPKPAAPTLQIIPPLPA 747
678 -IPPAQCPS--TSMRQSHRHGTSVPDGHSLVRI-PLPLPA 715

```

RESULT 6
US-09-177-650-7

```

; Sequence 7, Application US/09177650
; Patent NO. 6413719
; GENERAL INFORMATION:
; APPLICANT: Lepert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KGNQ2 AND KGNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BENC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147

```

EARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 129

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 872

TYPE: PR

ORGANISM: Homo sapiens

US-09-177-650-7

Query Match 34.2%; Score 1620.5; DB 4; Length 872;

Best Local Similarity 42.2%; Pred. No. 2.0e-135; Mismatches 111; Indels 173; Gaps 29;

```

7 GGEAGAGLWVSGAAAAAGGRLGSGKDVESGRGR-----VLNSAARGDILL 60
14 GGGGGGGG-----GGAANAGDAAGDEKRYGLAPDVEQVTLALGADKDGILL 68
61 LGTRAATLGGGGGLRESRGKQAGARSLIGK-PLSTSSQSCRNVKRVONYLVN 119
69 L-----EGGRDEGQRRTPOG--IGLAKTPLSRPVK--RNNAKYRRIQTLIDAL 115
120 ERPRGMATYAHAVFLVFCCLISVSTIPEHKLASSCLLLEFVIYVGLFEIIRI 179
116 ERPRGMATYAHAVFLVFCCLISVSTIPEHKLASSCLLLEFVIYVGLFEIIRI 175
180 WSAGCCCRKMGWRGRLFAKRPFCVIDIYLIASIAVAVSAKTOGNIFATSALRSRLFLQI 239
176 WAGCCCRKMGWRGRLFAKRPFCVIDIYLIASIAVAVSAKTOGNIFATSALRSRLFLQI 234
240 LRNVMDRGTWKLGSVYVAHSEKELITANYIGFLVILFESSFLVYLVKDKANKEFSTYADALMGTITLTIGYDKTPL 291
235 LRNVMDRGTWKLGSVYVAHSEKELITANYIGFLVILFESSFLVYLVKDKANKEFSTYADALMGTITLTIGYDKTPL 294
292 --NKEFSTYADALMGTITLTIGYDKTPLTWIGRLISAGFALLIGISFFALPAGILGSG 349
295 EKKEFEETYADALMGTITLTATIGYDKTPEKRWGRILIAATFSLIGVFFALPAGILGSG 354
350 FALKVOEHRKHFEKRRNPAANLIQVRSYAADEKSVSI-ATWK-----PHLKA 400
355 LALKVOEHRKHFEKRRNPAANLIQVRSYAADEKSVSI-ATWK-----PHLKA 414
401 HTCSPTNOKLSFEKRVMAASPROSISKROASVDGRSPSTDLTAGESTPKYQKMSFNDRTRFRL 460
415 QLEAASQKGLDLDRVRLSNRGSNTK--SKLFLPVLNDALEESPEKPVGLNN 468
461 RTFRPRLRLK-----SOPKPYIADATGALGTDDVYDEKGCQCDVSEDLTPPLKTVIRAIRIMFHAARKRF 514
469 KERFTRAFKKAFAFQSSQ-----DAGTG--DPMADRGVNDPFIEDMPLTKAAR 520
515 AIRIMFHAARKRFKETLRPYDKVAVIEQYSAGHILMLCRKISLQTRVDQILGKQITS 574
521 AVRLQPRLYKKNKKEKTLRPYDKVAVIEQYSAGHILMLCRKISLQTRVDQILGKQITS 580
575 KKSRR-----EKITAHEHTT--DDLMLGRVAVKVEQVOSIESKLDCLDI 615
581 KHKKSQKSAFTFSPDOSPRNEPYVAPRSTSEIQSMGKVFYKVEKRODQDKGLDFLY 640
616 DIYQOVLK-----KGSASALALASFOIPRECQTSYQSPVDSKDLGSAQNT 663
641 DMHQMHERLOVOYETEYPTKGTSS-----PALAEKKEDRYIS-DLKTICNISE 689
664 SGCLSRSTANISRGLOFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTI 723
690 TGPEPEPYSF-----QVITDKVSPYGFADHP-----VNLPRGPGSSGKYVAT-- 733
724 ANQINTAPKPAAPTLQIIPPLPAIKHLPRETLHPNPAGIOESISDVTTCVAKENYQ 783
734 -----PPSSATYVERPVLPITLLDSRVSC--SQADLOGPYD-----RIS 775
784 VAQSNLTKDRSMRKSFDWGGETLISVCPMPVKDLGKSLSVONLIRSTELNLTOLGSGESS 843
776 PRQ-----RSITRDSPTPLSL-----MSVNH-----EELERSPGSGFIS 810

```

QY 844 GSRGSDPFP---KWRESKLFITDEVPGETETDTF 877
 Db 811 QDRDDYVFCBPGSSWMRKRYLA---GETDITDTPF 845

RESULT 7

US-09-105-058C-27
 ; Sequence 27, Application US/09105058C
 ; Patent No. 6403360
 ; GENERAL INFORMATION:
 ; APPLICANT: Blanaer, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Grubkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Men-Pin
 ; TITLE OF INVENTION: KClO4 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: 3053-4052
 ; CURRENT APPLICATION NUMBER: US/09/105,058C
 ; CURRENT FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; PRIOR FILING DATE: 1997-08-12
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 854
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-105-058C-27

Query Match 33.9%; Score 1603.5; DB 4; Length 854;
 Best Local Similarity 42.7%; Pred. No. 8.2e-134;
 Matches 393; Conservative 109; Mismatches 252; Indels 167; Gaps 29;

QY 20 SGAAAAAGG--GRGSGMKDYESGRGVLLNSAARGCLLIGRAATLGGGGGLRE 77
 Db 11 AGCAAAAGDEBERKGLAPDVEQ---VTLAAGADKGGTLL-----GGGGDEG 59
 QY 78 SRRGKGAARMSILGK-PLSTYSOSCRNVKRYRNVLYNVLEPRGMAFIYHAFVELL 136
 Db 60 QRRPQG--IGLLAKTPLSRPVK---RNNAKYRIOTLIYDALERRGVALIHALVFLI 114
 QY 137 VEGLLISVSTIEBHTKLASSCLLILEFVMTVEGLEPIIRISAGCCCRYGWQRLR 196
 Db 115 VLGLLILAVLTFFKEFVSGDWMLLLEFFAIFGAEFALRIMAGCCCRYGWQRLR 174
 QY 197 FARKPCVIDITVLIASIAVYSAKTOGNIFATSLRLEFLOLRVVRMDRGGTWKLLG 256
 Db 175 FARKPLCMDLFLVLIASVPAVAVGQGNVLAIS-LRSLRFLQILRLMDRGGTWKLLG 233
 QY 257 SVVYAHSKELITAWYIGFLVLISSFLVLYLVKDA-----NKESTYADALMWGT 306
 Db 234 SAICAHSKELITAWYIGFLVLISSFLVLYLVKDOPEVDAQEGMEKEFTYADALMWGL 293
 QY 307 ITLTITIGYKPTPLTWIGRLLSAGFALLGISFPAIPAGLISGFAIKVBOBHRQHEKR 366
 Db 294 ITLTATIGYKPTPLTWIGRLLSAGFALLGISFPAIPAGLISGFAIKVBOBHRQHEKR 353
 QY 367 RNPAAALIQCVWRISYADDEKSVS-IATWK-----PHLKALHCSPTNOKISFERRV 417
 Db 354 RNPAAALIQCVWRISYADDEKSVS-IATWK-----PHLKALHCSPTNOKISFERRV 413
 QY 418 MASPRGOSISROASVQDRSPSTDTITAEISPTKQKSWNSFDRTRFRPSLRK----- 471
 Db 414 LSNPRGSNTK-----GLTFPLVNDALIEESPSKPKPGLNKKERFAPFRKAAVAFWQ 467
 QY 472 SSQPKPIVDALAGTDVYDEKGCQCQVSVEDLPLPLKTVIRAIKMFHVAKKRFFET 531
 Db 468 SSE-----DAGTG--DPMADREGNDPFLDMLPTLKAALRAVRILOFRLYKKKFFET 519
 QY 532 LRPDYADVIEOYSAGHLDMLCRISLOTRVDOILGKGQITSDDKSR----- 578
 |||||||

Db 520 LRPDYADVIEOYSAGHLDMLCRISLOTRVDOILGKGQITSDDKSR----- 579
 QY 579 -----EKITAHEHT--DLSMLGRVAVYKOVQSTIESKLDCLLDITYOVL----- 623
 Db 580 SPRNEPVYARSPSTSEIDQSMGKFKYVERQVODGKRLDPLVDHMQMERLOQVTEY 639
 QY 624 ---KGSASALALASFOIIPPECQTSQVQSVDSKDSLSAONSCLSTANISRGIO 680
 Db 640 YPKGTSS-----PAEAKEDRRYS-DLKTICNSETPEPPYSFH----- 682
 QY 681 FILTPNEFSQOTVYALSPTHSQATQVPIQSODSASAVATMTIANQIAPPAPTLQ 740
 Db 683 -QVTDKVSPEYGFADHP-----VNLPRGPPSSKQVAT-----PSSATTYE 725
 QY 741 IPPPLAIKRLPPEITHHPAGIQESISDYTTCLIVASKENVQAQSLTKDRSMKSF 800
 Db 726 RPYVLEPILTLILDSRVSCH-SQADLQGPYS-----RISPRQ-----RSTF 765
 QY 801 MGGETLIVCPMPVKDLGKSLSYONLIRSTPELNIQLSGSSSGSRGSDPFP---KWR 856
 Db 766 RSDTFLSL-----MSVNH-----EELERSPSGFSISQDRDDYVFCBPGSSWM 809
 QY 857 ESKLFTDEVPGETETDTF 877
 Db 810 REKRYLA---GETDITDTPF 827

RESULT 8

US-09-177-650-91
 ; Sequence 91, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; TITLE OF INVENTION: AND OTHER EPILEPSIES
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177,650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 91
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-177-650-91

Query Match 33.2%; Score 1570.5; DB 4; Length 870;
 Best Local Similarity 41.6%; Pred. No. 7.4e-131;
 Matches 388; Conservative 109; Mismatches 273; Indels 163; Gaps 28;

QY 7 GGEGBGAAGLWVKSAAAAAGG-----RLGSGMKDYESGRGVLLNSAARGDG 57
 Db 12 GGGEGGGG-----GGAANPAGDSAVAGDEERKGLAPDVEQ---VTLAAGADKDG 63
 QY 58 LILTLRAATLGGGGGGLRESRRGKGAARMSILGK-PLSTYSOSCRNVKRYRNVLY 116
 Db 64 TLL-----EGGREGGQRTPOG--IGLLAKTPLSRPVK---RNNAKYRIOTLTY 110
 QY 117 NVLEPRGMAFIYHAFVELLVEGCLLSVSTIEBHTKLASSCLLILEFVMTVEGLEFI 176
 Db 111 DALEPRGMAFIYHAFVELLVEGCLLSVSTIEBHTKLASSCLLILEFVMTVEGLEFI 170
 QY 177 IRISWAGCCCRYRGWQRLRFAKRPVCVITVLIASIAVYSAKTOGNIFATSLRLRF 236
 Db 171 LRIMWAGCCCRYRGWQRLRFAKRPVCVITVLIASIAVYSAKTOGNIFATSLRLRF 229
 QY 237 LQILMVRMDRGGTWKLLGSSVYVYAHSKELITAWYIGFLVLISSFLVLYLVKDA----- 291
 |||||||

```

Db 230 LQILRLMDRDRGTWKLGSALCAHSKELITAWYIGFLTLILSFLVYVEKDVEMDA 289
QY 292 -----NKESTYADALMWGITTLTIGYDKTPTLWIGRLLSAGFALLGISFPALPAGIL 346
Db 290 QGEMKEEFTYADALMWGITLTIATIGYDTPKTWEGRLIAAFSLIGVSFFALPAGIL 349
QY 347 GSGFALKVOHOKHEKRRNPANLIQCVRGSADEKSVS-IATK-----PHL 397
Db 350 GSGLALVQOHOKHEKRRNPANLIQAAMRYATNPNDLVATYRSIESVSPFPE 409
QY 398 KALHTCSPTNOKLSFKERVMAASPRGOSIKRSQASVGDRRSPSDITDAEGSPTKVQKWS 457
Db 410 RKQGLEAASQKGLDLRVRLSNRGSNTK-----GKLFPLPNDALIEESPKEPKPYG 463
QY 458 FNDTRFRLRLKS-----SQPKVYADPTALGTDVYDEKGCQCVSVEDLPLPLKT 511
Db 464 LNKRRERFRTAFRMKAYAFWQXSE-----DACTG---DEMAEDRGXNXLIDMIPXXKA 515
QY 512 VIRAIRIMKFPVAKRKKEETLRPYDKVDVIOYSAGHLDMLCRILSLQTRVDQILGKQI 571
Db 516 ATRAVRLQRLYKKKKEETLRPYDKVDVIOYSAGHLDMLSRILYLQTRIDMITTPGPP 575
QY 572 TSDK-KSREKIT-----AEHTTDDLMLGRVYVYKQVQSIIESKLD 612
Db 576 STPKHKKSQKGTATPTYSQSPRNEPYVARAATSETEDQSMGKFVYKVERQVHDMGKKLD 635
QY 613 CLLDIYQVLRKGSASALALASFQIPPECEOTSIYQSPV---SKLDSGSQNSGCLSR 669
Db 636 XLVDMHMQHMER-----LOVHYEYYPYTKASSPAEKEKEDNEYSLDKTLICNY 685
QY 670 STANISRGLOFILTP-NEFSAQTFYALSPMHQSOATQVPISSQSAVAATNTIANQIN 728
Db 686 SETPPPPPSFHOYPRIDRVCPYGFHNDP-----VKLTRGSPSSIKQAQNLPS--- 734
QY 729 TAPKPAATLQIPPLPAIKHLPREPLHPNPAQLQESISDVTCLVASKENVOYAQSN 788
Db 735 -----SSSTYAEPLVPIFLTLIDSCVSYH-----SQETLQPPSD 770
QY 789 LTKRSMKSPDMGCEITLSCPMWPKDLGKSLSYONLIRTEELNIQLSSESSSRSS 848
Db 771 HISPR-QRRSITRSDPLSL-----MSVNH-----EELERSPSGISISODRDD 813
QY 849 QDFYP-----KWRSKLFTIDEVGEPEETETDTE 877
Db 814 YVFGPSGGSSWMGKRYIAE---GETDIDTDF 843

RESULT 9
US-09-105-058C-4
; Sequence 4, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 300 amino acids of human KCNQ2

```

```

US-09-105-058C-4
Query Match 25.5%; Score 1207.5; DB 4; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.7e-99;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

QY 91 GKPLSTSSQSCRNVKRYRQVNTLYNLEBRPGMAFIYNAFVLLVFGCLISVFTIP 150
Db 5 GKP-----PKRNAFTRKQNLNLYNLEBRPGMAFIYNAFVLLVFGCLISVFTIP 56
QY 151 EHTKLASSCLLIEFWIVVGLFEITIRISAGCCCRYKQGLRPAKRFVYDITVL 210
Db 57 EYKSSGALYIIEIVYIVFGEYFVYIMAGCCCRYKGRGRRLKPAKRFVYDITVL 116
QY 211 IASIAVAAKQGNIFATSLRFLQILRMVMDRGTWKLGSVYVAHSEKELTAW 270
Db 117 IASIAVAAKQGNVATSLRFLQILRMVMDRGTWKLGSVYVAHSEKELTAW 176
QY 271 YIGFLVLFSSFLVYVEKDKANKESTYADALMWGITTLTIGYDKTPTLWIGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEGNDHFDYADALMWGITLTIIGYDKKYPQTWNGRLAAT 236
QY 331 FALGISFPALPAGILSGFALKVOEOROKHEKRRNPANLIQCVRGSADEKSVSI 390
Db 237 FFLIGVSFFALPAGILSGFALKVOEOROKHEKRRNPAGLIOSAMRYATNTLSRDL 296
QY 391 -ATW 393
Db 297 HSTM 300

```

```

RESULT 10
US-09-105-058C-6
; Sequence 6, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 300
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 300 amino acids of murine KCNQ2
US-09-105-058C-6
Query Match 25.5%; Score 1207.5; DB 4; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.7e-99;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

QY 91 GKPLSTSSQSCRNVKRYRQVNTLYNLEBRPGMAFIYNAFVLLVFGCLISVFTIP 150
Db 5 GKP-----PKRNAFTRKQNLNLYNLEBRPGMAFIYNAFVLLVFGCLISVFTIP 56
QY 151 EHTKLASSCLLIEFWIVVGLFEITIRISAGCCCRYKQGLRPAKRFVYDITVL 210
Db 57 EYKSSGALYIIEIVYIVFGEYFVYIMAGCCCRYKGRGRRLKPAKRFVYDITVL 116
QY 211 IASIAVAAKQGNIFATSLRFLQILRMVMDRGTWKLGSVYVAHSEKELTAW 270

```

Db 117 IASIVLAAGSGGNFATLSALSLRFLQILRMIRMDRGSTWKLGSVVAHSELYAW 176
 QY 271 YIGFVLVLFSSFLVYLVKEDANKFSTYADALMMGTTITLTIGYDGTPLTWLRLLSAG 330
 Db 177 YIGFCLILASFLVYLVKEDNDHFTYADALMMGLITTTIGDGYPTQWNRRLLAT 236
 QY 331 FALGISEFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLIQCVRSYAADKSVSI 390
 Db 237 FTLLGVSEFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLIQSAMRFATWLSRDL 296
 QY 391 -ATW 393
 Db 297 HSTM 300

RESULT 11
 US-09-177-650-3
 ; Sequence 3, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Lepfert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177, 650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063, 147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 807
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-177-650-3

Query Match 25.1%; Score 1188; DB 4; Length 807;
 Best Local Similarity 37.7%; Pred. No. 8, 1e-97;
 Matches 285; Conservative 118; Mismatches 186; Indels 166; Gaps 22;

QY 75 LRSRRKQKQARMMLKPLSTTSQSCRNVKRYRVONYLVNERPGW-AFIYHAFV 133
 Db 77 LHSEEGNR--KMSLVGKPLTY---KNYRTQFRFRMOKMNFLEPRGMKATYHLAV 131
 QY 134 FLVFGCLISVSTIPEHTKLASCLLLEFVMIVGSLERIRMSAGCCCRYRGMG 193
 Db 132 LFWVLMKLAISVSTPEDEFNATIVLYLLEIVYIMWATEYICRWASAGCRSRGIGSG 191
 QY 194 RLRFARKPCVIDITVILASIAVVSATQGNIFATSAULSLRFLQILRMVRMDRGSTW 253
 Db 192 RIRFATSAVCVIDIIVILASTIVLCIGATGVFAASAIRGLRFPQ-LRLMRIDRRAGTWM 250
 QY 254 LGSVYVAHSEKELTAMVIGLVLIFFSEFLVYLVKEDANKERSTADALMWGTTITLTIG 313
 Db 251 LGSVVAHSEKELTAMVIGLVLIFFSEFLVYLVKEDANKERSTADALMWGTTITLTIG 310
 QY 314 YGDKTPTLWMLGRLISAGFALLGISEFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLI 373
 Db 311 YGDKTPTLWMLGRLISAGFALLGISEFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLI 370
 QY 374 IOCVMSRYAADKSVSIATWKP--LKAALHTCSP--TNOKLSFKERYRMAAPRGOSIK 427
 Db 371 IOCLMRYSAAPSTSLATWKLHILARELPYVXLPLGSSNNAATGLINLRROSTKRTPNLN 430
 QY 428 SRQASVGDERS-----PSTDTT-----AEG-----SPTKQKSVS 457
 Db 431 NONLAIVNSQATSKNLSVPRVYHDTISLVSTDSIEOLGALGSLGWSKSKYGGSKK 490
 QY 458 FND-----RTRFRPSL-----RLKSQPRFVIDADALG-- 486

Db 491 ATDDSVLQSRMLAPSNNAHLDMMRRRRRSASLGRVYNTGQHLRPLQPRSTLSDSVICY 550
 QY 487 -----TDDVYD-----EKGCOC 498
 Db 551 SLMMAPYQCEQWVQNRSTPGEDEVNSQLSQLSOLTTCAATRTEDISDGEDEAVGY- 609
 QY 499 DVSDEDTPLKTVYIRAIRIMKFVAKRKEETLRPVYKQVIEYSAGHLMCRISKL 558
 Db 610 POTEIEFTPALKVCVRAIRKIQLLVARKKFEALPYDKVIEQYSAGHVLQSRKTV 669
 QY 559 QTRVDDILGKQITSDKSRREKITAHEHTTDLMSLGRVYVKEKQVOSIESKLDLDIY 618
 Db 670 QAKLDFTCG-----KNIEKTEPK-----IMFTRIALTEYTGKMDKDLDMVENVL 715
 QY 619 QOVLKRGASALALASQIPEPECEQTSIDQSPVDSKDLGSAQNSGLSRSTANISRG 678
 Db 716 M-----GROASQRFVQSNTSP-----RGESEPTSPARQ-----DLTRSRSRMVSD 756
 QY 679 LQFLTPNEFSAQTFYALSPTMHSQATQVPISQSD 713
 Db 757 MEM-----YTAHSH---SPGYHODANPIT-IAQID 781

RESULT 12
 US-09-135-021-2
 ; Sequence 2, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
 ; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135, 021A
 ; CURRENT FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 08/874, 655
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094, 477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 676
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-135-021-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2, 8e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSQSCRNVKVR-RYONLYXNLERPGW-AFIYHAFVFLVYVGLLSVSTIPEHTKL 155
 Db 92 SIYSTRRLPLATHTHOGRVNLFLEPTGKCFYHAAVFLIVVCLTFVSLSTEOYAL 151
 QY 156 ASSCLLLEFVAVIVFGLFIIRMSAGCCCRYRGMGRFLRFAKPCVIDITVILASIA 215
 Db 152 ATGTLFMEIYLVVEFGTYVVRWMSAGCRSKTVGLMGRFLRFAKPCISTIDILVYASW 211
 QY 216 VVSATQGNIRFATSAULSLRFLQILRMVRMDRGSTWKLGSVVAHSEKELTAMVIGFL 275
 Db 212 VLVGSKQGVAPTSAIRGIRFLQILRMHLDVDRQGTWRLGVSIVFIHQELITLTLYIGL 271
 QY 276 VLISSFLVYLVKKA-----NKESTVADALMWGTTITLTIGYDGTPLTWLGRLLSAG 330
 Db 272 GLIFSSIFVYLAEKNAVDSGVEFGSADALMWGVVYTTTIGYDGVDPQWTKTJASC 331
 QY 331 FALGISEFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLIQCVMSRYAADKSVSI 390
 Db 332 FSVVAISFPALPAGILGSGFALKVOEORHOKHFEKRRNPANLIQCVMSRYAADKSVSI 390
 QY 391 ATWKPHTKAL--HT-CSPYNOKLSFKERVNAPSPGOSIKSROASVGDERSPTDTTAA 446

Db 391 -TWKTIYRKAPRSHTLSPSPK---KSSVYVKKKKFKLDKNGVTPGKMLTVPHITCD 446
 QY 447 GSPTRVOKSWS---FNDTRRPRPSLRKSSQPKPYIDADTALGTDVDYDEKGCQCDVSVE 503
 Db 447 PPRERRLDHFVSDGSDSVRSKSPFL-LEYSMPH-----FMRTNSFAD---LDLEGE 494
 QY 504 DLTPPL-----KVIVAIRIRMKRHHVAKRKREKTLRPYDVYDVIQYSGHIDMLC 553
 Db 495 TLLTPITHISQREHNRATIKVIRMOYFVAKKFOQARKPYDVYDVIQYSGHIDMLV 554
 QY 554 RIKSLQTPVDOILGKGQ--ITSDDKSREKITAHEHTTDLISMLGRVYKVKQVOSIESKL 611
 Db 555 RIKELORRLDSDIGKPSLFISVSEKSKD-----GSNTIGARLNREDKATOLDORL 606
 QY 612 DCLDIYQOVL-----RKGSA-----SALALASFOIPPE 641
 Db 607 ALITDMLHQLLSLHGSGTPSGGPPREGAHITOPCGSGSVDPPELFLPSNMLPYE 663

RESULT 13
 US-09-135-020-2
 : Sequence 2, Application US/09135020
 : Patent No. 6274332

GENERAL INFORMATION:
 : APPLICANT: Keating, Mark T.
 : APPLICANT: Sanguinetti, Michael C.
 : APPLICANT: Splawski, Igor
 : TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
 : TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
 : TITLE OF INVENTION: KCNE1 AS AN IOT GENE
 : FILE REFERENCE: 2323-131
 : CURRENT APPLICATION NUMBER: US/09/135,020
 : CURRENT FILING DATE: 1998-08-17
 : EARLIER APPLICATION NUMBER: 08/921,068
 : EARLIER FILING DATE: 1997-08-29
 : EARLIER APPLICATION NUMBER: 08/739,383
 : EARLIER FILING DATE: 1996-10-29
 : EARLIER APPLICATION NUMBER: 60/019,014
 : EARLIER FILING DATE: 1995-12-22
 : EARLIER APPLICATION NUMBER: 60/094,477
 : EARLIER FILING DATE: 1998-07-29
 : NUMBER OF SEQ ID NOS: 114
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 676
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-135-020-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.8e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSOSCRANRYR-RVONYLYNVLEPRGM-AFIYHAFVFLVFCGLLSVFSITPEHTKL 155
 Db 92 SIYSTRPVLARHVOGRVYVNFLEPRGMCFYHFAVFLVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLILEFVIVGLEFIIRIWSAGCCRRYRGMGRLEFARKPCVIDITVLASIA 215
 Db 152 ATGTLFWMELIVLVFGTEVYVRLWSAGCSKYVGLMGRLEFARKPISIIDLIVVAVSMV 211
 QY 216 VVSATOGNINPATSAIRSLRFLQILRMVRDRRGCTKLLGSSVYVYASKEKITAMTIGFL 275
 Db 212 VLVCGSKGVFAFSAIRGIRFLQILRMVLHVDROGCTWRLLGSSVFIHRQELITLTYIGFL 271
 QY 276 VLIFFSFLVYLVKDA-----NKEFSYADALMWGTTTLTIGYGDKTPLTWLGRLSAG 330
 Db 272 GLIFSSFYVYLAEKDAVNESGRVFGSYADALMWGVYTVTTIGYGDVPOVWVGKTIASC 331
 QY 331 FALGISFFALPAGILSGSALKVQEOHROKHFEKRRPANLQOCVWRSTAADKSYSI 390
 Db 332 FSVAISFFALPAGILSGSALKVQOKOROKHFNROJPAASLIQIOTAWRCYAENPDSS- 390

QY 391 ATWPKHLKAL---HT-CSPNOKLSFKERVMAASRGOSIKSRQASVGRDRSPSYDTIAE 446
 Db 391 -TWKTIYRKAPRSHTLSPSPK---KSSVYVKKKKFKLDKNGVTPGKMLTVPHITCD 446
 QY 447 GSPTRVOKSWS---FNDTRRPRPSLRKSSQPKPYIDADTALGTDVDYDEKGCQCDVSVE 503
 Db 447 PPRERRLDHFVSDGSDSVRSKSPFL-LEYSMPH-----FMRTNSFAD---LDLEGE 494
 QY 504 DLTPPL-----KVIVAIRIRMKRHHVAKRKREKTLRPYDVYDVIQYSGHIDMLC 553
 Db 495 TLLTPITHISQREHNRATIKVIRMOYFVAKKFOQARKPYDVYDVIQYSGHIDMLV 554
 QY 554 RIKSLQTPVDOILGKGQ--ITSDDKSREKITAHEHTTDLISMLGRVYKVKQVOSIESKL 611
 Db 555 RIKELORRLDSDIGKPSLFISVSEKSKD-----GSNTIGARLNREDKATOLDORL 606
 QY 612 DCLDIYQOVL-----RKGSA-----SALALASFOIPPE 641
 Db 607 ALITDMLHQLLSLHGSGTPSGGPPREGAHITOPCGSGSVDPPELFLPSNMLPYE 663

RESULT 14
 US-09-135-010A-2
 : Sequence 2, Application US/09135010A
 : Patent No. 6277978

GENERAL INFORMATION:
 : APPLICANT: Keating, Mark T.
 : APPLICANT: Sanguinetti, Michael C.
 : APPLICANT: Curran, Mark E.
 : APPLICANT: Landes, Gregory M.
 : APPLICANT: Connors, Timothy D.
 : APPLICANT: Burn, Timothy C.
 : APPLICANT: Splawski, Igor
 : TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
 : FILE REFERENCE: 2323-133
 : CURRENT APPLICATION NUMBER: US/09/135,010A
 : CURRENT FILING DATE: 1998-08-17
 : PRIOR APPLICATION NUMBER: 60/094,477
 : PRIOR FILING DATE: 1998-07-29
 : PRIOR APPLICATION NUMBER: 08/921,068
 : PRIOR FILING DATE: 1997-08-29
 : PRIOR APPLICATION NUMBER: 08/739,383
 : PRIOR FILING DATE: 1996-10-29
 : PRIOR APPLICATION NUMBER: 60/019,014
 : PRIOR FILING DATE: 1995-12-22
 : NUMBER OF SEQ ID NOS: 116
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 676
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-135-010A-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.8e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSOSCRANRYR-RVONYLYNVLEPRGM-AFIYHAFVFLVFCGLLSVFSITPEHTKL 155
 Db 92 SIYSTRPVLARHVOGRVYVNFLEPRGMCFYHFAVFLVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLILEFVIVGLEFIIRIWSAGCCRRYRGMGRLEFARKPCVIDITVLASIA 215
 Db 152 ATGTLFWMELIVLVFGTEVYVRLWSAGCSKYVGLMGRLEFARKPISIIDLIVVAVSMV 211
 QY 216 VVSATOGNINPATSAIRSLRFLQILRMVRDRRGCTKLLGSSVYVYASKEKITAMTIGFL 275
 Db 212 VLVCGSKGVFAFSAIRGIRFLQILRMVLHVDROGCTWRLLGSSVFIHRQELITLTYIGFL 271
 QY 276 VLIFFSFLVYLVKDA-----NKEFSYADALMWGTTTLTIGYGDKTPLTWLGRLSAG 330
 Db 272 GLIFSSFYVYLAEKDAVNESGRVFGSYADALMWGVYTVTTIGYGDVPOVWVGKTIASC 331


```

Db 152 ATGTLFMMELIVLVEFGTEVYVRLMSAGCSKYYVGLMGRLRFARKPISIIDLIYVVASMV 211
QY 216 VSAKTOGNIFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 275
Db 212 VLVCSKQGVFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 271
QY 276 VLVCSKQGVFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 271
Db 272 GLIFSSFEVYLAEDAVNESGRVFEFSYADALMMGVTVTTIGYGDVPTWVGKTIASC 331
QY 331 FALLGISFPAFPAFAGILSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Db 332 FSVFAISFPAFPAFAGILSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
QY 391 ATWPKHUKAL---HT-CSPINOKLSFEKRYMASPRGOSISRSQASVGDERSPTDITAE 446
Db 391 -TWKIYIRKAPRSHLTLSPSPK---KSSVYVKKKKFKLDKNGVTPGEKMLTVPHITCD 446
QY 447 GSPTKYOKSWS---FNDRTFRPSLRKSSQPKVIDADTALGTDVYDEKGCOCDDVSE 503
Db 447 PPEERLDFHSVDGYDSVRSKSPFL-LEVSMPH-----FMRNSFAED---LDLGE 494
QY 504 DLTPPL-----KTYIRAIRIMKFAHAKKFKETLRPYDVYDEYQISAGHLMC 553
Db 495 TLTPPTHISQLEHHRATIKVIRMOYFAVAKKFKQARKYDVYDEYQISAGHLMC 554
QY 554 RIKSLQTRVDQILGKQO--ITSDKRSREKITAHEHTDLSMLGRVYKVEKOVOSIESKL 611
Db 555 RIKELQRLDQSIGKPSLFSVSEKSKDR-----GSNTIGARLNKVEKQVQLDQRL 606
QY 612 DCLLDIYQOVL-----RKGA-----SALALASFOIPFE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGPPREGAHITQPCGSGSVDPFLPNTLPTYE 663

```

RESULT 19

US-09-597-732-2

```

; Sequence 2, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-597-732-2

```

Query Match 23.3%; Score 1102; DB 4; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.8e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

```

QY 98 SSQSCRNNVYR-RVONTLYNVLRRPGW-AFITYHAFVLVFGCLLSVFTIPERTYL 155
Db 92 SITSTRPVARHNVQGVFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 151
QY 156 ASSCLLLEFVMIYVLEFIRISAGCCCRKRYMGRARRPAPFCVIDITVLASTA 215
Db 152 ATGTLFMMELIVLVEFGTEVYVRLMSAGCSKYYVGLMGRLRFARKPISIIDLIYVVASMV 211
QY 216 VSAKTOGNIFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 275
Db 212 VLVCSKQGVFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 271
QY 276 VLVCSKQGVFAFSAFSLRFLQILRMVMDRGCTKWLGSVYVAHSKELITAMYGFL 271
Db 272 GLIFSSFEVYLAEDAVNESGRVFEFSYADALMMGVTVTTIGYGDVPTWVGKTIASC 331
QY 331 FALLGISFPAFPAFAGILSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Db 332 FSVFAISFPAFPAFAGILSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
QY 391 ATWPKHUKAL---HT-CSPINOKLSFEKRYMASPRGOSISRSQASVGDERSPTDITAE 446
Db 391 -TWKIYIRKAPRSHLTLSPSPK---KSSVYVKKKKFKLDKNGVTPGEKMLTVPHITCD 446
QY 447 GSPTKYOKSWS---FNDRTFRPSLRKSSQPKVIDADTALGTDVYDEKGCOCDDVSE 503
Db 447 PPEERLDFHSVDGYDSVRSKSPFL-LEVSMPH-----FMRNSFAED---LDLGE 494
QY 504 DLTPPL-----KTYIRAIRIMKFAHAKKFKETLRPYDVYDEYQISAGHLMC 553
Db 495 TLTPPTHISQLEHHRATIKVIRMOYFAVAKKFKQARKYDVYDEYQISAGHLMC 554
QY 554 RIKSLQTRVDQILGKQO--ITSDKRSREKITAHEHTDLSMLGRVYKVEKOVOSIESKL 611
Db 555 RIKELQRLDQSIGKPSLFSVSEKSKDR-----GSNTIGARLNKVEKQVQLDQRL 606
QY 612 DCLLDIYQOVL-----RKGA-----SALALASFOIPFE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGPPREGAHITQPCGSGSVDPFLPNTLPTYE 663

```

RESULT 20

US-09-105-058C-24

```

; Sequence 24, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 24
; LENGTH: 605
; TYPE: PRT
; ORGANISM: mouse
US-09-105-058C-24

```

Query Match 23.3%; Score 1100.5; DB 4; Length 605;
 Best Local Similarity 43.6%; Pred. No. 3.1e-89;
 Matches 244; Conservative 99; Mismatches 148; Indels 69; Gaps 15;

[illegible]

Query Match Similarity	23.1%	Score 1092.5	DB 4	Length 677
Best Local Similarity	41.7%	Pred. No. 1.9e-88		
Matches	251	Conservative 105	Mismatches 167	Indels 79
				Gaps 17
Qy	94	LSYSSQSCRNVKVR-EVQNTLVNVERPRGM-AFIYHAFVLLVFCGLISVSTIPE	151	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	88	LPKSVISYTRRPVLARTHVQGRVYFLEPRPGMKCFEYVHFAVLLVCLLFSTVLTSEQ	147	
Qy	152	HTKLASSCLLIEFMIVFGELFIIIRLWSAGCCCRIRGWSGRLL-FARKPCPVDTIVL	210	
		: : : : : : : : : : : : : : : : : : : : : : : : :		

```

Db      148  TAAATATGTLFMMELIYLVFETGETEYVVRRLMSAGCRKYVGLMGRLFEAFKRPISIDLLIV  207
Qy      211  TASIAYVSAKTQGNIEATSAIRSLRFQILRMVDRMRGCTWKLIGSVYVAHAKSLITAM  270
Db      208  VASWVLLCVSGSGYEATSAIRGIRFQLILMLHIDRGGVRLIGSVYVEIHROELITTL  267
Qy      271  YIGVLVLIFFSSFLVYLVKDA-----NKEFSYAAALMWGTTLTITIGYDKTPELTWIGR  325
Db      268  YIGFGLGLFFSYFYLAEKDAVNESGRVFEFGSYADALMWGVTVTTITIGDKVPOTWGK  327
Qy      326  LLSAGFALIGISFFALPAGILGSGFALVQEOHROKHEKRRNPANLITQWRSYAAD  385
Db      328  TIASEFSVAFISFALPAGILGSGFALVQOQOROKHFNROJPAASAISLQTMRCYAAEN  387
Qy      386  KSVSIATWKPHLKAL--HT-CSPTNOKLSFEKERYRMASSPRGOSIKSRQASVGDGRSPST  441
Db      388  PDS--TWKIYIRKRPDRSHLTLLSPBKP--KSVYVVKKKKKFLKLDNGVTFGEKKLTVP  442
Qy      442  DITAGSGPRKYQKMS---FNDRTRFRLSLRLKSOPKVIDADADALGTDVYDEKGCQC  498
Db      443  HTTCPPREERLDRHSVDOGDSVRSKSPYL-LEVSAPH-----FMKPNSTAE-----L  490
Qy      499  DVSVEDLFPPL-----KTVIRAIRIMKEFHAHAKRFKETLRPRDYDKVIEOYSAGH  548
Db      491  DLEGETLPLPIIHQILREHHRNATIKVIRRMQYFAKKKFKQARKRYDYRVDIYEOYSQH  550
Qy      549  IDMLCRISLQTRVQDQILGKGQ--ITSDDKSSEKITAHEHTTDDLSMLGRVYVKEQVOVS  606
Db      551  LMLVWIRKELQRRDLDSIGKPSLFIETVSEKSDR-----GSNTIGARLNLNVEAPQVO  602
Qy      607  IESKLDCLIDIYQVYL-----RKGSA-----SALALASQIPIP  639
Db      603  IDQRLALITDMLQILSLHGSGSTPGSGGPPRREGAHITOPCGSGSGSVDPDELPLPSNTLPT  662
Qy      640  FE 641
Db      663  YE 664

```

```

      RESULT 22
US-09-135-021-80
; Sequence 80, Application US/09135021A
; Patent No. 6150104
;
; GENERAL INFORMATION:
; APPLICANT: SPLAWSKI, IGOR
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVL0T1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 581
;
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-135-021-80

```

	Query Match	23.1%	Score 1091.5	DB 4	Length 581
	Best Local Similarity	41.8%	Pred. No. 1.8e-88		
	Matches 243	Conservative 105	Mismatches 157	Indels 77	Gaps 15
Qy	112 QNLYVLEPRGQ-AFTYHAFFVLLVECLLSVSTIPERTKLASSCLLLEFVMYV	170			
Db	12 QGVHYVLEPRGQKCFVYHFAVFLVLCVLSVSTIEQAAALATGTLFMEVLYVF	71			
Qy	171 FGLFEILIRISMGCCCRYSRGMGRLEFARPPCVIDITVLISIAVVSAKTGNIPTSA	230			


```

QY 112 QNYLYNLEBPRGW-APYHAFLVFLVGCILISVSTIPBHTKLASSCLLILEFMYIV 170
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 QGRYINLEBPTGKCFVHFAVFLVLYVCLIFSVLSTIEQALATATGLTLMELVLYVF 60

QY 171 FGLEFIIRMSAGCCCRGMQGRLEFARKPCVYDITVLAIAVSAKTOGNIFATSA 230
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 FGEYVVRMSAGCRSKYVGLMGRLEFARKPISITIDLIVVAMSVLVCSGOYFATSA 120

QY 231 LRSLEFIQIIRMYMDRGGTWMKLLGVSVAHSEKELTAWYIGLVLFSSFLVLYVEKD 290
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 IRGIRFIQIIRMLVHDGOGTWMRLGVSVFIRHRELITLTYIGFLGLFSSYFVYLAERD 180

QY 291 A-----NKESTYADALMWGTITLTIGYDGTPLTWIGRLLSAGFALLGISFPALPAGI 345
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 181 AVNMSGHVEFGSYADALMWGVVTVTTIGYDGVPTWGTWKTASCFVFAISFPALPAGI 240

QY 346 LGSFALKVQBOHQHFEKRRNPANLIQCWRSYADAEKSVSIATWPKHAKAL---HT 402
| | | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 241 LGSFALKVQOKQKHNRQIPAAASLIQTAMRCYAAENPDSS--TWKTYIRKAPRSH 298

QY 403 -CSPTNOKLSFEKERVMA SPRGOSIKSQA SVGDRSPSTDTITAGSPTKVSMS---F 458
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 299 LLSPPRP---KKSUVVKKKKFKLDKONGVTPGEMKLTVPHTCDPPEERRLDHFSVDGY 355

QY 459 NDRTRFPRSLRKSOPKRVYIDADTALGTDDVYDEKGCOCOVSVEDLPPPL----- 509
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 356 DSSVRKSPPTL-LEVSMRP-----FMRTNSFAED---LDLEGTLTPHTHISOLREH 403

QY 510 -KTYIRAIRIMKFFVAKRKETLRPYDVKYIEOYSAGHLDMLCRISLQTRVDIOLGK 568
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 404 HRATIKVIRMOYVFAKKKFOARKPYDVRYIEQYSGHLMIMVYIKELORLDOISICK 463

QY 569 GQ--ITSKRSREKITAHEHTTDDLMLGRVYKVEKOVQSIKDLCLDIYQOVL---- 622
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 464 PSLTIVSEKSKDR-----GSNTIGARINRVEDKYVQLDQRLALITDMLHQLLSLHG 515

QY 623 -----RKGA-----SALALASFOIPPE 641
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 516 GSTPGSGGPPREGAHITQPCGSGSVDPBELFLPNTLTPTYE 557

RESULT 29
US-09-444-871-114
; Sequence 114, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-444-871-114

```

```

Query Match 22.9%; Score 1081.5; DB 4; Length 570;
Best Local Similarity 41.6%; Pred. No. 1,4e-87;
Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

QY 112 QNYLYNLEBPRGW-APYHAFLVFLVGCILISVSTIPBHTKLASSCLLILEFMYIV 170
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 QGRYINLEBPTGKCFVHFAVFLVLYVCLIFSVLSTIEQALATATGLTLMELVLYVF 60

QY 171 FGLEFIIRMSAGCCCRGMQGRLEFARKPCVYDITVLAIAVSAKTOGNIFATSA 230
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 FGEYVVRMSAGCRSKYVGLMGRLEFARKPISITIDLIVVAMSVLVCSGOYFATSA 120

QY 231 LRSLEFIQIIRMYMDRGGTWMKLLGVSVAHSEKELTAWYIGLVLFSSFLVLYVEKD 290
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 IRGIRFIQIIRMLVHDGOGTWMRLGVSVFIRHRELITLTYIGFLGLFSSYFVYLAERD 180

QY 291 A-----NKESTYADALMWGTITLTIGYDGTPLTWIGRLLSAGFALLGISFPALPAGI 345
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 181 AVNMSGHVEFGSYADALMWGVVTVTTIGYDGVPTWGTWKTASCFVFAISFPALPAGI 240

QY 346 LGSFALKVQBOHQHFEKRRNPANLIQCWRSYADAEKSVSIATWPKHAKAL---HT 402
| | | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 241 LGSFALKVQOKQKHNRQIPAAASLIQTAMRCYAAENPDSS--TWKTYIRKAPRSH 298

QY 403 -CSPTNOKLSFEKERVMA SPRGOSIKSQA SVGDRSPSTDTITAGSPTKVSMS---F 458
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 299 LLSPPRP---KKSUVVKKKKFKLDKONGVTPGEMKLTVPHTCDPPEERRLDHFSVDGY 355

QY 459 NDRTRFPRSLRKSOPKRVYIDADTALGTDDVYDEKGCOCOVSVEDLPPPL----- 509
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 356 DSSVRKSPPTL-LEVSMRP-----FMRTNSFAED---LDLEGTLTPHTHISOLREH 403

QY 510 -KTYIRAIRIMKFFVAKRKETLRPYDVKYIEOYSAGHLDMLCRISLQTRVDIOLGK 568
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 404 HRATIKVIRMOYVFAKKKFOARKPYDVRYIEQYSGHLMIMVYIKELORLDOISICK 463

QY 569 GQ--ITSKRSREKITAHEHTTDDLMLGRVYKVEKOVQSIKDLCLDIYQOVL---- 622
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 464 PSLTIVSEKSKDR-----GSNTIGARINRVEDKYVQLDQRLALITDMLHQLLSLHG 515

QY 623 -----RKGA-----SALALASFOIPPE 641
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 516 GSTPGSGGPPREGAHITQPCGSGSVDPBELFLPNTLTPTYE 557

RESULT 30
US-09-597-735-114
; Sequence 114, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0

```

;; SEQ ID NO 114
;; LENGTH: 570
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-597-735-114

Query Match 22.9%; Score 1081.5; DB 4; Length 570;
Best Local Similarity 41.6%; Pred. No. 1.4e-87;
Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

```

OY 112 ONLVNVLPRPGW-AFIYHAFVLLVFGCLLSVSTIEPHTKLASSCLLLEFVMIYV 170
D 1 QGRVYNELEPRTGKCFVHFAVFLVLCVLFVSLTIEOYALATGTFMMEIVLVF 60
OY 171 FGLEFIIRWSAGCCCRKRGMOGRLEFARKPCFVITIVLAVASAKTOGNIFATSA 230
D 61 FGLETVVRLMSAGCRSKYVGLMGRLEFARKPCISIIDLIYVASMVLCVSGKGVFATSA 120
OY 231 LRSLEFLQILRMVMDRGGTWKLLGSVYVASHKELITAWYIGFLVLIFFSFLVLYEKD 290
D 121 IRCIRFLOILRLMHDVROGGTWRLGVSVEFHROELITLTYIGFLGIFSSFYVLAEKD 180
OY 291 A-----NKESTYADALMWGTTITLTIGYGDKTPLTWGLSLGAFALLGISFALPAGI 345
D 181 AVNESGRVEGSDADALMWGVVTVTTIGYDKVPQVWGTIASCFVSFAISFALPAGI 240
OY 346 LSGSFALKVOEQHROKHFERRRNPANLIQCVRSYADEKSVSIATWPKHLKAL--HT 402
D 241 LGSFALKVQOKORQHFNQIPAAASLIOTAMRCYAAENPDS--TWKTIYIKAPRSHT 298
OY 403 -CSPTNOKLSKERVMAASPRGOSIKRQASVGDRRSPSTDTITAEGPSPTKVOKWS--F 458
D 299 LLSPSKPK--KKSIVVKKKKFKLDKNGVTPGKMLTPHITCDPREERLDFHSVDGY 355
OY 459 NDRTFRRLRLKSSQPKPYIDADTLGTDVYDEKCCQDVSEDLTPPL----- 509
D 356 DSSVRKSPYL-LEVSMPH-----FMKRNFAED--LDLEGETLTPPTHTISQLREH 403
OY 510 -KTVIRAIRIMKFNHAKRREKTELRPYDVADVEYQSAGHLMCLRIKSLQTRVDQILGK 568
D 404 HRATIKVIRRMQYFAVAKKFFQARKPYDVADVEYQSQHLMNMRVYIKELORLDQSIGK 463
OY 569 GQ--ITSDKSKREKITAHEHTDDLSMLGRVYVKEKOVOSIESKLDCLDIYQOVL---- 622
D 464 PSLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDORLALITDMLHQLLSLHG 515
OY 623 -----RKGSA-----SALALASFOIPPE 641
D 516 GSTPGSGGPRREGAHTIOPCGSGSVDPFLPSPNTLPTYE 557

```

RESULT 31
US-09-444-295-114
; Sequence 114, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN IOT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444, 295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135, 020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921, 068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739, 383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019, 014
; PRIOR FILING DATE: 1995-12-22

;; PRIOR APPLICATION NUMBER: 60/094,477
;; PRIOR FILING DATE: 1998-07-29
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 114
;; LENGTH: 570
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-444-295-114

Query Match 22.9%; Score 1081.5; DB 4; Length 570;
Best Local Similarity 41.6%; Pred. No. 1.4e-87;
Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

```

OY 112 ONLVNVLPRPGW-AFIYHAFVLLVFGCLLSVSTIEPHTKLASSCLLLEFVMIYV 170
D 1 QGRVYNELEPRTGKCFVHFAVFLVLCVLFVSLTIEOYALATGTFMMEIVLVF 60
OY 171 FGLEFIIRWSAGCCCRKRGMOGRLEFARKPCFVITIVLAVASAKTOGNIFATSA 230
D 61 FGLETVVRLMSAGCRSKYVGLMGRLEFARKPCISIIDLIYVASMVLCVSGKGVFATSA 120
OY 231 LRSLEFLQILRMVMDRGGTWKLLGSVYVASHKELITAWYIGFLVLIFFSFLVLYEKD 290
D 121 IRCIRFLOILRLMHDVROGGTWRLGVSVEFHROELITLTYIGFLGIFSSFYVLAEKD 180
OY 291 A-----NKESTYADALMWGTTITLTIGYGDKTPLTWGLSLGAFALLGISFALPAGI 345
D 181 AVNESGRVEGSDADALMWGVVTVTTIGYDKVPQVWGTIASCFVSFAISFALPAGI 240
OY 346 LSGSFALKVOEQHROKHFERRRNPANLIQCVRSYADEKSVSIATWPKHLKAL--HT 402
D 241 LGSFALKVQOKORQHFNQIPAAASLIOTAMRCYAAENPDS--TWKTIYIKAPRSHT 298
OY 403 -CSPTNOKLSKERVMAASPRGOSIKRQASVGDRRSPSTDTITAEGPSPTKVOKWS--F 458
D 299 LLSPSKPK--KKSIVVKKKKFKLDKNGVTPGKMLTPHITCDPREERLDFHSVDGY 355
OY 459 NDRTFRRLRLKSSQPKPYIDADTLGTDVYDEKCCQDVSEDLTPPL----- 509
D 356 DSSVRKSPYL-LEVSMPH-----FMKRNFAED--LDLEGETLTPPTHTISQLREH 403
OY 510 -KTVIRAIRIMKFNHAKRREKTELRPYDVADVEYQSAGHLMCLRIKSLQTRVDQILGK 568
D 404 HRATIKVIRRMQYFAVAKKFFQARKPYDVADVEYQSQHLMNMRVYIKELORLDQSIGK 463
OY 569 GQ--ITSDKSKREKITAHEHTDDLSMLGRVYVKEKOVOSIESKLDCLDIYQOVL---- 622
D 464 PSLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDORLALITDMLHQLLSLHG 515
OY 623 -----RKGSA-----SALALASFOIPPE 641
D 516 GSTPGSGGPRREGAHTIOPCGSGSVDPFLPSPNTLPTYE 557

```

RESULT 32
US-09-597-732-114
; Sequence 114, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQTI - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597, 732
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135, 010
; PRIOR FILING DATE: 1998-08-17

RESULT 33
US-09-105-058C-8
Sequence 8, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blanner, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin

```

RESULT 34
US-09-105-058C-2
: Sequence 2, Application US/09105058C
: Patent No. 6403360
: GENERAL INFORMATION:
: APPLICANT: Blanaer, Michael A.
: APPLICANT: Dworetzky, Steven
: APPLICANT: Gribkoff, Valentin K.
: APPLICANT: Levesque, Paul C.
: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauer, Michael G.
: APPLICANT: Yang, Wen-Pin
: TITLE OF INVENTION: KCONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: 3053-4052
: CURRENT APPLICATION NUMBER: US/09/105,058C
: CURRENT FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 60/055,599
: PRIOR FILING DATE: 1997-08-12
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:Consensus amino
: OTHER INFORMATION: acid sequence as shown in Fig. 17A-17B
: OTHER INFORMATION: xaa is any amino acid
US-09-105-058C-2

```

Query Match	20.2%;	Score 957;	DB 4;	Length 298;
Best Local Similarity	67.0%;	Pred. No. 5.7e-77;		
Matches 189;	Conservative 12;	Mismatches 79;	Indels 2;	Gaps 2


```
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQTL - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-113
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-135-010A-113
```

```
Query Match          19.0%; Score 898.5; DB 4; Length 376;
Best Local Similarity 55.3%; Pred. No. 1.4e-71;
Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5;
```

```
QY 98 SSQSCRNVKVR-RVQNTLVNLEPRGM-AFIYHAFVLLVFGCLLSVSTIPEHTKL 155
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 SIYGRRLPFRSTINQGRVNFLEPRGMKCFVHFVFLVLLICLIFSVLSTIOQYNNL 117
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 156 ASSCLLLEFMYIVFEGLEFIIRIWSAGCCCRKRYGMQGRLPARKPCVYDIIVLASIA 215
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 ATEFLFMEIYLVVFFGAEYVVRILMSACRSKYVGMGRLPARKPCVYDIIVLASIA 177
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 216 VSAKTOGNIFATSLRFLQILRMVMDRGGTWKLLGSVYAHSELTIAWYIGFL 275
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 178 VLVGSNGQVFAISIRGIRFLQILRMVMDRGGTWKLLGSVYAHSELTIAWYIGFL 237
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 276 VLIFFSFLVYLVKDA-----NKESTYADALMMGTITLTIGYDGTPLTWLGRLLSAG 330
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 GLIFSSYFVYLAERKALDSSGEYFGSYADALMMGVYVTTTIGYDGTPLTWLGRLLSAG 297
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 331 FALGISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 390
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 298 FSVAISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 355
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 391 ATWKPHLAL----HTCSPT 406
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 ATWKIYIKRSRHHIMSPS 375
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 38
US-09-444-871-113
; Sequence 113, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: KCE1 AS AN LOT GENE
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
```

```
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-444-871-113
```

```
Query Match          19.0%; Score 898.5; DB 4; Length 376;
Best Local Similarity 55.3%; Pred. No. 1.4e-71;
Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5;
```

```
QY 98 SSQSCRNVKVR-RVQNTLVNLEPRGM-AFIYHAFVLLVFGCLLSVSTIPEHTKL 155
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 SIYGRRLPFRSTINQGRVNFLEPRGMKCFVHFVFLVLLICLIFSVLSTIOQYNNL 117
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 156 ASSCLLLEFMYIVFEGLEFIIRIWSAGCCCRKRYGMQGRLPARKPCVYDIIVLASIA 215
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 ATEFLFMEIYLVVFFGAEYVVRILMSACRSKYVGMGRLPARKPCVYDIIVLASIA 177
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 216 VSAKTOGNIFATSLRFLQILRMVMDRGGTWKLLGSVYAHSELTIAWYIGFL 275
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 178 VLVGSNGQVFAISIRGIRFLQILRMVMDRGGTWKLLGSVYAHSELTIAWYIGFL 237
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 276 VLIFFSFLVYLVKDA-----NKESTYADALMMGTITLTIGYDGTPLTWLGRLLSAG 330
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 GLIFSSYFVYLAERKALDSSGEYFGSYADALMMGVYVTTTIGYDGTPLTWLGRLLSAG 297
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 331 FALGISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 390
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 298 FSVAISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 355
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 391 ATWKPHLAL----HTCSPT 406
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 ATWKIYIKRSRHHIMSPS 375
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 39
US-09-597-735-113
; Sequence 113, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQTL - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-597-735-113
```

```
Query Match          19.0%; Score 898.5; DB 4; Length 376;
```

Best Local Similarity 55.3%; Pred. No. 1.4e-71;
Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5

```

OY 88 SOSORRANKYV-RVONYLYNLERGRM-AFYHAFVFLVYGCILSVESTIBETKL 155
Db 58 SYISGRRLPESRTNIQGRVYNFLERPTGKCFYHFTVFLVLICLIFSVLSTIQOYNL 117
OY 156 ASSCLLIEFWIYVVEGLEFIRISAGCCCRKRGQIRFRARFKPCYDITVLASIA 215
Db 118 ATEILFMEIYLVVEFGAEYVRLVMSAGCRKIVYGRRIRFRKPIYDILLVVAASVL 177
OY 216 VVSATQGNIFATSRLRFLQILRMVMDRGRGTWKLGSVYVHSELEITAWYIGFL 275
Db 178 VLVCSNQGVEFATSIRGIRFQILRLMLHVDROGGTWRLLGSVVF IHRQELITLYIGFL 237
OY 276 VLISSFLYLYVERKA-----NKESTYADALMWGITLTITIGYCKPTLYMLGRLLSAG 330
Db 238 GLIRSSSYVYLAEKADALDSSGEYOGSYADALMWGVYVTTITIGYGKVPQWTWIGKTIASC 297
OY 331 FALGILSEFPALPAGILGSGFALKVOEORHOKHFEEKRNRNPANLIIQCVRSYADEKSVSI 390
Db 298 FSVFALISFPALPAGILGSGFALKVOOKQKQKHFNRQIPAAASLIQVAMCYAAE--NPDS 355
OY 391 ATWKPHLKAL-----HTCSPT 406
Db 356 ATWKYIRKQSNHNIHIMSPS 375

```

RESULT 40
US-09-444

Sequence 113, Application US/09444295
Patent No. 6432644
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REFERENCE: 2323-131
CURRENT APPLICATION NUMBER: US/09/444,295
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 09/135,020
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 113
LENGTH: 376
TYPE: PRF
ORGANISM: *Xenopus laevis*
US-09-444-295-113

Query Match	19.0%	Score 898.5	DB 4	Length 376
Best Local Similarity	55.3%	Pred. No. 1,4e-71		
Matches 177; Conservative	53;	Mismatches 77;	Indels 13;	Gaps 5

QY 98 S\$OSCRNMYKR -NQVNYLYVLETRPGMW -FEIYAEFELLVCGCLISVSTIDEHNRKL 155
Db 58 SIYSGRRPLESRNTIOGRVYVNFLETRPGMKCFYHFEVLLVILICLISVSTIOQYNNL 117
QY 156 ASSCLLLEFPMIVVFGLEFTIRW\$G\$CCCR\$G\$MGRLL\$REARK\$PEVIDITIVY\$ASA 215
Db 118 ATFEFLFEMELVLYVFGAEYVYVR\$MS\$OC\$R\$KRY\$G\$W\$GR\$LF\$PA\$R\$K\$IS\$VIDI\$V\$V\$AST 177
QY 216 V\$AK\$OG\$N\$F\$AT\$S\$AL\$SR\$FL\$QL\$LR\$V\$RD\$RD\$RG\$T\$K\$L\$G\$S\$V\$V\$Y\$H\$SK\$EL\$IT\$AM\$Y\$IG\$FL 275

Db 178 VLCVSGNGVFATSAIRGLRFLQILMLHVDPRQGGTWMLDGSVYFIHRQELITTLVIGFL 237

QY	2/6	VLIISSFFVYIVAEKKA----	NKESTYADALAMWGITITLTITIGYSGKPTLTWIGKTLISAG	330
Db	238	GLIISSSYVYVYIAEKPAIDSSGEYQGSYADALAMWGCVIVTITIGYGDVKEPQTWIGKTLTASC	297	
QY				
Db	331	FALGIISSFPAIPAGILGSGFALKVQEOHQRCKHFKEKRNPANALICQVMSYADEKSVSI	390	
Db	298	FSVFALISFPALPAGILGSGFALKVQGKQKQKHFNRQIPAAASLIQTAMMCYAAE--NPDS	355	
QY				
Db	391	ATWKPDKAL-----HTCSPT	406	
	356	ATWKIYIKQSRNHHHIMSPS	375	

RESULT 41
US-09-507

```

Sequence 113, Application US/09597732
Patent No. 6451534
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burr, Timothy C.
APPLICANT: Splasko, Igor
FILE OF INVENTION: KVL071 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,732
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 113
LENGTH: 376
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-597-732-113

```

Query Match	19.0%;	Score 898.5;	DB 4;	Length 376;
Best Local Similarity	55.3%;	Pred. No. 1.4e-71;		
Matches 177;	Conservative 53;	Mismatches 77;	Indels 13;	Gaps 5

QY	98	SSOSCRNNVYXR-RVQNYLVNVLVERPGQM- FEITHAEFELLVFGCLLIVSEITDEHNTL	155
Db	58	SIYSGRRPLESRNIGQGRVYNYFLERPLPGKCFVYH FEYLVLLICLISVSLTIOQYNNL	117
QY	156	ASSCLLIEVYMYVEGLEFIRIKWSAGCCCRYGMOGLR PARKPECVIDTYLIASIA	215
Db	118	ATTELTLMMEIVLVFFGAEEYVVRMLMSAGCRSKY GVGWRGLFARPKDISVIDLIVVAVSYI	177
QY	216	VWEAKTOGNIFATSAIRLSRFLQLIRNVRMDRPGT MLSSVYVYAHSKELITAYIGTL	275
Db	178	VLCVSGNSGYCFANISAIKINGIRFLOLRMLNHL ADROGCTWRLLSSVYFIHNOELITTYIGTL	237
QY	276	VLIFFSFLVYLVEKDA-----NKEESTYADAL MWGTLTTLTIGYGDKTPLTLGRLLSAG	330
Db	238	GLIFFSFFVYVLAKDAIDSSGEYVQFSGSYADAL MMGVVTYLTIGYGDVKPQTMIGKTIASC	297
QY	331	FALIGISFFLPLPGIGLISGFALMKQEOEHROK HEKRRNPANLILQCVARSVYADKSVSI	390
Db	298	FSVFALISFPALPGIGLISGFALMKVQOKROKH ENKQIPDAASLIQTARCKTAAE--NDS	355

QY 336 ISFPALPAGILSGSFGAL 352
Db 121 ISFPALPAGILSGSFGAL 137

RESULT 45

US-09-597-735-109
Sequence 109, Application US/09597735
Patent No. 6420124
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,735
CURRENT FILING DATE: 2000-06-19
EARLIER APPLICATION NUMBER: 09/135,010
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-597-735-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1.6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

QY 221 TCGNIFATSAIRLQILRMVMDRGCTWKLGSVVAHASKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGCTWRLGSVVFIRHQLITTYIGFLGIFS 60

QY 281 SFYVLYAEKDA-----NKEESTYADALMWGTTITTTIGYDGTPLTWLGRLLSAGFALLG 335
Db 61 SYFYVLYAEKDAVNESGRVEFGSYADALMWGVVYTTTIGYDGPQTWGWKTIASCSFVFA 120

QY 336 ISFPALPAGILSGSFGAL 352
Db 121 ISFPALPAGILSGSFGAL 137

RESULT 46

US-09-444-295-109
Sequence 109, Application US/09444295
Patent No. 6432644
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/444,295
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 09/135,020
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/921,068

PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-444-295-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1.6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

QY 221 TCGNIFATSAIRLQILRMVMDRGCTWKLGSVVAHASKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGCTWRLGSVVFIRHQLITTYIGFLGIFS 60

QY 281 SFYVLYAEKDA-----NKEESTYADALMWGTTITTTIGYDGTPLTWLGRLLSAGFALLG 335
Db 61 SYFYVLYAEKDAVNESGRVEFGSYADALMWGVVYTTTIGYDGPQTWGWKTIASCSFVFA 120

QY 336 ISFPALPAGILSGSFGAL 352
Db 121 ISFPALPAGILSGSFGAL 137

RESULT 47

US-09-597-732-109
Sequence 109, Application US/09597732
Patent No. 6451534
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,732
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-597-732-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1.6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

QY 221 TCGNIFATSAIRLQILRMVMDRGCTWKLGSVVAHASKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGCTWRLGSVVFIRHQLITTYIGFLGIFS 60

[illegible]

RESULT 48
HS-08-46A

US-08-404-340A-13
Sequence 13, Application US/08464340A
Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

Query Match	5.3%:	Score 250;	DB 1;	Length 539;
Best Local Similarity	23.3%:	Pred. No. 1.6e-13;		
Matches	91:	Conservative 77;	Mismatches 131;	Indels 72;
				Gaps 13

```

OY 330 GFALLIGEFPLPAGILLSGFALTKVOEJHRKCHFEKRRRPPANLIGQVWRSTYADEKSYS 389
Db 394 LCCIALGVIALPIDIPIDIVNNFSEFYKEOKROEKAIRK-----EALERARRNGS 442
OY 390 IATWPHLKALHTCSPTNOKLSFKERVRM-----ASPRGOSIKSRQASVGDNRSPDITIA 445
Db 443 IVS-----MMKKDAFANSIEMDIVERKNGENMKDKVDONHLSPNRWKWT 489
OY 446 EGSPTKVQSWSFNDTRFRPSILRLKSSQPK 476
Db 490 KRLTSETSSSKSFETKEOGSPKAKASSSSPQ 520

```

RESULT 49

```

US-09-336-643A-10
: Sequence 10, Application US/09336643A
: Patent No. 6399761
:
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian Wang
: TITLE OF INVENTION: No. 6399761el Human Potassium Channels
: FILE REFERENCE: SEQ-15P
: CURRENT APPLICATION NUMBER: US/09/336,643A
: CURRENT FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 646
: TYPE: PRT
: ORGANISM: H. sapiens
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(646)
: OTHER INFORMATION: Xda = Any Amino Acid
US-09-336-643A-10

```

Query Match	5.2%	Score 245;	DB 4;	Length 646;
Best Local Similarity	22.5%;	Pred. No. 6.2e-13;		
Matches 107;	Conservative 81;	Mismatches 170;	Indels 118;	Gaps 22;

OY 416 VMASPRGOSIKRQAS---VG-----DRRSPSTDITAGSPTKYKQSMFNDRT 463
DB 503 LGAVSPGKRTSRSTVSQPGPSLLSSCCPRRAKRAIRLANSTASVSRG-SMOELDM 561
OY 464 FRPSLRKRSQPKPIDADTALGTDVYDEKGCOC-----VSEDLTPPLKT 511
DB 562 LAGLRSHAPQSRSSLANKP-----HDSLDLNCDSRDFVAALISIP--TPPANT 608

RESULT 50

US-09-336-643A-4
; Sequence 4, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rulter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 601
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-4

Query Match 5 1%; Score 243; DB 4; Length 601;

Best Local Similarity 23.8%; Pred. No. 8.2e-13; Matches 82; Conservative 65; Mismatches 109; Indels 88; Gaps 13;

OY 65 AATLGGGGGGLRESRGRGKAGMSLIGKPLSYSSQSCRNMVYRYQNYLYNLERP-- 122
DB 159 AAGLGCPD-----GKSG-----RMRRLQPRMMLFEDPYS 188
OY 123 -RGNAFYHAFVFLVFG---CL-----ILSVSTIPEHTKLASSCLLI 162
DB 189 SRARFFIAFASLFFLVSITTEPCLETHEAFNIYKNKTEPIYNGTSVLYQEIETDPALTY 248
OY 163 LEFMIIVVEGLEFIRIMWAGCCCRGMQGLRFAKPCPCVDTIYLI-----ASIAVY 217
DB 249 VEGCVVWFTEFLVRIYFS-----PNKLEFTKNLNIIDFAILPFYLEVGLSGL 299
OY 218 SAKTOGNIFATSAULSLRFLQILRMVMDRGGTWSLLGSVYVYHSKE-LITAWYIGFLV 276
DB 300 SSKAKVDYL--GELHVRFRVILRIKFLTRHFEVGLRVLGHTRASTNEFLLIIFLAGV 357
OY 277 LIFSEFLVLYLEK-----DANKKESTYADALMWGITTLTIGYGDKPLTWLGR 326
DB 358 LIFAT-MITYAERVGAQPNPDSASEHTQKNIPIGFWMAVYMTTLGYGDMYFOTWSGML 416
OY 327 LSAGFALGISFPALPAGIL---GSGFALKVQEQ---HROKH 362
DB 417 VGALCALAGVLTIANPVIYVNNFGMYISLAMAKOKLPRKKKH 460

Search completed: June 14, 2003, 17:45:42
Job time : 34 secs

84	255	5.4	446	22	AAW57124	Human brain expres
85	255	5.4	446	22	AAW69516	Human bone marrow
86	255	5.4	446	22	AAW17348	Peptide #3782 encoc
87	255	5.4	446	22	AAW29655	Peptide #3892 encoc
88	255	5.4	446	22	AAW05037	Peptide #3719 encoc
89	255	5.4	446	22	ABG31941	Human peptide encoc
90	250	5.3	1057	23	ABG00601	Novel human diagno
91	248	5.2	647	22	AAW25597	Human protein sequ
92	247	5.2	481	20	AAW50342	Murine Kv6.2 protei
93	245	5.2	646	20	AAW34123	Human potassium ch
94	245	5.2	646	20	AAW86318	Human Kv4.1 protei
95	243	5.1	601	20	AAW34120	Human potassium ch
96	243	5.1	638	22	AAW14201	Human transporter
97	242	5.1	1019	23	AAW67198	Drosophila melanog
98	239.5	5.0	616	20	AAW32713	Drosophila melanog
99	239	5.0	985	22	AAW57704	Drosophila melanog
100	235.5	5.0	630	20	AAW13523	Amino acid sequenc
101	234	4.9	283	20	AAW49495	Mutant human KVLOT
102	232.5	4.9	655	19	AAW79590	Human Kv potassium
103	232.5	4.9	655	23	ABW79584	Human Kv4.3 potass
104	229.5	4.8	495	20	AAW32014	Human cation chann
105	229	4.8	636	19	AAW79589	Human Kv potassium
106	229	4.8	636	19	AAW79591	Human Kv potassium
107	229	4.8	636	23	ABW79585	Human Kv4.3 potass
108	227.5	4.8	629	22	AAW86319	Human Kv4.2 protei
109	226	4.8	495	23	ABW57250	Mouse ischemic co
110	226	4.8	556	20	AAW32016	Caenorhabditis ele
111	224	4.7	477	20	AAW34127	Human potassium ch
112	223	4.7	466	20	AAW50341	Human Kv6.2 protei
113	223	4.7	466	22	ABG11444	Novel human diagno
114	223	4.7	499	20	AAW34122	Human potassium ch
115	222.5	4.7	571	22	ABW71712	Drosophila melanog
116	222	4.7	526	21	ABG14353	Novel human diagno
117	220.5	4.7	506	21	AAW44564	Mouse Voltage-gate
118	220.5	4.7	506	21	AAW44566	Mouse Voltage-gate
119	220.5	4.7	506	21	AAW44567	Mouse Voltage-gate
120	220.5	4.7	506	21	AAW44568	Mouse Voltage-gate
121	217.5	4.6	655	22	AAW86321	Human Kv4.3 protei
122	214.5	4.5	495	20	AAW33766	hKv5.1 human brain
123	213	4.5	41	23	AAW16611	Human KCNQ5 immuno
124	213	4.5	869	22	ABG06674	Novel human diagno
125	212	4.5	498	22	ABW59446	Drosophila melanog
126	212	4.5	519	21	AAW44565	Human Voltage-gate
127	212	4.5	519	21	AAW44569	Human Voltage-gate
128	212	4.5	519	21	AAW44570	Human Voltage-gate
129	212	4.5	519	21	AAW44571	Human Voltage-gate
130	212	4.5	519	21	AAW44572	Human Voltage-gate
131	209.5	4.4	532	16	AAW89337	Mouse Kv1.7 voltage
132	209	4.4	559	22	ABW11807	Human K channel ho
133	209	4.4	559	22	AAW08660	Human NOVA protein
134	208.5	4.4	249	22	AAW087098	Novel central nerv
135	208.5	4.4	250	22	AAW18283	Human K+ channel 2
136	206.5	4.4	494	17	AAW90765	Human K+ channel 2
137	206.5	4.4	494	19	AAW42996	Putative mature po
138	204.5	4.3	431	22	AAW99519	Human polypeptide,
139	204.5	4.3	456	23	AAW23655	Human ion channel
140	204.5	4.3	490	20	AAW34121	Human potassium ch
141	204.5	4.3	491	21	AAW70454	Human membrane ch
142	204.5	4.3	491	21	AAW53780	Novel human diagno
143	204	4.3	406	22	ABW11445	Novel human diagno
144	203.5	4.3	446	23	ABW60654	Human potassium ch
145	203.5	4.3	518	22	AAW90765	Drosophila melanog
146	199.5	4.2	513	17		

ALIGNMENTS

RESULT 1

AAB47678
ID AAB47678 standard; protein; 923 AA.
XX AC AAB47678;
XX DT 21-JAN-2002 (first entry)
XX DE Human ion-channel forming protein.
KW Ion-channel forming protein; voltage-gated potassium channel;
KM fetal; brain; thymus; prostate; heart; skeletal muscle; probe.
OS Homo sapiens.
XX WO200175108-A1.
PN 11-OCT-2001.
PD 03-APR-2001; 2001WO-US10875.
PF 03-APR-2000; 2000US-194255P.
PR 03-APR-2000; 2000US-194255P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
XX PT Sands AT;
XX DR WPI: 2001-656987/75.
XX N-PSDB; AAH43633, AAH43634.

New human ion channel protein and polynucleotides encoding the protein,
useful in diagnosing or treating diseases, in drug screening, and in
clinical trial monitoring

Claim 2: Page 35-37; 41pp; English.

This sequence represent a novel ion-channel forming protein. This
protein shares structural similarity with mammalian ion channel
proteins, particularly voltage-gated potassium channel proteins. The
protein is expressed in many human cell lines including fetal brain,
brain, thymus/prostate, heart and skeletal muscle. The novel protein
can be used in the diagnosis or treatment of diseases, in drug
screening, and in clinical trial monitoring. The oligonucleotides may
be used as hybridization probes for screening libraries, and assessing
gene expression patterns (particularly using a micro array or high
throughput chip format). The nucleic acids and novel protein can also be
used in the identification, selection and validation of novel molecular
targets for drug discovery, to screen collections of genetic material
from patients who have a particular medical condition, to identify
mutations associated with a particular disease, as a diagnostic or
prognostic assay, and to screen for drugs which can be used to treat
CC symptomatic or phenotypic manifestations of perturbing the normal
function of novel human protein. The polypeptides are further used in
generating antibodies.

Sequence 923 AA:

Query Match 100.0%; Score 4733; DB 22; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 923; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MPRHHAGEEGGGAAGLWVKSAAAAAAGGGGRIGSGMKDVEGRGVLLNSAAARGDGLL 60
|||||
1 MPRHHAGEEGGGAAGLWVKSAAAAAAGGGGRIGSGMKDYESRGVLLNSAAARGDGLL 60
|||||
61 LGTRATITGGGGGGLRESRRKQGARMSILGKPISYTSQSQRNVKYRRVONYLYNVL 120
|||||
61 LGTRATITGGGGGGLRESRRKQGARMSILGKPISYTSQSQRNVKYRRVONYLYNVL 120
|||||
121 RPRGAIFYHAFFLVFLVGCLILSVFSTIPPEHTKLASSCLILFEVMIVPELEFIIRTW 180
|||||
121 RPRGAIFYHAFFLVFLVGCLILSVFSTIPPEHTKLASSCLILFEVMIVPELEFIIRTW 180
|||||

```

QY 181 SAGCCRYRGWQGLRFAARKPECVIDITVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
DB 181 SAGCCRYRGWQGLRFAARKPECVIDITVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
QY 241 RMVMDRRGGTGWKLLGSVYVAHAKSKELLTAMWYIGFLVLFFSSFLVYLVEKDANKKESTYAD 300
DB 241 RMVMDRRGGTGWKLLGSVYVAHAKSKELLTAMWYIGFLVLFFSSFLVYLVEKDANKKESTYAD 300
QY 301 ALMMGTITLTTIGYDGTPLTWLGRLLSAGFALLGISFPALAGILGSGFALKVQDQHQ 360
DB 301 ALMMGTITLTTIGYDGTPLTWLGRLLSAGFALLGISFPALAGILGSGFALKVQDQHQ 360
QY 361 KHFEKRRNPANLITOCVWRSYAADAESVSIAATWPKHLALHTCSPTNOKLSFKERERMS 420
DB 361 KHFEKRRNPANLITOCVWRSYAADAESVSIAATWPKHLALHTCSPTNOKLSFKERERMS 420
QY 421 PRGOSIKRSQASVGDRRSPSTDITAEGSPTVKQKSMSEFDRTRFRPSRLKSSQKPEVID 480
DB 421 PRGOSIKRSQASVGDRRSPSTDITAEGSPTVKQKSMSEFDRTRFRPSRLKSSQKPEVID 480
QY 481 ADTALGTDVYDEKGCOCVSVEDLTPPLKTYIRAIRIMKFMHAKRKKEETLRPYDKVY 540
DB 481 ADTALGTDVYDEKGCOCVSVEDLTPPLKTYIRAIRIMKFMHAKRKKEETLRPYDKVY 540
QY 541 IEQYSAGHLDMLCRISLQTRVDQILGKQILTSKRSREKITAHEHTTDLISMLGRVAVY 600
DB 541 IEQYSAGHLDMLCRISLQTRVDQILGKQILTSKRSREKITAHEHTTDLISMLGRVAVY 600
QY 541 IEQYSAGHLDMLCRISLQTRVDQILGKQILTSKRSREKITAHEHTTDLISMLGRVAVY 600
DB 541 IEQYSAGHLDMLCRISLQTRVDQILGKQILTSKRSREKITAHEHTTDLISMLGRVAVY 600
QY 601 EKQVOSIESKLDCLDITVOYLKRSASALASFOIPPEECQISDYOSPVDSKDLGSG 660
DB 601 EKQVOSIESKLDCLDITVOYLKRSASALASFOIPPEECQISDYOSPVDSKDLGSG 660
QY 661 AONGCISRSNTSANISRGLOFLTPNESAOFYALSPMHSAOTVPISSOSGSAVAAT 720
DB 661 AONGCISRSNTSANISRGLOFLTPNESAOFYALSPMHSAOTVPISSOSGSAVAAT 720
QY 721 NTIANQINTAPKPAATLQIPPLPAIKHLPRPETLHPNPAJLOESISDVTTCLVAASKE 780
DB 721 NTIANQINTAPKPAATLQIPPLPAIKHLPRPETLHPNPAJLOESISDVTTCLVAASKE 780
QY 781 NVQVAOSMLTKDRSKRSKFDMDGFTLLSVCMPVPKDLGKSLSVONLIRSTEELNIOGSG 840
DB 781 NVQVAOSMLTKDRSKRSKFDMDGFTLLSVCMPVPKDLGKSLSVONLIRSTEELNIOGSG 840
QY 841 ESSSGRSQDFFPKKRESKLFITDEVEGPEETDTFDAAPOPARAAASDLSLRTGRSR 900
DB 841 ESSSGRSQDFFPKKRESKLFITDEVEGPEETDTFDAAPOPARAAASDLSLRTGRSR 900
QY 901 SSOSICKAGESTDALSLPHVKLK 923
DB 901 SSOSICKAGESTDALSLPHVKLK 923

```

```

RESULT 2
AAB86979
ID AAB86979 standard; Protein: 932 AA.
AC
XX AAB86979:
DT 11-DEC-2001 (first entry)
DE
XX Human KCNQ5 protein.
XX KCNQ5: potassium channel protein; human; neurological; cardiovascular;
XX anticonvulsant; excitability modulator; membrane potential; neuron;
XX voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
XX screening; central nervous system disease; cardiovascular disease.
OS Homo sapiens.
XX
XX DE10013732-A1.
XX
XX 27-SEP-2001.
PD

```

```

XX 21-MAR-2000; 2000DE-1013732.
PE
XX 21-MAR-2000; 2000DE-1013732.
PR
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX Steimeyer K, Lerche C, Scherer C, Seebold G, Busch AE;
XX WPI; 2001-571700/65.
XX N-PSDB; AAH49499.
XX
XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX for specific modulators, potential agents for treating central nervous
XX system and cardiovascular diseases.
XX
XX Claim 1b; Page 10-14; 20pp; German.
XX
XX This invention describes a novel DNA sequence (I) encoding: (i) a
XX polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
XX polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
XX the invention have neurological, cardiovascular and anticonvulsant
XX activity and act as modulators of the voltage-dependent KCNQ5 potassium
XX channel, a key regulator of membrane potential and modulator of
XX excitability of electrically activated cells such as neurons and
XX cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (ii)
XX are used to screen for compounds that modulate the activity of KCNQ5,
XX potentially useful for treating central nervous system (e.g. epilepsy)
XX and cardiovascular diseases. This sequence represents the human
XX potassium channel KCNQ5 protein described in the invention.
XX
XX Sequence 932 AA:
XX
XX Query Match 99.3%; Score 4699.5; DB 22; Length 932;
XX Best Local Similarity 98.7%; Pred. No. 0;
XX Matches 920; Conservative 1; Mismatches 2; Indels .9; Gaps 1;

```

```

QY 532 LRPDYKQVIEQYSGAGHLMCRKISQTRVDQILGQITSDKKSREKITAHEHTTDDL 591
DB 541 LRPDYKQVIEQYSGAGHLMCRKISQTRVDQILGQITSDKKSREKITAHEHTTDDL 600
QY 592 SMLGRVYKVEKQVIESKLDCLLDIYQOVLKKSASALALASFOIPPEECOTSDYOSP 651
DB 601 SMLGRVYKVEKQVIESKLDCLLDIYQOVLKKSASALALASFOIPPEECOTSDYOSP 660
QY 652 VDSKIDSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYALSPYMSQAOTVPISQ 711
DB 661 VDSKIDSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYALSPYMSQAOTVPISQ 720
QY 712 SSGSAVAANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPETLHPNPAQLQESISDY 771
DB 721 SSGSAVAANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPETLHPNPAQLQESISDY 780
QY 772 TTCLVASKENVOYAQSNLTKDRSMKRSFDMGGETLLSYCPVWPDKLGSLSYONLIRSTE 831
DB 781 TTCLVASKENVOYAQSNLTKDRSMKRSFDMGGETLLSYCPVWPDKLGSLSYONLIRSTE 840
QY 832 ELNIDLSGSESSGSGSODFYPKWRESKLETTDEEVPEETETDTPDAAPQAPAREAPAS 891
DB 841 ELNIDLSGSESSGSGSODFYPKWRESKLETTDEEVPEETETDTPDAAPQAPAREAPAS 900
QY 892 DSLRTGRSRSSOSICKAGESTDALSLPHVRLK 923
DB 901 DSLRTGRSRSSOSICKAGESTDALSLPHVRLK 932

RESULT 3
AAU09021
ID AAU09021 standard: Protein; 888 AA.
AC AAU09021;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human voltage gated potassium channel hKCNQ5-2.
DE
XX
XX Human: voltage-gated potassium channel; hKCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.
XX
XX Homo sapiens.
OS
XX
XX WO200170759-A1.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 20-MAR-2001; 2001WO-US09328.
PE
XX
XX 21-MAR-2000; 2000US-190954P.
PR
XX
XX (ICAG-) ICAGEN INC.
PA
XX
XX Jegla TJ;
PI
XX
XX WPI; 2001-611467/70.
XX
XX N-PSDB; AAS14653.
DR
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits
XX
XX Claim 17; Page 64; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of

```

```

CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC encoded by a splice variant of hKCNQ5 and is hKCNQ5-2.
XX
SQ Sequence 888 AA;
Query Match 96.1%; Score 4547; DB 22; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 MKDVESSGRGVILNSAARGDGLLIGTRAATLGGGGGLRRSRGKQAGRMSLGKPLS 95
DB 1 MKDVESSGRGVILNSAARGDGLLIGTRAATLGGGGGLRRSRGKQAGRMSLGKPLS 60
QY 96 YTSQSCRRNVKRYRVOYLYNVLEPRGMAFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
DB 61 YTSQSCRRNVKRYRVOYLYNVLEPRGMAFIYHAFVLLVFGCLLSVFSTIPEHTKL 120
QY 156 ASSCLLLEFVMYVFLFEFTIRIMSAGCCCRYRMOGRRLRARRPCYDITVILASTA 215
DB 121 ASSCLLLEFVMYVFLFEFTIRIMSAGCCCRYRMOGRRLRARRPCYDITVILASTA 180
QY 216 VSAKTQGNIFATLSALSLRFLQILRMVRRMRRGRTWKLGSVVAHSELTAWYIGTL 275
DB 181 VSAKTQGNIFATLSALSLRFLQILRMVRRMRRGRTWKLGSVVAHSELTAWYIGTL 240
QY 276 VLISSFLVYLVKEDANKFESTYDALMWGTTITTTIGYGKTPPLTWLGRLLSAGFALLG 335
DB 241 VLISSFLVYLVKEDANKFESTYDALMWGTTITTTIGYGKTPPLTWLGRLLSAGFALLG 300
QY 336 ISFFALPAGILGSGFALKVOEHOHROKHFERKRNPAANLIOCWRKYADEKSVSTATWKP 395
DB 301 ISFFALPAGILGSGFALKVOEHOHROKHFERKRNPAANLIOCWRKYADEKSVSTATWKP 360
QY 396 HUKALHTCPTNOKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAECSPTKRVKS 455
DB 361 HUKALHTCPTNOKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAECSPTKRVKS 420
QY 456 WSPNDRTRRRPSRLKSSQPKPVADDTALGTDYVDEKGGQCDVSEDLPLPLTVIRA 515
DB 421 WSPNDRTRRRPSRLKSSQPKPVADDTALGTDYVDEKGGQCDVSEDLPLPLTVIRA 480
QY 516 IRIKMFHVAKRKKEKTELRPYDKVDTIOYSAGHDMCRKISQTRVDQILGQITSDK 575
DB 481 IRIKMFHVAKRKKEKTELRPYDKVDTIOYSAGHDMCRKISQTRVDQILGQITSDK 540
QY 576 KSRKETAHEHTTDDL SMLGRVYKVEKQVIESKLDCLLDIYQOVLKKSASALALASF 635
DB 541 KSRKETAHEHTTDDL SMLGRVYKVEKQVIESKLDCLLDIYQOVLKKSASALALASF 600
QY 636 QIPPECEQTSDYQSPVDSKIDSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYA 695
DB 601 QIPPECEQTSDYQSPVDSKIDSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYA 660
QY 696 ISPTMSQAOTVPISSDGSAAVAATNTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPE 755
DB 661 ISPTMSQAOTVPISSDGSAAVAATNTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPE 720

```

QY 756 TLHPNPAGIYESIDVTCTCLVASKENVOYAOSNLTKDRSMRKSEFDMGGETLLSYCPVWP 815
 DB 721 TLHPNPAGIYESIDVTCTCLVASKENVOYAOSNLTKDRSMRKSEFDMGGETLLSYCPVWP 780
 QY 816 DLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLFITDEVEGETETD 875
 DB 781 DLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLFITDEVEGETETD 840
 QY 876 TFDAPQAPAREAFASDSLRTGSRSSQSTCKRAGESTDALSLPHVKL 923
 DB 841 TFDAPQAPAREAFASDSLRTGSRSSQSTCKRAGESTDALSLPHVKL 888

RESULT 4
 AAU09020
 ID AAU09020 standard; Protein; 897 AA.
 AC AAU09020;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human voltage gated potassium channel hKvN05-1.
 KM Human: voltage-gated potassium channel; hKCN05-1; nontropic;
 KM cerebroprotective; neurotropic; analgesic; vision disorder;
 KM central nervous system disorder; epilepsy; migraine; hearing disorder;
 KM psychologic disorder; seizure; learning disorder; memory disorder;
 KM stroke; pain; gene therapy; splice variant.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 343..640
 FT /label="Conserved region
 FT /note="This sequence is specifically claimed in
 FT claim 13."
 PN MO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR MPI: 2001-611467/70.
 DR N-PSDB; AAS14652.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCN05 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCN0 alpha
 PT subunits
 XX
 PS Claim 17; Page 64; 78pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNO potassium channel, with a subsequence having
 CC 658 sequence identity to amino acids 343-640 of hKCN05-1 amino acid
 CC sequence and forms a KCNO potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNO alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCN05 (including splice variants encoding hKCN05-1 and hKCN05-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNO containing potassium channel and modulate ion flux through the
 CC channel. The KCNO polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNO nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNO5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNO5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNO5. The present sequence is
 CC encoded by a splice variant of hKCN05 and is hKCN05-1.
 XX
 SQ Sequence 897 AA;
 Query Match 95.7%; Score 4527.5; DB 22; Length 897;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
 QY 36 MKDVEGGRVLLNSAARGDGLLLGTRAAVLGGGGGLRESRKGARMSLGPPLS 95
 DB 1 MKDVEGGRVLLNSAARGDGLLLGTRAAVLGGGGGLRESRKGARMSLGPPLS 60
 QY 96 YTSOSCRNRYRKYONLTVLWLEPRGMATFYHAFVFLVNGCLLSVFTIPETKL 155
 DB 61 YTSOSCRNRYRKYONLTVLWLEPRGMATFYHAFVFLVNGCLLSVFTIPETKL 120
 QY 156 ASSCLLIEFVMIYVEGFEITRIMSAGCCCRYGOGRLRFARKPCVDTIVLASIA 215
 DB 121 ASSCLLIEFVMIYVEGFEITRIMSAGCCCRYGOGRLRFARKPCVDTIVLASIA 180
 QY 216 VVSATGQNIPTALSRLSLFLQILRMVMDRRGRTWKLGSVYVASHKELITAWYIGFL 275
 DB 181 VVSATGQNIPTALSRLSLFLQILRMVMDRRGRTWKLGSVYVASHKELITAWYIGFL 240
 QY 276 VLISSFLYLYVEKQANKFEFTYADALMMGTITLTITIGYDKPLTWLGLSAGFLLG 335
 DB 241 VLISSFLYLYVEKQANKFEFTYADALMMGTITLTITIGYDKPLTWLGLSAGFLLG 300
 QY 336 ISFPALPAGILSGFALQVOEOHROKHFEKRRNPANLQCVRSYAADKSVSIATWK 395
 DB 301 ISFPALPAGILSGFALQVOEOHROKHFEKRRNPANLQCVRSYAADKSVSIATWK 360
 QY 396 HLKALHTCSPT-----NKLSPKERVRAASPRGOSTKSSQASVGRDRSPSTDTAE 446
 DB 361 HLKALHTCSPTKKEQGEASSQKLSFKERVRMASPRGOSTKSSQASVGRDRSPSTDTAE 420
 QY 447 GSPTVQKWSFNDRTRFRPSLRLKSSQRPVADATAGTDVYDEKGCQCDVSVDLT 506
 DB 421 GSPTVQKWSFNDRTRFRPSLRLKSSQRPVADATAGTDVYDEKGCQCDVSVDLT 480
 QY 507 PPLKTYIRAIRIMKFFVAKRKFEKTLRPYDVKVIDEQYSAGHDMLCRISLQTRVQIL 566
 DB 481 PPLKTYIRAIRIMKFFVAKRKFEKTLRPYDVKVIDEQYSAGHDMLCRISLQTRVQIL 540
 QY 567 GKGQITSDDKSRREKITAHEHTTDDLSMLGRVYVERKOVOSIESKLDCLDIYQVLRKS 626
 DB 541 GKGQITSDDKSRREKITAHEHTTDDLSMLGRVYVERKOVOSIESKLDCLDIYQVLRKS 600
 QY 627 ASALALASFOIPPEEEOGTSIDVOSPYDSKDLSSAQNOSGLSSTANSIRGLQITIPN 686
 DB 601 ASALALASFOIPPEEEOGTSIDVOSPYDSKDLSSAQNOSGLSSTANSIRGLQITIPN 660
 QY 687 ERSAGTFVALSPFMISQANOVPTISODSGSAVAANTINTANINAPKRAAFTTQIPPLP 746
 DB 661 ERSAGTFVALSPFMISQANOVPTISODSGSAVAANTINTANINAPKRAAFTTQIPPLP 720
 QY 747 AIKHLRPREPTLHPNPAGIYESIDVTCTCLVASKENVOYAOSNLTKDRSMRKSEFDMGGETL 806
 DB 721 AIKHLRPREPTLHPNPAGIYESIDVTCTCLVASKENVOYAOSNLTKDRSMRKSEFDMGGETL 780
 QY 807 LSYCPVWPDLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLFITDEE 866
 DB 781 LSYCPVWPDLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLFITDEE 840

RESULT 6
AAE16599
ID AAE16599 standard; Protein: 897 AA.
XX
AC AAE16599;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNO5.
XX
KW Human: potassium channel polypeptide; KCNO5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 191..209
FT /note= "pore region"
FT 265..285
FT /note= "S4 voltage sensor region"
XX
PN MO200192526-A1.
XX
PD 06-DEC-2001.
XX
PE 24-MAY-2001; 2001WO-US17314.
XX
PR 26-MAY-2000; 2000US-207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan GS, Trojnecki JT, Boissard CG;
PI Grubkoiff VK;
XX
DR WPI: 2002-122069/16.
DR N-PSDB: AAD27192.
XX
PT Novel potassium channel polypeptide, KCNO5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases
XX
PS Claim 25; Fig 2; 128bp; English.
XX
XX The invention relates to potassium channel polypeptides referred to
XX as KCNO5 and nucleic acid molecules encoding such polypeptides. KCNO5
XX polypeptides are useful for identifying compounds that modulate their
XX biological activity. The compounds identified and KCNO5 polynucleotides
XX are useful for treating acute and chronic pain, migraine, acute stroke,
XX dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
XX (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
XX disorders, depression, bipolar disorders, sleep disorders, eating
XX disorders, addiction, myokymia, Alzheimer's disease, age-associated
XX memory loss, learning deficiencies, cognitive disorders and motor
XX neuron diseases. The nucleic acid molecules of the invention are
XX further useful for treating neurophysiological, neuropsychological
XX disorders, asthma, neuron cell death and brain tumours. They are also
XX used in gene therapy and antisense therapy. KCNO5 polypeptides modulate
XX synaptic transmission and electrical excitability in the brain and are
XX useful for generating antibodies. They are also useful to affinity
XX purify biological effectors from biological materials e.g. disease
XX tissues or cells. The present sequence is human KCNO5 protein.
XX
SQ Sequence 897 AA;

Query Match 95.7%; Score 4527.5; DB 23; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 36 MKDVESGRGRVLLNSAARGDGLLLGTRATLGGGGGGLRESRRKGAGRNILGKPLS 95
DB 1 MKDVESGRGRVLLNSAARGDGLLLGTRATLGGGGGGLRESRRKGAGRNILGKPLS 60
QY 96 YTSQSCRRNVKRRVONLYLVLEPRGNAFYTHAFVLLVFGLLISVSTIDEHKL 155
DB 61 YTSQSCRRNVKRRVONLYLVLEPRGNAFYTHAFVLLVFGLLISVSTIDEHKL 120
QY 156 ASSCLLLEFMIYVFGLEFIRIMSAGCCCRYRGMORLRFARKPCVIDIVLIIASIA 215
DB 121 ASSCLLLEFMIYVFGLEFIRIMSAGCCCRYRGMORLRFARKPCVIDIVLIIASIA 180
QY 216 VSAKTQGNIFATSAISSLRLFLQILRMVMDRGGTWKLLGSVYAHSEKELITAVYIGFL 275
DB 181 VSAKTQGNIFATSAISSLRLFLQILRMVMDRGGTWKLLGSVYAHSEKELITAVYIGFL 240
QY 276 VLISSFLVLYVEKDANKKESTYADALMWGTTTTLTIGYGDKPTLWTIGRLISAGFALLG 335
DB 241 VLISSFLVLYVEKDANKKESTYADALMWGTTTTLTIGYGDKPTLWTIGRLISAGFALLG 300
QY 336 ISFPALPAGILGSGFALKVQEOHOKHPEKRRNPANLIQCVWRSYAADEKSVSIATWKP 395
DB 301 ISFPALPAGILGSGFALKVQEOHOKHPEKRRNPANLIQCVWRSYAADEKSVSIATWKP 360
QY 396 HLKALHTCSPT-----NKLSEKERVMASSPRGOSIKSRQASVGDGRSPSDITAE 446
DB 361 HLKALHTCSPTKKRQGEASSSQKLSFKERVMASSPRGOSIKSRQASVGDGRSPSDITAE 420
QY 447 GSPTRKQKSWSEFNDRTPRPSLRKSSQPKPYIDADTLGDDVDYDEKCCQCDVSEDLT 506
DB 421 GSPTRKQKSWSEFNDRTPRPSLRKSSQPKPYIDADTLGDDVDYDEKCCQCDVSEDLT 480
QY 507 PPLKTVIRAIRIMFHVAKRKEKTLRPYVDVDEYVYSAHIDMLCRITKSQTRVDQIL 566
DB 481 PPLKTVIRAIRIMFHVAKRKEKTLRPYVDVDEYVYSAHIDMLCRITKSQTRVDQIL 540
QY 567 GKQGITSDKRSREKITAHEFTDDISLGRVVKVEKQVSIKSLDCLDIYQOVLARKGS 626
DB 541 GKQGITSDKRSREKITAHEFTDDISLGRVVKVEKQVSIKSLDCLDIYQOVLARKGS 600
QY 627 ASALALASFOIPEPCQSDSYOSPVDSKDLSSGSAONSGLSRSTANISRGLOFTLTPN 686
DB 601 ASALALASFOIPEPCQSDSYOSPVDSKDLSSGSAONSGLSRSTANISRGLOFTLTPN 660
QY 687 EFSAQTEFALSPTHMSQATQVPISSDSGSAVAATNTIANQINTAPKPAATTLQIIPPLP 746
DB 661 EFSAQTEFALSPTHMSQATQVPISSDSGSAVAATNTIANQINTAPKPAATTLQIIPPLP 720
QY 747 AIKHLPRPETLHPNPAIGQESISDVTTCLVASKENVQVQASNLTKDRSKRKSDDMGETL 806
DB 721 AIKHLPRPETLHPNPAIGQESISDVTTCLVASKENVQVQASNLTKDRSKRKSDDMGETL 780
QY 807 LSVCPMVPKDKLSVQNLINSTEELINQLSGSESSGSGSGSODFFPKKRRESKLFITDEE 866
DB 781 LSVCPMVPKDKLSVQNLINSTEELINQLSGSESSGSGSGSODFFPKKRRESKLFITDEE 840
QY 867 VGPETETDTFDPAOPAREAFASDSLTGSRSSQSIKAGESTDALSLPHVKLK 923
DB 841 VGPETETDTFDPAOPAREAFASDSLTGSRSSQSIKAGESTDALSLPHVKLK 897
RESULT 7
AAU09023
ID AAU09023 standard; Protein: 897 AA.
XX
AC AAU09023;
XX
DT 18-DEC-2001 (first entry)

Human voltage gated potassium channel hKvNO5-1 variant #2.

Human; voltage-gated potassium channel; hKCNQ5-1; noctropic; cerebroprotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder; psychotic disorder; seizure; learning disorder; memory disorder; stroke; pain; gene therapy; mutant; muten.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 50 /note="Wild-type Ala substituted by Ser"

Region 343..640 /label="Conserved_region" /note="This sequence is specifically claimed in claim 13"

MO200170759-A1.

27-SEP-2001.

20-MAR-2001; 2001WO-0509328.

21-MAR-2000; 2000US-190954P.

(ICAG-) ICAGEN INC.

Jegla TJ;

WPI; 2001-611467/70.

Polypeptides and polynucleotides of potassium channel KCNQ5 for identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ alpha subunits

Disclosure; Page - : 78pp; English.

The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modeling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a polymorphic variant of hKCNQ5-1.

Note: The present sequence does not appear in the specification but is based on hKCNQ5-1 sequence appearing as AAU09020.

Query Match 95.6%; Score 4524.5; DB 22; Length 897; Best Local Similarity 98.8%; Pred. No. 0; Matches 886; Conservative 2; Mismatches 0; Indels 9; Gaps 1;

36 MKDVESGRGVLLNSAARGDGLLLGTRATLGGGGGLRSRSGKQAGARSILGKPLS 95

1 MKDVESGRGVLLNSAARGDGLLLGTRATLGGGGGLRSRSGKQAGARSILGKPLS 60

96 YTSOSCRNRVKKRRVONYLYNLEPRPGMAFYHAFFLVFGLLSVFSTIDPHTKL 155

61 YTSOSCRNRVKKRRVONYLYNLEPRPGMAFYHAFFLVFGLLSVFSTIDPHTKL 120

156 ASSCLLLEVMIVFLEFIRISAGCCCRHYGMORLPARPFCVIDITVILASTA 215

121 ASSCLLLEVMIVFLEFIRISAGCCCRHYGMORLPARPFCVIDITVILASTA 180

216 VVSAKTQGNIFATSAISLRFQLLRVWRMDRGSTWKLGSVYVYHASKELITANYIGFL 275

181 VVSAKTQGNIFATSAISLRFQLLRVWRMDRGSTWKLGSVYVYHASKELITANYIGFL 240

276 VLFSSFLVYLVKDKANKESTYADALWGTITLTIGYCKPTLWGLRSLASGAFALG 335

241 VLFSSFLVYLVKDKANKESTYADALWGTITLTIGYCKPTLWGLRSLASGAFALG 300

336 ISFFALPAGILSGFALKVOEHRQKHFERRRPAANLQCVMSRYADEKSVSIATWKP 395

301 ISFFALPAGILSGFALKVOEHRQKHFERRRPAANLQCVMSRYADEKSVSIATWKP 360

396 HLKALHTCSPT-----NKLSEKERYRMASSPRQSIKROASVGDRRSPSTDTIAE 446

361 HLKALHTCSPTKEGEASSQKLSFKERYRMASSPRQSIKROASVGDRRSPSTDTIAE 420

447 GSPTKVOKSMSEFDRFRFRSLRLKSSQPKPVVDADPAGLDVYDEKCCQDVSEDLT 506

421 GSPTKVOKSMSEFDRFRFRSLRLKSSQPKPVVDADPAGLDVYDEKCCQDVSEDLT 480

507 PLKTVIRAIRIMKFNVAKRKFETLPRYVKVDEIYQYSAGHLMCLRIKSLQTFVDDIL 566

481 PLKTVIRAIRIMKFNVAKRKFETLPRYVKVDEIYQYSAGHLMCLRIKSLQTFVDDIL 540

567 GKGQITSDKKSREKITAHEHTDLSMLGVRVYKVKOVQSIKSLDCLDITYQVLRKGS 626

541 GKGQITSDKKSREKITAHEHTDLSMLGVRVYKVKOVQSIKSLDCLDITYQVLRKGS 600

627 ASALALASFOIPPEEOTSDYOSPYDSKDLGSAONGCISRSTSANISGLQFTLPN 686

601 ASALALASFOIPPEEOTSDYOSPYDSKDLGSAONGCISRSTSANISGLQFTLPN 660

687 EFSAGTFVALSPTMSQATQVPIQSOGSAVAANTIANQINAPKPAAPTLQIPPLP 746

661 EFSAGTFVALSPTMSQATQVPIQSOGSAVAANTIANQINAPKPAAPTLQIPPLP 720

747 ATKHLPRPETLHPNPAGLQESTIDVTCLVASKENVOVAOSNLTKDSMRKSPFMGGTLL 806

721 ATKHLPRPETLHPNPAGLQESTIDVTCLVASKENVOVAOSNLTKDSMRKSPFMGGTLL 780

807 LSVCPMPKDLKSLSVQMLIRSTEELNQLSGSSSGSGSGSODFYFKWRSKLFTIDEE 866

781 LSVCPMPKDLKSLSVQMLIRSTEELNQLSGSSSGSGSGSODFYFKWRSKLFTIDEE 840

867 VGPETETDTPDAAPAPAREAFASPSLRTGSRSSOSICKAGESTDALSPHYK 923

841 VGPETETDTPDAAPAPAREAFASPSLRTGSRSSOSICKAGESTDALSPHYK 897

RESULT 8

AAU09025 standard; Protein; 897 AA.

AAU09025;

18-DEC-2001 (first entry)

Human voltage gated potassium channel hKvNO5-1 variant #4.

Human; voltage-gated potassium channel; hKCNQ5-1; noctropic; cerebroprotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder;

XX WPI: 2000-647417/62.
 DR N-PSDB: AAC64370, AAC64371.
 XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Claim 8; Fig 2; 99pp; English.

CC The present sequence represents the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.

XX Sequence 846 AA:

Query Match 90.2%; Score 4269.5; DB 21; Length 846;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 835; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

DB 87 MSLLGKPLSTSSOSCRRVKKRRQNYLYNLEERGNAFYHAFVLLVFGCLISVF 146
 1 MSLLGKPLSTSSOSCRRVKKRRQNYLYNLEERGNAFYHAFVLLVFGCLISVF 60
 QY 147 STPEHTKLASSCLLLEFVIVFGLFETIRIMSGCCCRYGWOGRLFEARKPFQVID 206
 DB 61 STPEHTKLASSCLLLEFVIVFGLFETIRIMSGCCCRYGWOGRLFEARKPFQVID 120
 QY 207 TIVILASIAVYSAKTQGNIFATSLRLNFLQILRVNDRDRGCTWKLGSVYVAHSEL 266
 DB 121 TIVILASIAVYSAKTQGNIFATSLRLNFLQILRVNDRDRGCTWKLGSVYVAHSEL 180
 QY 267 ITAVYIGFLVLFSSFLVYVEKDKANKERSTADALMKGITLTITGGYGTPLTWIGRL 326
 DB 181 ITAVYIGFLVLFSSFLVYVEKDKANKERSTADALMKGITLTITGGYGTPLTWIGRL 240
 QY 327 LSAGFALLGISFFALPAGILSGFALKVQEHROKHFEKRRNPANLIGCVMSYADEK 386
 DB 241 LSAGFALLGISFFALPAGILSGFALKVQEHROKHFEKRRNPANLIGCVMSYADEK 300
 QY 387 SVSIAATKPKHKAHTGSPET-----NOKLSFRERVRMASPRGOSIKSRQASVGD 437
 DB 301 SVSIAATKPKHKAHTGSPET-----NOKLSFRERVRMASPRGOSIKSRQASVGD 360
 QY 438 SPSTDITAEAGSPKTVOKSWSFNDRTFRPRLSLKSSQRPVDAADALGTDVYDEKGCQ 497
 DB 361 SPSTDITAEAGSPKTVOKSWSFNDRTFRPRLSLKSSQRPVDAADALGTDVYDEKGCQ 420
 QY 498 CDVSVEDELTPPLKIVYAIRIMKRVAKRKEKRLPYDVYKVIQYISAGHLDMLCRIS 557
 DB 421 CDVSVEDELTPPLKIVYAIRIMKRVAKRKEKRLPYDVYKVIQYISAGHLDMLCRIS 480
 QY 558 LQTRVDIILKGQITSPDKSKREKITAHEHTDDLSMLGVYVVEKOVQSIESTLDDLDI 617
 DB 481 LQTRVDIILKGQITSPDKSKREKITAHEHTDDLSMLGVYVVEKOVQSIESTLDDLDI 540
 QY 618 YQOVLKRGASALALASFOIIPFECQTSYOSPYVDSKDLSSAONSGLSNSTANISR 677
 DB 541 YQOVLKRGASALALASFOIIPFECQTSYOSPYVDSKDLSSAONSGLSNSTANISR 600
 QY 678 GLOFILLPNEFSQTFALSPTHMSQATQVPISSOSGSAVAANTNTIANDINTAPKPAAPT 737
 DB 601 GLOFILLPNEFSQTFALSPTHMSQATQVPISSOSGSAVAANTNTIANDINTAPKPAAPT 660

QY 738 TLOIPPLPAIKHLPRPETHLPNPAIGLOESTDYVTCVASKENVOVQASNLTKDSMRK 797
 DB 661 TLOIPPLPAIKHLPRPETHLPNPAIGLOESTDYVTCVASKENVOVQASNLTKDSMRK 720
 QY 798 SFDWGGTLLSYCPMPVFKDLGKSLSYVNLIRSTEELINQIOLSSGSSGSGSODFYPKWR 857
 DB 721 SFDWGGTLLSYCPMPVFKDLGKSLSYVNLIRSTEELINQIOLSSGSSGSGSODFYPKWR 780
 QY 858 SKLFITDEEYGPETETDTPDAPQAPAREAPASDSLRTGRRSSQSICKAGESTDALSL 917
 DB 781 SKLFITDEEYGPETETDTPDAPQAPAREAPASDSLRTGRRSSQSICKAGESTDALSL 840
 QY 918 PHYKLK 923
 DB 841 PHYKLK 846

RESULT 12
 AAB01476
 ID AAB01476 standard; Protein: 695 AA.

AC AAB01476;

DT 08-NOV-2000 (first entry)

DE KCNQ4 Potassium channel protein.

KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
 death; probes; treatment; therapy; transgenic animal; antibody;
 agonist; antagonist; faintness; hearing loss; neonatal deafness;
 presbycusis; affective disorder; Alzheimer's disease; anxiety;
 ataxia; cognitive deficits; compulsive behavior; dementia;
 depression; Huntington's disease; mania; memory impairment;
 motor disorder; neurodegenerative disease; Parkinson's disease;
 Pick's disease; psychosis; schizophrenia; spinal cord damage;
 stroke; tremor.

OS Homo sapiens.

PN W0200044786-A1.

PD 03-AUG-2000.

PF 19-JAN-2000; 2000WC-DK00024.

PR 26-JAN-1999; 99DK-0000076.

PR 19-MAY-1999; 99DK-0000693.

PA (NEUR-) NEUROSEARCH AS.

PI Jentsch TJ.

DR WPI: 2000-548813/50.

XX N-PSDB: AAA47618.

PT Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
 PT useful e.g. for treating tinnitus, deafness, Alzheimer's and
 PT Parkinson's diseases

PS Claim 8; Page 48-51; 65pp; English.

CC Mutations in 3 known genes of the KCNQ branch of the potassium
 CC channel gene family underlie inherited cardiac arrhythmia's, neonatal
 CC epilepsy and in some cases associated with deafness. KCNQ4 has been
 CC mapped to the DFNA2 locus for autosomal dominant hearing loss, and
 CC a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
 CC pedigree has been identified. KCNQ4 is the first potassium channel
 CC gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
 CC channels with other KCNQ channel subunits, especially KCNQ3.
 CC Nucleotides encoding the KCNQ4 protein and the protein itself may be
 CC used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate KCNQ4 expression. The nucleotides may
 CC also be used as DNA probes in diagnostic assays (e.g. polymerase

CC chain reactions (PCR)) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function
 CC of KCNQ4 polypeptides and their role in metabolism, for example
 CC through the production of transgenic animals. The KCNQ4 polypeptides
 CC may be used as antigens in the production of antibodies and to
 CC identify modulators (agonists and antagonists) of KCNQ4 expression
 CC and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may
 CC also be used to down regulate KCNQ4 expression and activity. They may
 CC be used in this way to treat tinnitus, loss of hearing (especially
 CC progressive hearing loss), neonatal deafness and presbycusis
 CC (deafness of the elderly) and disease or adverse conditions of the
 CC central nervous system (CNS) such as affective disorder, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders and dysfunctions, motion disorders, motor disorders,
 CC neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
 CC disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
 CC cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
 CC molecules may be administered to down regulate KCNQ4 expression by
 CC binding with the cells own KCNQ4 genes and-preventing their
 CC expression.

CC Sequence 695 AA;

Query Match 42.1%; Score 1991; DB 21; Length 695;

Best Local Similarity 57.8%; Pred. No. 8,1e-165;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

25 AAGGGRGSGMKVSGRGRVLLNSAARGDILLGTRAAITLGGGGGLRESRKGOG 84
 DB | | | | | : : : : : | | | | |
 2 AEAAPRRLGLGPPGADARAEVLAITAVOSEG-----EAGGGGSPR----- 43
 QY | | | | | : : : : : | | | | |
 85 ARMSLGLKPL-----SYSSQSCRNVKRYRVOVLYLVLEPRGAFIT 130
 DB | | | | | : : : : : | | | | |
 44 -RLGLLSPLPGAPLPFGSGSGSACGCRSSAAKRRYRLONWVYVLERPGMAFYVH 102
 QY | | | | | : : : : : | | | | |
 131 AFVFLVAGCLILVSTIPEHTKLASSCLILEFVMTVFGLEFIRIRMSAGCCCRYG 190
 DB | | | | | : : : : : | | | | |
 103 VFIFLVFSCVLTSTIQEHLANECLILEFVMTVFGLEFIRIRMSAGCCCRYG 162
 QY | | | | | : : : : : | | | | |
 191 WGRRLRFARKEPCVDTIVLTIASIVASAKTOGNIFFATSLRLRLQILIRVMRDRG 250
 DB | | | | | : : : : : | | | | |
 163 WGRFRFRARKEPCVDTIVLTIASIVASAKTOGNIFFATSLRLRLQILIRVMRDRG 222
 QY | | | | | : : : : : | | | | |
 251 TWKLLGVSVAHAKSKELITAWYIGFLVLFSSFLVYLVKEDANKESSTYDALMWTITLT 310
 DB | | | | | : : : : : | | | | |
 223 TWKLLGVSVAHAKSKELITAWYIGFLVLFSSFLVYLVKEDANKESSTYDALMWTITLT 282
 QY | | | | | : : : : : | | | | |
 311 TIGGDKPLTWLWGLLISAGFALLGISFPALPAGILISGFALKVORHOKHKEKRNP 370
 DB | | | | | : : : : : | | | | |
 283 TIGGDKPLTWLWGLLISAGFALLGISFPALPAGILISGFALKVORHOKHKEKRNP 342
 QY | | | | | : : : : : | | | | |
 371 ANLIQCVRSYAAD-EKSVSIATW----- 393
 DB | | | | | : : : : : | | | | |
 343 ANLIQCVRSYAAD-EKSVSIATW----- 393
 QY | | | | | : : : : : | | | | |
 394 -----KPHLAKLHT-----CSPTNOKLSFKRRVMAASRGOSISRQ--ASVGR 436
 DB | | | | | : : : : : | | | | |
 403 PVPDGPAPSRYPVAVACHRPSTSPFCGESSRMGIKIRIRGSSQRTGEPKQDLAPPTMP 462
 QY | | | | | : : : : : | | | | |
 437 RSPSTDIATAG-SPTKVOKSMGFNDTRPRPSLRKSSQPRVIDATGALDQVYVEKG 495
 DB | | | | | : : : : : | | | | |
 463 TSPSEQYGEATSPKVKOKSMGFNDTRPRPSLRKSSQPRVIDATGALDQVYVEKG 516
 QY | | | | | : : : : : | | | | |
 496 CQCDVSVEDLPPLTVINAIRIMKFRVAKRKEKTLRPYDVADVTEQYSAGHLMLCRI 555
 DB | | | | | : : : : : | | | | |
 517 YQCELTVDDIMPAVTVIRISIRIKFLVAKRKEKTLRPYDVADVTEQYSAGHLMLCRI 576
 QY | | | | | : : : : : | | | | |
 556 KSLQTRVDDIILKGQITSPKKSRE---KTAHEHTDDLSMLGRVYKVEQVOSTIEKLD 612
 DB | | | | | : : : : : | | | | |

DB 577 KSLQTRVDDIIVGNG--PGGRKAREKDGKPSDAEVEVDISEMGRVYKVEQVOSTIEKLD 634
 QY 613 CLLDIYQOYLKRGKSASALATASFOIPPEEQTSDYQSPYDSKDLGSAQNSGLSRSTS 672
 DB 635 LLIGFISRLSRISTSA--SLGAVQVPLFDDIISDHPDHEDISVSAQTLISRSVS 691
 QY 673 ANI 675
 DB 692 TNM 694
 RESULT 13
 AAEL6621
 ID AAEL6621 standard; Protein: 695 AA.
 XX AAEL6621.
 AC
 DT 09-APR-2002 (first entry)
 XX
 DE Human potassium channel polypeptide, KCNQ4.
 KW Human: potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neuropsychological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; KCNQ4 protein;
 KW hearing loss.
 XX
 OS Homo sapiens.
 XX
 PN W0200192526-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17314.
 XX
 PR 26-MAY-2000; 2000US-207389P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;
 XX Gribockoff VK;
 XX
 DR WPI: 2002-122069/16.
 XX
 XX Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
 PT it, for diagnosing, treating and identifying modulators useful in
 PT treating neurological, neuropsychological and neuropsychological
 PT diseases
 PS
 PS Disclosure: Fig 5; 128pp; English.
 XX
 CC The invention relates to potassium channel polypeptides referred to
 CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
 CC polypeptides are useful for identifying compounds that modulate their
 CC biological activity. The compounds identified and KCNQ5 polynucleotides
 CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for treating neuropsychological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease

CC tissues or cells. The present sequence is human KCNQ4 protein.
 CC Mutations in this protein is associated with particular disease
 CC e.g. hearing loss.
 CC XX

SO Sequence 695 AA:

Query Match 42.1%; Score 1991; DB 23; Length 695;
 Best Local Similarity 57.8%; Pred. No. 8,1e-169;
 Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

```

QY 25 AAAGGRLGSGMKDVEGSGRVLNSAARGDGLLIGTRAATLGGGGGLRESRRKOG 84
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 2 AEAARRRIGLGPDPDAPRAELVALTAVOSEOG-----EAGGSGSPR----- 43
QY 85 ARMSLLGKPL-----SYTSSQSCRNNKYRVQVLYNVLERPRGMATYH 130
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 44 -RLDLLSGPLPGGAPLPBGSGSGSAGGORSANHRRLQWVNVLEPRGMATYH 102
QY 131 AFVELVFGCLILSVSTIPEHTKLASSCLLLEFVMIIVFGLEFIIRISAGCCCRYRG 190
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 103 VFIFLVFSCIVLAVSTIOHELANECLLLEFVMIIVFGLEFIIRISAGCCCRYRG 162
QY 191 WQGLRFRARPCVYDITVLASINAVSAKTGNTFATSLNSLRFLLQILRMVMDRRGG 250
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 163 WQGFRRARPCVYDITVLASINAVSAKTGNTFATSLNSLRFLLQILRMVMDRRGG 222
QY 251 TWKLLGSVVAHSEKELTAWYIGFLVLFSSFLVYVEVDANKFESTYDALMNGTTLT 310
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 223 TWKLLGSVVAHSEKELTAWYIGFLVLFSSFLVYVEVDANKFESTYDALMNGTTLT 282
QY 311 TIGGDKTPTLWLGRLLSAGFALLGISFPALGILSGFALKVQDQHRKHFEKRRNPA 370
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 283 TIGGDKTPTLWLGRLLSAGFALLGISFPALGILSGFALKVQDQHRKHFEKRRNPA 342
QY 371 ANLIQCVWRSYAAD-EKSVSIATM----- 393
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 343 ANLIQCVWRSYAAD-EKSVSIATM----- 393
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 394 -----KPHKALHT-----CSPYNOKLSFEKERVMAASPRGOSIKSRQ--ASVGD 436
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 403 PVPDGAPSRPVATVCHRPSTSCPGSSRMGINDRIMGSSQRTGSGKQALPPTMP 462
QY 437 RSPSTDTIAG-SPTKQKSSFNDRTRFRSLKSSQPKVVDADTALGTDVYDEKG 495
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 463 TSSSEVGATSPSTKQKSSFNDRTRFRSLKSSQPKVVDADTALGTDVYDEKG 516
QY 496 CQCDVSEDELTPLKTYIRATIRIKMFHAKRFEKTLRPYDKVDEOYSAGHLMICRT 555
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 517 YQGLVYDDIMPAVKYIRISIRILKFLVAKKFKETLRYDKVDEOYSAGHLMICRT 576
QY 556 KSLQTRVDQILGKQITSDKRSRE--KITAEHETTDLSMLGRVYKVEKQVOSIESKID 612
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 577 KSLQTRVDQILGKQITSDKRSRE--KITAEHETTDLSMLGRVYKVEKQVOSIESKID 634
QY 613 CLVDIYQVARKSASALASFOIPPEECQTSYQSPVDSKIDSGAQNKGCLSRSTS 672
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 635 LLLGFTSRCLRSQTS--SLGAVQVPLEDPDITSDYHSPVHEDITSVSAQTLS--ISRSYS 691
QY 673 ANI 675
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 692 TNN 694

```

RESULT 14

ID AAE16619 standard; Protein: 844 AA.

AC AAE16619;

DT 09-APR-2002 (first entry)

DE Human potassium channel polypeptide, KCNQ2.

KW Human: potassium channel polypeptide: KCNQ5; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neuropsychological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; KCNQ2 protein.

OS Homo sapiens.

PN MO200192526-AL.

PD 06-DEC-2001.

PF 24-MAY-2001; 2001MO-US17314.

PR 26-MAY-2000; 2000US-207389P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Dworesky SI, Ramanathan CS, Trojacek JT, Boisard CG;
 PI Gribkoff VK;

DR WPI: 2002-122069/16.

PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
 PT it, for diagnosing, treating and identifying modulators useful in
 PT treating neurological, neuropsychological and neuropsychological
 PT diseases

PS Example 1; Fig 5; 128pp; English.

CC The invention relates to potassium channel polypeptides referred to
 CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
 CC polypeptides are useful for identifying compounds that modulate their
 CC biological activity. The compounds identified and KCNQ5 polynucleotides
 CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for treating neuropsychological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease
 CC tissues or cells. The present sequence is human KCNQ2 protein.
 CC Mutations in this protein is associated with particular disease
 CC e.g. epilepsy.

CC Sequence 844 AA:

CC XX

SO Query Match 37.9%; Score 1793; DB 23; Length 844;
 SO Best Local Similarity 48.2%; Pred. No. 6,1e-151;
 SO Matches 411; Conservative 92; Mismatches 195; Indels 154; Gaps 25;

```

QY 21 GAAAAAGGRLGSGMKDVEGSGRVLNSAARGDGLLIGTRAATLGGGGGLRESRR 80
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 9 GVPYGPSEKELTKVFGVLDPA-----PDSTRGALLIAGSEAK--RGSILSKPRA 59
QY 81 GKQARMSLLGKPLSYTSSQCRNNKYRVQVLYNVLERPRGMATYHAFVLLVFGC 140
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 60 GGAGA-----GKP-----PKRNAFYKRLQNFLYNVLEPRGMATYHAFVLLVESC 106
QY 141 LILSVFTIPEHTKLASSCLLLEFVMIIVFGLEFIIRISAGCCCRYRGMGRRLRARK 200
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 107 LVLSVFSTIKYKESSEGALYILETVTVFVEVEFVRIMAGCCCRYRGMGRRLRARK 166

```


QY 201 PCVIDITVLIASTAVSAKTGNIATFATSLRLEFLOILRMVRRDRRGTKLLGSVY 260
 DB 167 PCVIDITVLIASTAVSAKTGNIATFATSLRLEFLOILRMVRRDRRGTKLLGSVY 226
 QY 261 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 286
 QY 321 TWIGRLLSAGFALLGISFFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCWRS 380
 DB 287 TWNGRLLAATFTLLIGVSPFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCWRS 346
 QY 381 YAAD-----EKSVAIATWK--PHLKALHTC-----SPT 406
 DB 347 YATNLSRDLHSTWQYERTVTPMRLPLPNOLELRLNLKSKSGILTRKROPPPEPSP- 405
 QY 407 NOKLSFERVMAASPRGOSIKRSQASVGD--RRSPSTDTAEGSPTRKVSMSFNDRTRE 464
 DB 406 SOKVSLKDRV-FSSPRGMAAKGSPQAOVTRSPADSLDPSKVKPSWFGDRSRA 464
 QY 465 RPSLRKSSQPKPVADATLCTDGVYDEKGCOCVSVEDLPPPLKTVIRAIRIMFHYA 524
 DB 465 RQAFRIKGAASRQNSE-EASLPEGEDIYDKSCPEFVEDLPPGLKVSIRAVCMRFLVS 523
 QY 525 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGQOITSDKRSREKITA 584
 DB 524 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGQOITSDKRSREKITA 582
 QY 585 HETTDLSMLGRVYKVOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPPEC-- 642
 DB 583 AELPEDPMGMRLGKVEKQVLSMEKKLDPLVNIYMQ--RMG-----IPPETEA 629
 QY 643 -----EQTSPYQSPVDSKDLSSGSAQNSGCLSRISANISRLQFILIPNESAOFTYA 695
 DB 630 YFAGKEPPAPPYHSPEDSR--HYDRHGCTVKKIVRSSSTG-----QKNASAP- 678
 QY 696 LSPTHMSOATGVPIOS-----DGSAAVTNTITANOINTPAKPAAPPTLOI----- 741
 DB 679 APP-----VQCPSTSMQPOSHPRQGHGTSIPVGDHLSIVRIPPAHERSLAYGGGNR 732
 QY 742 -----PP-----PLPAIKHLPRPETLHPNPAAGLOESISDVTCL 775
 DB 733 ASMEFLROEDPRGCRPEGLTRDSPTISIPSYDH-----EELERSFSGF--SISQ----- 781
 QY 776 VASKENNOVAOS 787
 DB 782 --SKENDALNS 791
 RESULT 15
 ID AAY01530 standard: Protein: 722 AA.
 AC AAY01530:
 XX
 DE 16-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of murine KCNQ2/KvLRI.
 XX
 KM KCNQ protein; nervous system-specific potassium channel;
 KM neuronal excitability; neurotransmitter release; KCNQ modulator;
 KM ataxia; myokyma; seizure; Alzheimer's disease; Parkinson's disease;
 KM age-associated memory loss; learning deficiency; motor neuron disease;
 KM epilepsy; stroke.
 XX
 OS Mus sp.
 XX
 PN WO9907832-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 26-JUN-1998; 98WO-US13276.
 XX

PR 12-AUG-1997; 97US-0055599.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Blananar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 PI Little WA, Neubauer MG, Yang W;
 XX
 DR WPI: 1999-190047/16.
 DR N-PSDB: AAX26588.
 XX
 PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
 PS
 PS Claim 4; Fig 10A-D; 6app; English.
 XX
 CC The present sequence represents murine KCNQ2/KvLRI. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokyma, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.
 XX
 SQ Sequence 722 AA;
 Query Match 37.9%; Score 1792.5; DB 20; Length 722;
 Best local similarity 53.4%; Pred No 5.2e-151;
 Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;
 QY 21 GAAAAAGGGRIGSGMKDVESGRGVLLNSAARDGILLGTRATLGGGGGGRRESRR 80
 DB 9 GYVGTSGEKKLKVGFGLDPCA-----PDSTRGALLILIASAPK--RGSVLSKPRPT 59
 QY 81 GKQGRMSLKGKPLSTSSQCRNRYKTRVNYLYNVEERRRGAFTIHAFFLLVFGC 140
 DB 60 GGAGA-----GKP-----PKRNAFYKLIQNFYLVNERPRGMAFTIHAFFLLVESC 106
 QY 141 LILSVFTIPHTKLASSCLILEFMYVFGLEFIRISAGCCCRYGWGRFLPARK 200
 DB 107 LVLSVFTIKEREKSEGALEYLTIVTIVFGEVFRVMAAGCCCRYGWGRFLPARK 166
 QY 201 PCVIDITVLIASTAVSAKTGNIATFATSLRLEFLOILRMVRRDRRGTKLLGSVY 260
 DB 167 PCVIDITVLIASTAVSAKTGNIATFATSLRLEFLOILRMVRRDRRGTKLLGSVY 226
 QY 261 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 286
 QY 321 TWIGRLLSAGFALLGISFFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCWRS 380
 DB 287 TWNGRLLAATFTLLIGVSPFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCWRS 346
 QY 381 YAAD-----EKSVAIATWK--PHLKALHTC-----SPT 406
 DB 347 YATNLSRDLHSTWQYERTVTPMRLPLPNOLELRLNLKSKSGILTRKROPPPEPSP- 405
 QY 407 NOKLSFERVMAASPRGOSIKRSQASVGD--RRSPSTDTAEGSPTRKVSMSFNDRTRE 464
 DB 406 SOKVSLKDRV-FSSPRGMAAKGSPQAOVTRSPADSLDPSKVKPSWFGDRSRT 464
 QY 465 RPSLRKSSQPKPVADATLCTDGVYDEKGCOCVSVEDLPPPLKTVIRAIRIMFHYA 524
 DB 465 RQAFRIKGAASRQNSE-EASLPEGEDIYDKSCPEFVEDLPPGLKVSIRAVCMRFLVS 523
 QY 525 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGQOITSDKRSREKITA 584
 DB 524 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGQOITSDKRSREKITA 582
 QY 585 HETTDLSMLGRVYKVOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPPEC-- 642
 DB 583 TELPEPDMGMRLGKVEKQVLSMEKKLDPLVNIYMQ--RMG-----IPPETEA 629

OY 643 -----EQTSYQSPVDSKDLSSAONSGC---LSRSTSANISRGLOFILTPNESAO 692
 DB 630 YFGAKPEEPAPYPHSPEDSRD---HADKHGCIIVRSTSS-----TGCR 671
 OY 693 FYALSPTHMSQATQVPIPSOS 712
 DB 672 NYAAPPAI--PPAQCPEPSTS 689
 RESULT 16
 ABG10644
 ID ABG10644 standard; protein; 912 AA.
 AC ABG10644;
 XX 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #10635.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS74831.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS
 PS Claim 20; SEQ ID No 41003; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of drugs and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SX Sequence 912 AA;
 Query Match 37.8%; Score 1790.5; DB 22; Length 912;

Best Local Similarity 47.7%; Pred. No. 12e-150;
 Matches 411; Conservative 91; Mismatches 196; Indels 164; Gaps 25;
 OY 21 GAAAAAGGGLGSGMKDVEGRGRVULNSAARGDGLLTGTAATLGGGGGLRESRR 80
 DB 67 GYPPGSPGEEKLKVGFGVLDPGA-----PDSIRGALLIAGSEAK---RGSILKPR 117
 OY 81 GKQAGMSLCKPLSTYSQSCRNVKRRVQNYLYNLERGRGAFYTHAFVLLVFGC 140
 DB 118 GGAGA-----GKP-----PKRNFYRKLNFLNLYLERPRGMFIYHAYVFLVFC 164
 OY 141 LILVFSTIPEHTKLASSCLLILEFVMTVEFGLFIRITWMSGCCCRYGMGRLEFAR 200
 DB 165 LVLSVFSTIEKESSEBGLATILEVTIVGVEFVRMAAGCCCRYGMGRLEFAR 224
 OY 201 PCFVIDITVLIASTAVVSAKTQGNIFATSLRFLQILRMVRRDRGTGKLLGSVY 260
 DB 225 PCFVIDIMVLIASTAVVLAAGSQGNVFAFSALRSLRFLQILRMVRRDRGTGKLLGSVY 284
 OY 261 AHSKELITAWYIGFLVIFSSFLVYVKEKANKESTYADALMNGTITITIGYGTPL 320
 DB 285 AHSKELITAWYIGFLVIFSSFLVYVKEKANKESTYADALMNGTITITIGYGTPL 344
 OY 321 TWLGRLLSAGFALLGISFALPAGILGSGFALKVQEOGRKHFEKRRNPANILQVMS 380
 DB 345 TWNGRLLAATFTLIGVFEFALPAGILGSGFALKVQEOGRKHFEKRRNPANILQVMS 404
 OY 381 YAAD-----EKSYIATWK-----PHLKALHTC----- 403
 DB 405 YATNLSRTDLSHWYERYTVPVMSQOTYGSRLPLPLQDELRLNLKSGSLAR 464
 OY 404 -----SPTNOKLSFKERYMASPPROGSIKRSROASVGD--RRSPDTITAGSPKRYOK 454
 DB 465 KOPPEPESP-SQAVSLKDRV-FSSPRGVAAGKSSPAQATVRRSSAQSLEDSKVPK 522
 OY 455 SMSFNDTRFRPRLRLKSSQPKPVYIDATLGTVDYDEKQCQCDVSVEDLPPPLKTVR 514
 DB 523 SMSFGDRSRAKQAFRIKGAASRQNSE-EASLPGEDIVDKSCPEFVEDLTPGLKVSIR 581
 OY 515 AIRIMKEHVAKRKFKETLRPYDVYDEYVSAGHLMDCIRKSLQTRDOILGKQITSD 574
 DB 582 AYCVMRFVLSKRFKESLRPYDVMDVLEQYSAGHLMDSIRKSLQTRDOILGKQITSD 641
 OY 575 KKSREKITAHEHTDLSMLGRVYVKEQVQISKLDCLDIYQOVLKGSASALALAS 634
 DB 642 -KDRTKGPAEALPEPDSMGMRLGKVKQVLSMEKIDFLVNIYMQ--RMG----- 689
 OY 635 FQIPPEEC-----EQTSYQSPVDSKDLSSAONSGCLSRSTSANISRGLOFILTP 685
 DB 690 --IPPEETAVYFGAKPEEPAPYPHSPEDSRD---HYDRHGCIIVRSTSSSTG-----Q 738
 OY 686 NEFSAQTFYALSPTHMSQATQVPIPSOS-----DGSAAVATNTIANQINAPAPAPT 737
 DB 739 KNFSAPP--AAP-----VQCPSTSWQPSHRQGHGSPVDGHSVNIIPPAHHR 790
 OY 738 TLQI-----PP-----PLPAIKHLPRPETHLPAPLQ 765
 DB 791 SISAVGGGNRASMEFLRQEDTPGCRPEPTLRDSDTISIPSVH-----ELHNSFSGF 845
 OY 766 ESISDYTTLVASKEWVAQS 787
 DB 846 -SISQ-----SKENLDALINS 859
 RESULT 17
 AA08347
 ID AA08347 standard; protein; 930 AA.
 AC AA08347;
 XX 22-JUL-1999 (first entry)
 XX
 DE Human mutant KCNQ2 protein.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Blannar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 XX Little WA, Neubauer MG, Yang W;
 XX MPI: 1999-190047/16.
 XX N-PSDB; AAX26587.
 XX
 XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 XX neurotransmission and neuroprotection, used to treat, e.g. ataxia
 XX
 XX Claim 2: Fig 2: 6pp; English.
 XX
 XX The present sequence represents human KCNQ2/KVLRI. KCNQ proteins are
 XX nervous system-specific potassium channels. In neurons, potassium
 XX channels regulate neuronal excitability, action potential shape
 XX and firing pattern, and neurotransmitter release. KCNQ modulators
 XX may be used to treat disorders such as ataxia, myokymia, seizures,
 XX Alzheimer's disease, Parkinson's disease, age-associated memory
 XX loss, learning deficiencies, motor neuron diseases, epilepsy, and
 XX stroke.
 XX
 XX Sequence 871 AA:
 SQ
 Query Match 37.8%; Score 1788.5; DB 20; Length 871;
 Best Local Similarity 46.8%; Pred. No. 1.6e-150;
 Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;
 21 GAAAAAGGGRGSGMKDVGSGRVLLNAAAGDGLLLGTAAATLGGGGGCGGRESRR 80
 9 GYPPSPGSKKLVGFGVGDPCA-----PDSTRDGLALTAGSEAPK---RGSILSKPRA 59
 81 GKQAGMSLLGKPLSYTSSQSRNRYKRVQMYLVNLEPRGMAFYHAFFVLVFGC 140
 60 GGAGA-----GKP-----PKRNAFYRLQNFIVNLEPRGMAFYHAFFVLVFGC 106
 141 LILSFTITPEHTKLASSCLLIEFYMIYVFGLEFTRIMSAGCCCRYGKQGRLEPARK 200
 107 LVLSFTIKEKESSEKALYLTLYIVFVGEYFVRIMAAAGCCCRYGKGRLEPARK 166
 201 PCVADITVLILSIIVASAKTGNIFATSLRLSLRFLQILIRMYMDRGGKWLGLSVY 260
 167 PCVADITVLILSIIVASAKTGNIFATSLRLSLRFLQILIRMYMDRGGKWLGLSVY 226
 261 AHSKELTAWYIGFLVLFSEFLVLYVERDANKFEFTYADALWGTTLTIGYGDXTPL 320
 227 AHSKELTAWYIGFLVLFSEFLVLYVERDANKFEFTYADALWGTTLTIGYGDXTPL 286
 321 TWLGRLLSAGFALLGISFPALPAGILGSGFALKVOQHQRKHEKRRNPAANLIQCVWRS 380
 287 TWNGRLATFTLLIGVSPFALPAGILGSGFALKVOQHQRKHEKRRNPAANLIQCVWRS 346
 381 YAAD-----EKVSIAITWK-----PHLALHT----- 402
 347 YATMLSRITDLSTWQYERTVAVPMYSSQTYTGASRLPLPMLDELRLMLKSKSGIAFR 406
 403 -----CSP--TNOKLSFEKERYRNASPPGQSTIKSROASVD--RR 437
 407 KDPPEPSPSKSGPCRGPLCGCCPGRSQKVSILKDRV-FSSPGVAAKAGSGPOAQVRR 465
 438 SPSVDITAEQSPPTKOKSMFMDRTFRPSRLKSSQRPVIDADNALGDDVYDEGCQ 497
 466 SPSADQSIEDSPSKPKMSFQDRRARQAFRIKGAASQ--NSEASLPDEDIVDDKSCP 523
 498 CDVSEVEDLTPPLKTVIRAIRIMKFFVARKKFEETLRLPYDVKDIIEQYSAGHLMCRITS 557
 524 CEFTVEDLTPGLKTVIRAVCWRLFLVSKRKESLRLPYDVYMDVIEYSAGHLMCRITS 583
 558 LQTVNDQILGQGITSDKSKREKITAHEHTDLSMLGNVAVKEKOVOSTESKLDCLDT 617
 584 LQSRVDQIVGPAITD-KDRTKGPAAEALPEDPSMMGRIGLKEKVOVLSMEKKLDFLNI 642

QY 618 YQVLRKSGASALALASFOIPPEEC-----EOTSQSPVDSKDLSGSANGCGLS 668
 DB 643 YMQ--RNG-----IPPTETEAIFGAKEPEPAPRYHSPEDSRE--HYDRRGCIY 686
 QY 669 RSTSANISRGIOFLTPNEFSAQTFYALSPTHMSQATQVPIQS-----DGSAYVAP 720
 DB 687 KIVRSSSSSTG-----QKNFSAP--AAP-----VCCPSTSMQPSQHRGCHGSPV 732
 QY 721 NTIANQINTAPKPAAPTLQI-----PP-----FLPAL 748
 DB 733 GDHSLVRIPPPAPHENLSAYGGGNRASMELRQEDPPGCRPEGTLDSDTSISIPV 792
 QY 749 KHLPRPETLHPNPAQLOESISDVITCLVASKENVOAQS 787
 DB 793 DH-----ELERSFSGF--SISQ-----SKENLDALNS 818
 RESULT 19
 ABG10643
 ID ABG10643 standard; Protein; 914 AA.
 AC ABG10643;
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #10634.
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN MO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001MO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HSE-) HYSBQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR MPI: 2001-693362/73.
 DR N-PSDB; AAS74830.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX
 XX Claim 20: SEQ ID NO 41002; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridization probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. ABG00010-ABG30377 represent novel human
 XX diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 914 AA:

Query Match 37.8%; Score 1788.5; DB 22; Length 914;

Best Local Similarity 45.6%; Pred. No. 1.7e-150; Indels 199; Gaps 27; Matches 420; Conservative 91; Mismatches 211;

```

QY 2 PRHAGGEEGAGAGIWM-----VKSAAAAAGGRLGSGMKDVEGSGRGLVLSA----- 51
DB 5 PPRCGSGRPGGLG--WGRRRPRRSAPAPPEPDGRLPQGTWQKSNNGCVYGPSEKKL 62
QY 52 -----AARGDCLLLGTRAAATLGGGGGLRESRGGKOGARMSLLGKPLSYTS 98
DB 63 KVGFGVLDPGAPADSTRDGLALLIAGSEAPK---RGSILSKPRAGAGAG-----GKP----- 109
QY 99 SSGSRANRYKRYOVYLYNVLERPRGMAFIYHAFVLVFGGLIISVFSTIPEHTKLASS 158
DB 110 ---PKRAFYKFLQVLYNVLERPRGMAFIYHAFVLVFGGLIISVFSTIPEHTKLASS 166
QY 159 CLILFEYVIVFGLFIIRIWSAGCCCRYRGMOGRLEPARKPCVYIDTVLLASIAVVS 218
DB 167 ALYILEIYIVFVGEYEVRIWAGCCCRYRGMRGRLEPARKPCVYIDTVLLASIAVLA 226
QY 219 AKTQGNITATSLRLRLQILIRMYRMDRGSTWKLISVYVAHSELTAWYIGFLVLI 278
DB 227 AGSGGNVATSAFLRLRLQILIRMYRMDRGSTWKLISVYVAHSELTAWYIGFLVLI 286
QY 279 FSSFLVYVVEKDANKEFSTYADALMWGTTTLTIGYDGTPLTWLGLRLSAGFALLGISF 338
DB 287 LASFLYVLAEGENHFDYADALMWGLTTLTIGYDGTPLTWLGLRLSAGFALLGISF 346
QY 339 FALPAGILGSGFALVQEOHROKHFEKRRNPAANLIQCYWRSTYAD-----E 385
DB 347 FALPAGILGSGFALVQEOHROKHFEKRRNPAANLIQCYWRSTYAD-----E 406
QY 386 KSVSIATATK-----PHIKALHT----- 402
DB 407 RTVYPMYSSQOTYVYASRLPLPLNOLLELRNLKSKSGLAFFKDPPEPSFGSGPCRCR 466
QY 403 ---CSP--TNOKLSFEREYRMAAPRQOSIKSRQASVGD--RSPSPTDTAEGSPTRVQKS 455
DB 467 LCGCCPGRSQKVKSLKDRY-FSSPRGVAAKKGSPQAQYVRRSPASQSLSDSPSKVPS 525
QY 456 WSENDTRPRPSRLKSSQPKPYIADTALGTDVYDEKCCQCDVSEDTLPPLKTYIRA 515
DB 516 IIRKMFHAKRKKEFTLRPYDVYDEYQYSGHLMICRKSLOTRVDOILLGKQIISDK 575
QY 555 VCVMEFLVSKRKFKESLRPYDVYDEYQYSGHLMISRKISQSRKQDQVGRPALTD- 643
DB 576 KSRKRTAHEHTTDLISMLGRVYVYKQVQIESKIDCLLDIYQVLRKKSASALALASF 635
QY 644 KORTGPAPAELEPDEPSMGRGKVEKQVLSMEKIDELVINYIMQ--RMG----- 691
QY 636 QIIPPEEC-----EOTSQVQSPYDSKNDLSSAQNQSGLSSTANISIRGLFIILPN 686
DB 692 -IIPPEYEAPEGAKEPEPAPYPHSPEDSRK---HVDHGGIVIKVIRSSSG---OK 741
QY 687 EFSAGTFYALSPTMHSQATOVPISSQ-----DGSANVATNTIANDINTAPKPAFTT 738
DB 742 NNSAPP--AAPP-----VQCPSTSMQPSHPRQGHGTSRPGVGHSLVIRPPPAHRS 793
QY 739 LQI-----PP-----PLPAIKLPPPELTHPPACIQE 766
DB 794 LSAVGGNRAEMFLRQEDTPGCRPEGNLRDSDTISISPSVDH-----EELERSFSG-- 847
QY 767 STSDVTTCLVASKENOVQAS 787
DB 848 STSQ-----SKENDALNS 861

```

RESULT 20

AAV23215

ID AAV23215 standard; Protein: 854 AA.

AAV23215;

25-AUG-1999 (first entry)

Human brain-derived potassium channel protein.

Human; brain-derived potassium channel; neurophysiology;
 cognitive disorder; behavioural disorder; psychiatric disorder;
 neurodegenerative disorder; developmental disorder; mental retardation;
 autism; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
 Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 amyotrophic lateral sclerosis; retinitis pigmentosa;
 cerebellar degeneration; urinary incontinence; diabetes; asthma;
 premature labour; hypertension; cardiac ischemia; arrhythmia;
 autoimmune disease; cancer; graft rejection; inflammation; allergy;
 proliferative disorder; anaemia; autoimmune disease;
 type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 Sjogren's syndrome; mixed connective tissue disease;
 experimental allergic encephalomyelitis; rheumatoid arthritis.

Homo sapiens.

W09931232-A1.

24-JUN-1999.

11-DEC-1998; 98WO-GB03720.

13-DEC-1997; 97GB-0026339.

(ZENEC) ZENEC LTD.

Allyer J, Christian EP, Iannotti CA, Logsdon NJ;

WPI: 1999-395178/33.

N-PSDB; AAX81547.

New isolated potassium channel polypeptide

Claim 6; Fig 3; 151pp; English.

The present sequence represents a human brain-derived potassium channel.
 The polynucleotides and polypeptides can be used for identifying
 compounds that modulate the biological activity of a potassium channel
 or neurophysiology. It is used as a method of treatment for patients
 with conditions which are mediated by the biological activity of a
 human potassium channel. Antagonists can be used in modulating cognitive,
 behavioural, psychiatric, neurodegenerative and developmental disorders
 (mental retardation) as well as asthma, migraine, epilepsy and stroke
 and brain tumours. They can be used for treating diseases such as
 Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 autoimmune diseases, cancer, graft rejections, acute and chronic
 inflammation, allergies, proliferative disorders, anaemias,
 neurodegenerative diseases with immunological components, as well as
 autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 syndrome, mixed connective tissue disease, and experimental allergic
 encephalomyelitis (EAE).

Sequence 854 AA:

Query Match 37.7%; Score 1786; DB 20; Length 854;
 Best Local Similarity 47.7%; Pred. No. 2.6e-150;
 Matches 411; Conservative 91; Mismatches 196; Indels 164; Gaps 25;

```

QY 21 GAAAAAGGRLGSGMKNKDVESGGRVYLNLSAARGDCLLLGTRAAATLGGGGGURESR 80
DB 9 GYPPSPSGEKKLVGFGVLDPCA-----PDSTRDGLALLAGSAPK---RGSILSKRA 59
QY 81 GKGARMSLLGKPLSTSSOSCRNRYKRYVQNTLYVLERPRGMATYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRLQNFNLVLEPRGMATYHAYVLLVFGC 106
QY 141 LILSVFTIPRHTKLASSCLLLEFVMIYVGFLEFIRMSAGCCCRGMRGRLRPAK 200
DB 107 LVLVSFTIKEYEKSEGLATILEIYTYVGEYEFRIYAAAGCCCRGMRGRLRPAK 166
QY 201 PCVVDITVLIASIVASAKTOGNIATSLRSLRFLQILRMVMDRGGTWMKLLGSVY 260
DB 167 PCVVDIIVLIVASIVLAAGSOGNVPATSLRSLRFLQILRMVMDRGGTWMKLLGSVY 226
QY 261 AHSKELTAWYIGFVLIFSSFLVYLVENDANEFSTYDALMWGTTTLTIGYDKTPL 320
DB 227 AHSKELTAWYIGFVLIFSSFLVYLVENDANEFSTYDALMWGTTTLTIGYDKTPL 286
QY 321 TWLGRLLSAGFALLGISFPFALPAGILSGFALKVQDQHRKHFEKRRNPANLQCVWRS 380
DB 287 TWNGRLAATFTLLIVSFPFALPAGILSGFALKVQDQHRKHFEKRRNPANLQCVWRS 346
QY 381 YAAD-----EKSVSIATWK-----PHLKALATC----- 403
DB 347 YATMLSRITDLSTWQYERTVIVPMYSQTYGASRLPLNQLLELLRLKSKSGLAFR 406
QY 404 -----SPTNOKLSFKERVNRASPRGOSIKSKQASVGD--RSPSPDITAEGETVYOK 454
DB 407 KDPPEPSP-SQKSLKDRV-FSSPFGVAAKGGSSQAOQTVRSKSDQSLSDSPSKVPK 464
QY 455 SMSFNDRTRFRPSRLKSSQPRVIDADATLGDYDYDEKQCCQDVSEDLTPPLKVIYR 514
DB 465 SMSFGDSRRAQAFRIKGAASRQNSE-EASLPGEDIVDDKSCCEFTEDTLPLKAKSIR 523
QY 515 AIRIMKFPVARKKPEETLRPYVQVYIEQYSAGHLDMLCRIKSLQTRVQDILKGQITSD 574
DB 524 AVCYMRFLVSKRKESLRPYDVMDVIEQYSAGHLDMLCRIKSLQSRVQDILKGQITSD 583
QY 575 KKSREKTAHEHTDDLSMLGRVYVKEKQVQSIKSLDCLLDYQVLRKGSASALALAS 634
DB 584 -KDRTKGPAEALPEDPFSMGRGLKVEKQVLMKELDLVNTYMQ--RMG----- 631
QY 635 FQTPPEFC-----EQTSDYQSPVDSKDLSGSAGNSGCSRSSTANISRLQITLTP 685
DB 632 --IPTELEAYFGAKPEPPAPYHSPEDSR--HYDRHGCIYKIVRSSSTG-----Q 680
QY 686 NEFSAQTFYALSPYHMSQATQVPISS-----DGSVAANTNTIANQINTAPKPAAP 737
DB 681 KNFSAPR--AAPP-----VOCFPTSMQPOSHPRQGHGTSVGDHGLVIRPPPAHER 732
QY 738 TLOI-----PP-----PLPAIKHLPRPETHLPNPAQLQ 765
DB 733 SLSSAYGGNBSAMEFLRQEDTPGCRPEGLRLDSDTSLISIPVDH-----EELERSISGF- 767
QY 766 ESISDVTYTCIVASKENQVAVOS 787
DB 788 -SISQ-----SKENLDALNS 801

```

```

RESULT 21
AA08341
ID AA08341 standard; Protein: 872 AA.
XX AA08341;
XX AC
XX 22-JUL-1999 (first entry)
XX Human KCNQ2 protein.
XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;

```

```

KM benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW detection; gene therapy; drug screening.
OS Homo sapiens.
XX
XX MO9921875-A1.
XX
XX 06-MAY-1999.
XX
XX 23-OCT-1998; 98WO-US22375.
XX
XX 24-OCT-1997; 97US-0063147.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Charlier C, Leppert MF, Singh NA;
XX WPI; 1999-312938/26.
XX DR N-PDB; AAX57057.
XX
XX Nucleic acid encoding potassium channels KCNQ2 and 3
XX
XX Claim 1; Page 122-125; 195pp; English.
XX
XX This invention describes novel human and mouse potassium channel proteins
XX KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
XX KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
XX prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
XX epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
XX that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
XX in cell-free form) are used to screen for agents that can be used to
XX treat or prevent these forms of epilepsy. Fragments of the encoding
XX nucleic acids are used as probes or primers, either for detecting
XX mutations or for isolation of related sequences, while the complete
XX sequences may be used in gene therapy to provide wild-type protein.
XX Antibodies specific for mutant or wild-type proteins are used as
XX diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
XX useful in rational design of drugs and therapeutically (in replacement
XX CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
XX CC 3 sequences can now be diagnosed early (before symptoms are manifest),
XX and better treatment options will be available.
SQ Sequence 872 AA:
Query Match 37.7%; Score 1784; DB 20; Length 872;
Best Local Similarity 46.8%; Pred. No. 4; 1e-150;
Matches 411; Conservative 92; Mismatches 196; Indels 180; Gaps 25;
QY 21 GAAAAAGGRLGSGMKNKDVESGGRVYLNLSAARGDCLLLGTRAAATLGGGGGURESR 80
DB 9 GYPPSPSGEKKLVGFGVLDPCA-----PDSTRDGLALLAGSAPK---RGSILSKRA 59
QY 81 GKGARMSLLGKPLSTSSOSCRNRYKRYVQNTLYVLERPRGMATYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRLQNFNLVLEPRGMATYHAYVLLVFGC 106
QY 141 LILSVFTIPRHTKLASSCLLLEFVMIYVGFLEFIRMSAGCCCRGMRGRLRPAK 200
DB 107 LVLVSFTIKEYEKSEGLATILEIYTYVGEYEFRIYAAAGCCCRGMRGRLRPAK 166
QY 201 PCVVDITVLIASIVASAKTOGNIATSLRSLRFLQILRMVMDRGGTWMKLLGSVY 260
DB 167 PCVVDIIVLIVASIVLAAGSOGNVPATSLRSLRFLQILRMVMDRGGTWMKLLGSVY 226
QY 261 AHSKELTAWYIGFVLIFSSFLVYLVENDANEFSTYDALMWGTTTLTIGYDKTPL 320
DB 227 AHSKELTAWYIGFVLIFSSFLVYLVENDANEFSTYDALMWGTTTLTIGYDKTPL 286
QY 321 TWLGRLLSAGFALLGISFPFALPAGILSGFALKVQDQHRKHFEKRRNPANLQCVWRS 380
DB 287 TWNGRLAATFTLLIVSFPFALPAGILSGFALKVQDQHRKHFEKRRNPANLQCVWRS 346

```

QY 381 YAAD-----EKSYSIATWK-----PHLKALHT-----402
 Db 347 YATNLSRFDLHSTWQYERYVTVPWYSSQOTQYASRLIPLNQLELRLNLSKSGLAFR 406
 QY 403 -----CSP--TNQKLSFERVEMASPGOSIKRSQASVGD--RR 437
 Db 407 KDPPEPSPSKSGPCRCRGLCCGCCPERSQOKYSLKRV--FSSRGVAANKGSPQAQTVAR 465
 QY 438 SPSTDTAEGSPYVQKSMFSNDRTFRPRLKLSQPKPVADTALCTDDVYDEKGCQ 497
 Db 466 SPASDQSLIEDSPSKYKPSKMSFGDSRSRAQAFRIKGAASRQNSE--EASLPGEDIVDKSCP 524
 QY 498 CDVSEVELTPPLKTVIRAIRIMKHFVARKKFKETLRPDVKVITQYSAGHIDMLCRIS 557
 Db 525 CEVTEDELTPGLKVSIRAVCVARFLVSKRKESLRPDVMDVIEQYSGHIDMLSRIS 584
 QY 558 LGTFVDDILGKQITSDKRSREKITYAEHTTDDLSMLGRVYVKEKOVQSIKSLDCLDI 617
 Db 585 LQSHVDDQVGRGPAITD--KDRTKGPAEALPEDPMSMGRLGKVEKQVLSMEKKLDPLVNI 643
 QY 618 YQOVLKRGASALALASFOIPEEC-----EQTSYQSPVDSKDLSGSANOAGCLS 668
 Db 644 YMO--RMG-----IPPTTEAYFGAKEPEPAPPYHSPEDSRE--HYDRHGCIY 687
 QY 669 RSTGANISRGLOFILTPEEFSAQTFYALSPTMHSQATQVPISOS-----DGSAYVAT 720
 Db 688 KIVSSSSSTG-----QKNFSAP--AAP-----VQCPPTSMQPSHPRQGHGTSY 733
 QY 721 NTIANQINTAPKPAAPTLLQI-----PP-----PLPAT 748
 Db 734 GDHDSLVIRIPPPAHERSLSAYGGNRRASMEFLRQEDTGCRRPEGNLRDSDTSISIPSV 753
 QY 749 KHLRPERFLHNPAGLQESISDVYTCVASKENVOYAO 787
 Db 794 DH---EELERSFSGF--SISQ-----SKENLDALNS 819

RESULT 22

AA08345
 ID AA08345 standard: Protein: 757 AA.

AA08345;

22-JUL-1999 (first entry)

Mouse partial KCNQ2 protein.

KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;

benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;

KME; rolandic epilepsy; mutant; treatment; screening; epilepsy;

detection; gene therapy; drug screening.

Mus musculus.

MO9921875-A1.

06-MAY-1999.

23-OCT-1998; 98WO-US22375.

24-OCT-1997; 97US-0063147.

(UTAH) UNIV UTAH RES FOUND.

Charlier C, Leppert MF, Singh NA;

WPI; 1999-312938/26.

N-PSDB; AAX57140.

Nucleic acid encoding potassium channels KCNQ2 and 3

CC This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 or KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.

Sequence 757 AA;

Query Match 37.2%; Score 1761; DB 20; Length 757;

Best Local Similarity 51.8%; Pred. No. 3.7e-148;

Matches 395; Conservative 77; Mismatches 200; Indels 90; Gaps 18;

21 GAAAAAGGGRGSGMKDVEGGRGVLLNSAARGDGLLTGTAATLGGGGGLRESR 80
 Db 9 GYVGTGSEXXLKTGVGLDPC-----XPXSTRGKLLIAGSEAPK---RGXIXLKPRPT 59
 QY 81 GKQGRMSLKLKPLSTYSQSCRNVKRRVONYLYNVLERRGNAFYHAFFVLLPFC 140
 Db 60 GGAGG-----GKPKX-----RNAFYKLNFLYNLERRGNAFYHAFFVLLPFC 106
 QY 141 LILVSTPIPTHTKLAASCLLLEFVMTYFGLFIRIRMSAGCCCRYGMQGRLEFARK 200
 Db 107 LVLSVFSTIKKESSEBALTYLTYTVFGEVYFVRMAAGCCCRYGMGRLEFARK 166
 QY 201 PCVYDITVILASIAVSAKTQGNIFATSAISRFLQILIRVNRDRRGCTWKLGSVY 260
 Db 167 PCVYDITVILASIAVSAKTQGNIFATSAISRFLQILIRVNRDRRGCTWKLGSVY 226
 QY 261 AHSKELTAWYIGFLVLFSSFLVYLVEKDAKEPSTVDALMWGTTITLTGGYKPTL 320
 Db 227 AHSKELTAWYIGFLVLFSSFLVYLVEKDAKEPSTVDALMWGTTITLTGGYKPTL 286
 QY 321 TWLGRLLSAGFALGISEFPALPAGILGSGFALKVQEOHOKHFKERKRNPAANLIQCVMS 380
 Db 287 TWNGRLLAATFTLIGVSFPALPAGILGSGFALKVQEOHOKHFKERKRNPAANLIQCVMS 346
 QY 381 YAADKESVSI-ATWK-----PHLKALHTGSPNTOK--LSRK 413
 Db 347 YATNLSRFDLHSTWQYERYVTVPWYSSQOTQYASRLIPLNQLELRLNLSKSGITFR 406
 QY 414 ERYR---WASPRGOSIKRSQASVGD--RSPSTDTIAEESPTKVQKSWSFNDTRPRPSL 468
 Db 407 KEQPEPSPSPRGMAKAGSGPOAQTVRSFSDOSLDSPSKVSKMSFGDSRSRROAF 466
 QY 469 RLKSSOPKPVADADALGTDVYDEKGCQDVSEDELTPPLKTVIRAIRIMKHFVARKKF 528
 Db 467 RIKGAASRONSSEASIPGEDIYEDNKSCEFTEDLTGKAKSIRAVCMRFLVSRKF 526
 QY 529 KETLRPDYDKVIEQYSAGHIDMLCRINKSLQTRVDDIILGKQITSDKRSREKITYAEHTT 588
 Db 527 KESLRPDYDMQVIEQYSAGHIDMLCRINKSLQTRVDDIIVGGRPTTD--KDRTKGPAETELP 585
 QY 589 DDLMLGRVYKVEKQVQSIKSLDCLDIYQVLRKGSASALALASFOIPEECQSDY 648
 Db 586 EDPMSMGRLGKVEKQVLSMEKKIDFLVSYTQ--RMGIQPAETEAFTGAK--EPEPAPPY 641
 QY 649 GSPVDSKDLGSAQNSGC---LSRSTANISRGLOFILTPEEFSAQTFYALSPTMHSQAT 705
 Db 642 HSPEDSRD---HADKHGCIITKIVRSNS-----TGGRNVAAAPA----- 677
 QY 706 QVPISQDGSAAVATNTIANQINTAPKPAAPTLLQIPPLPA 747

OS Homo sapiens.
 XX NC09921875-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98MO-US22375.
 XX PR 24-OCT-1997; 97US-0063147.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX Charlier C, Leppert MF, Singh NA;
 XX WPI; 1999-312938/26.
 XX N-PSDB; AAK57059.
 XX Nucleic acid encoding potassium channels KCNQ2 and 3
 PS Claim 1; Page 136-139; 1999p; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 CC
 XX Sequence 872 AA:
 S0 Query Match 34.2%; Score 1620.5; DB 20; Length 872;
 Best Local Similarity 42.2%; Pred. No. 1.8e-135;
 Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;
 QY 7 GGEBCGAAGLWVKSAAAAAGGRLGSGMKDVEGRCR-----VLNSAARGGCLL 60
 DB 14 GGGGGGGGG-----GGAANPAGGDAAGADEERKYGAPDVEQVTLAAGADKDGTL 68
 QY 61 LGTAAATLGGGGGGLRESRKGOGARMISLTK-PLSTYSQSGRRVVKYRRVQNYLYNL 119
 DB 69 L-----EGGGRDEGGRTPQG--TGLAATPLSRPVK---RNNAKTRIDTTLTYDAL 115
 QY 120 ERPRGMAFIHAFVFLVFGCLLSVSTFIPHTKLASSCLLLEFVMVFGLEFIRI 179
 DB 116 ERPRGMAFIHAFVFLVFGCLLSVSTFIPHTKLASSCLLLEFVMVFGLEFIRI 175
 QY 180 WSAGCCCTRYRKGOGRLRPARKPFVITVILASTAVSAKQGNFATSAKSLRFLQI 239
 DB 176 WAAGCCCTRYRKGOGRLRPARKPFVITVILASTAVSAKQGNFATSAKSLRFLQI 234
 QY 240 LRMVMDRGGTGWKLGGSVVVAHSHKELTAWTIGFVLTFSSFLVVLVERDA----- 291
 DB 235 LRLMDRGGTGWKLGGSVVVAHSHKELTAWTIGFVLTFSSFLVVLVERDA----- 294
 QY 292 --NKEESTYADALMWGITLTITIGYGDKTPLTWGLLGSAGFALLGISFPALPAGILGSG 349
 DB 295 EKKEEFETTYADALMWGITLTITIGYGDKTPLTWGLLGSAGFALLGISFPALPAGILGSG 354
 QY 350 FALKVOEORHOKHFEKRRRPAANLQCVKRSYAADEKSY-SITWK-----PHIKAL 400
 DB 355 FALKVOEORHOKHFEKRRRPAANLQCVKRSYAADEKSY-SITWK-----PHIKAL 414

QY 401 HTCSPTNOKLSFEKRYVMASPRQSLKRSOASVGRDRSPSTDTIAEGSPTRKQKSWSEND 460
 DB 415 QLEAASSQKGLDRVRLSNPRGSGNTK-----GKLFPLVNDALIEEPPSEKRPVGLNN 468
 QY 461 RTFRPSRLK-----SSQPKPYIDADLTGTDVYDEKGCQCDVSDVETLPLKTYIR 514
 DB 469 KERFRTAFRMKAYAFMQSS-----DAGTG---DPMEDRGYGNDFPLEDMIPULKAIR 520
 QY 515 AIRIMKRVAKRKFEKTLRPYDVYDEOXSAGHLDMLCRKSLQTRVDOILGQOLTS 574
 DB 521 AVRILQRLYKKKFKETLRPYDVADVIEQYSAGHLDMLSRKTYQTRIDMLFTPEPSTP 580
 QY 575 KRSR-----EKTAHEETP--DLSMLGRVYVVKQVOSIESKLDCL 615
 DB 581 KHKKSQKGSATFPSPQSGSPRNEPVARPSTSEIDQSMGKFKVYERQVDMGKRLDPLV 640
 QY 616 DTYQOYIR-----KGSASALALASFOJPPPECDETSYQSVSDKSLGSGM 663
 DB 641 DMHQMHERLOVOYTEYPTKGTSS-----PAEAEKEDNRRS-DKTTICNTSE 689
 QY 664 SGCLSRSTSANISGLQFILTNPESQTFYALSPMTMSQATQVPISQDSGSAVAATWTI 723
 DB 690 TGPEPEPSFH-----QVTDKVSPTGFPAHD-----VNLPRGSPSSGKVAT-- 733
 QY 724 ANQINTAPKPAAPTLLQIPPLPAIKLPRBETLHPNPAGIQESIDVTTCLVASKENVQ 783
 DB 734 -----PPSATYVERPVLPLTLLDSRVSCH--SQADLQGPYSD-----RIS 775
 QY 784 VAQSNLTKDSMKRSFDMGCTLLSCVPMVRKDLKSLSYONLTSTELNQLSGSES 843
 DB 776 PRQ-----RRSITRDSPTPLT-----MSVNH-----BELERSPGFSIS 810
 QY 844 GSRGQDFYP-----KWRSEKLFITDEYGPETENDTF 877
 DB 811 QDRDYYFGPNVGSSMKREKRYLAE--GETDTIDTF 845
 RESULT 25
 ID AAE16620 standard; Protein: 872 AA.
 AC AAE16620;
 DT 09-APR-2002 (first entry)
 XX
 DE Human potassium channel polypeptide, KCNQ3.
 XX Human; potassium channel polypeptide; KCNQ3; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neurophysiological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; KCNQ3 protein.
 OS Homo sapiens.
 XX NC0200192526-A1.
 XX PD 06-DEC-2001.
 XX PF 24-MAY-2001; 2001WO-US17314.
 XX PR 26-MAY-2000; 2000US-207389P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Dwoletzky SI, Ramanathan CS, Trojnecki JT, Boisard CG;
 PI Gribkoff VK;
 XX WPI; 2002-122069/16.

CC diseases, epilepsy, and stroke.

XX Sequence 854 AA;

Query Match 33.9%; Score 1603.5; DB 20; Length 854;
Best Local Similarity 42.7%; Pred. No. 5,8e-134;
Matches 393; Conservative 109; Mismatches 252; Indels 167; Gaps 29;

20 SGAAAAAAGG--GRLSGMKDYESGRCRVLNLSAARGDGLLIGTRATLGGGGGLRE 77
DB AGDAAAAGDEERKVGGLAPDVEQ---VTALGAGADKDTLL-----EGGGRDEG 59
QY 11 AGDAAAAGDEERKVGGLAPDVEQ---VTALGAGADKDTLL-----EGGGRDEG 59
QY 78 SRGKGQARMSLGLK-PLSTSSQSCRNVKRRQNTLVNLEPRGMATFYHAFVFL 136
DB 60 QRRTPQG--IGLAKTPLSRPVK--RNNAKYRRQTLIDALEPRGALLVHALVFL 114
QY 137 VFGCLISVFSTIEHTKLASSCLLIEFVMIIVVGFELIRMSAGCCCRKRGMRRLR 196
DB 115 VLGLLILAVLTTEKEVEYVSGDWMLLLETFALIFGAFALRIMAGCCCRKRGMRRLR 174
QY 197 FARRPCVIDITVLIASIAVSAQTQNIETASLRSLFQILDMVRDRRGTKLIG 256
DB 175 FARRPLCMLDIFVLIAVPAVAVGNOGNVLAIS--LRSLRFQILRLMRDRRGTKLIG 233
QY 257 SVVYAHSEKLTAVKIGFLVLIFFSEFLVYLVKDA-----NKESTYADALMNGT 306
DB 234 SAICAHSEKLTAVYIGFLTLILSEFLVYLVKDAPEVDAQGEKKEEFTYADALMNGT 293
QY 307 ITLTIGGDKTPTLWLGRLSAGFALLGISFALPAGILGSGFALKVOEHRKHFERR 366
DB 294 ITLTATIGGDKTPTWEGRLIAATFSLIGVSFALPAGILGSGFALKVOEHRKHFERR 353
QY 367 RNPANLIGQVRSYADAEKVS--IAWK-----PLKALHCSPLNOKLSFEERR 417
DB 354 RKPAAELIQAAARRYATNPNRIDLVAIFWREYVVSFPFRRQOLEAASOKGLDRLVR 413
QY 418 MASRGSIKSRQASVGRDRSPSTDTAEGSPTKQKSSFPDRFRFSRLRK----- 471
DB 414 LSNRGSMTK-----GKLTPTPLNDALFEESPEKPKPGLNKEFRFAFRKAAFAWQ 467
QY 472 SSQKRPVIDADTALGTDVYDEKGGQCDVSEDLTPPLKTVIRAIRIMKFAKRRKET 531
DB 468 SSE-----DAGTG--DMAEDRGYGNDFIEDMPTLKAIRAVRIILOFLYKRRKET 519
QY 532 LRPDVKVIOYSAGHIDMLCRISLQTRVQIILKGQITSDKRS----- 578
DB 520 LRPDVKVIOYSAGHIDMLSRIRYLOTRIDMIFTPGPPSPKHKKSOKGSAFTPSQ 579
QY 579 ----EKTAHEHTT--DDLMLGRVYKVKQVQSIKSLDLIDLYQVYLR----- 623
DB 580 SPRNEPYVARSSTIEQSSAMGKFKYKVRQVQDMKKIDFLVDMQHMHERLOVQTEY 639
QY 624 ---KGSASALALASFQIPPECEQTSYQSPVDSKDLSSAONSGLSRSTANISRLQ 680
DB 640 YPTKGTSS-----PAAEAKEKEDNRY--DLKTIICNYSETGPEPEYSPH----- 682
QY 661 FILTPNESAQTFFALSPMHQAQVPIQSQDGSVAVAENTIANINAPKRAAPTLL 740
DB 663 -QVITDKVSPYGFHAP-----VNLPRGSPSSGKVQAT-----PPSSATTIVE 725
QY 741 IPPPLPAKHLPRPETLHPNAGLQESISDVTTCLVASKENNVQVQASNLTKDRMSRFS 800
DB 726 RPTVPIILTLDARSCH--SQADLQGYSD-----RISPRQ-----RISIT 765
QY 801 MGGFTLLVCPWVPKDLKSLSVONLIRSTELNOLSGSESSGSRQDFFP---KWR 856
DB 766 RSDPPLSL-----MSVNH-----EELERSPSGFSISQDRDYVFGPGSSSM 809
QY 857 ESKLFTDEVGPEETETDTF 877
DB 810 REKRIYLAEG--GETDTIDPF 827

RESULT 27

AY08346
ID AAY08346 standard; Protein: 870 AA.

XX AAY08346;

XX 22-JUL-1999 (first entry)

DE Mouse KCNQ3 protein.

KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;

benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;

KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;

OS Mus musculus.

PN W09921875-A1.

PD 06-MAY-1999.

PF 23-OCT-1998; 98WO-US22375.

PR 24-OCT-1997; 97US-0063147.

PA (UTAH) UNIV UTAH RES FOUND.

PI Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

DR N-PSDB; AAX57141.

PT Nucleic acid encoding potassium channels KCNQ2 and 3

PS Claim 1; Page 164-167; 195pp; English.

XX This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available.

XX Sequence 870 AA;

Query Match 33.2%; Score 1570.5; DB 20; Length 870;
Best Local Similarity 41.6%; Pred. No. 5,4e-131;
Matches 388; Conservative 109; Mismatches 273; Indels 163; Gaps 28;

QY 7 GGEBCGAAGLVKSGAAAAAGG-----RLGSGMKDYSGRVLNLSAARGDG 57
DB 12 GGEBCGGGG-----GGAANPAGDVAVAGDEERKVGILAPDVEQ---VTALGAGADKDG 63
QY 58 LLLLTGTRATLGGGGGRLSRGOGAMSLGK-PLSTSSQSCRNVKRRQNTLVNLEPRGMATFYHAFVFL 116
DB 64 TLLT-----EGGGRGEGQRRTPQG--IGLAKTPLSRPVK--RNNAKTRRIOTLLY 110
QY 117 NVLERPRGMATFYHAFVFLVFGCLILSVSTPIPEHTKLASSCLLIEFVMIIVFGLEFL 176
DB 111 DALERPRGMATLYHALVFLVIVGCLILAVLTTFKEVEYSGDWMLLLETFALIFGAEEFA 170
QY 177 IRMSAGCCCRKRGQGRLEFARKPCVIDITVLIASIAVSAKTQGNIFATSLASLR 236

```

Db      171 LRIWAGCCCRKYGWGRGLKFAKKPLCLMDLIFVLASVPVAVAGNOCNVLATS-LRSLRF 229
QY      237 LQILNVRMDRGGCTFKLIGSVYVAHSHKELITAMYTIFELVIESFLYVLEKDA----- 291
Db      230 LQILNVRMDRGGCTFKLIGSAICASHKELITAMYTIFELVIESFLYVLEKDEPDA 289
QY      292 ----NKEFSTYADALMWGITLTITLTIGGDKTPLTWGLRLSAGFALIGSFALPAGIL 346
Db      290 QGEMKEEFETAYADALMWGITLTITLTIGGXTPKTWGRLIAAFSLIGVFPALPAGIL 349
QY      347 GSGFALKVOEHQKHFEKRRNPAANLIQCVMSYAADEKSVS-IATWK-----PHL 397
Db      350 GSGALKVQEHQKHFEKRRRPAELIQAMRYATNPNDIIVATWRSYEVSVSFPF 409
QY      398 KALHTCSPTNQLSEFERMASPRGOSISRQASVDRSRSPDIAEGSEPTVQKWS 457
Db      410 RKEOLEAASOKLGLDRVRLSNPRGSNTK-----GKLTPLNVAIDIESPSKEPKVG 463
QY      458 FNDKTRFRPSLTKS-----SQPKVIDADATLGTDDVYDEKGCQCDVSVEDLPLPKT 511
Db      464 LNNKRFRTAFMKAVAFWQXSE-----DAGTG---DPMADRGYGNDXLIXDMIPXXKA 515
QY      512 VIRAIRIKFHAHAKKREKTELPRDYKDYIEQYSAGHLDMLCRKSLQTRVDQLLKGQI 571
Db      516 AIRAVRIQLFYLKKKFKETLPYDKVDIEQYSAGHLDMLSRKYLQTRIDMFTPGPP 575
QY      572 TSDR-KSREKIT-----AEHETDLSMLGRVYVKEVOQVSIESTLD 612
Db      576 STPKHKRSOKGATFYPSQSPRNEPYVARAATSEDEDOSMGKRYVEKQVHMGKKLD 635
QY      613 CLLDITQVQLKKGSAALASFOIPPECEOTSDYQSPVD---SKDLSSAQNQSGCLSR 669
Db      636 XLVMMHMHMR-----LOVHVTEYYPYXGASSPAEGEKKEEDNRYSDLEITICNY 685
QY      670 STSNISRGLOFILTP-NEFSAQTFALSPTHMSQTOVPISSQSDGSAVATNTIAQIN 728
Db      686 SETGPDPDPYFHOVPIRVGCGYGFANP-----VKLTGGRPSSTQAQANLPS-- 734
QY      729 TAPRPAFTLQIPPLPAIKHLPRPETHLPNPAGLOESISDVTVLASKENVOVAQSN 788
Db      735 ----SGSTVABRPVLPILITLDDCSVSH-----SOTELGPPYSD 770
QY      789 LTKRSMKSPDMGCEITLVCVPMYPKDLGKLSVONLIRSTEELNIQLSGSESSGRGS 848
Db      771 HISPR-QRRSITRSDTPLSL-----MSVNH-----ELERSPSGFSISQDRD 813
QY      849 QDEYF---KWRESKLFITDEVGPEETDTDF 877
Db      814 YVFGPSGGSSWMGKRYLAE---GETDITDTPF 843

```

RESULT 28
ABG09080 ID ABG09080 standard; Protein: 877 AA.

AC AC ABG09080;

DT DT 13-FEB-2002 (first entry)

DE DE Novel human diagnostic protein #9071.

XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.

OS OS Homo sapiens.

PN PN WO200175067-A2.

PD PD 11-OCT-2001.

PF PF 30-MAR-2001; 2001WO-US08631.

```

PR      31-MAR-2000; 2000US-0540217.
PR      23-AUG-2000; 2000US-0649167.
XX      (HYSE-) HYSEQ INC.
PI      Drmanac RT, Liu C, Tang YT;
XX      WPI: 2001-639362/73.
XX      N-PSDB; AAS73267.
PT      New isolated polynucleotide and encoded polypeptides, useful in
PT      diagnostics, forensics, gene mapping, identification of mutations
PT      responsible for genetic disorders or other traits and to assess
PT      biodiversity
XX      Claim 20; SEQ ID No 39439; 103pp; English.
XX      The invention relates to isolated polynucleotide (I) and
XX      polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX      polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX      and gene mapping, and in recombinant production of (II). The
XX      polynucleotides are also used in diagnostics as expressed sequence tags
XX      for identifying expressed genes. (I) is useful in gene therapy techniques
XX      to restore normal activity of (II) or to treat disease states involving
XX      (II). (II) is useful for generating antibodies against it, detecting or
XX      quantitating a polypeptide in tissue, as molecular weight markers and as
XX      a food supplement. (II) and its binding partners are useful in medical
XX      imaging of sites expressing (II). (I) and (II) are useful for treating
XX      disorders involving aberrant protein expression or biological activity.
XX      The polypeptide and polynucleotide sequences have applications in
XX      diagnostics, forensics, gene mapping, identification of mutations
XX      responsible for genetic disorders or other traits to assess biodiversity
XX      and to produce other types of data and products dependent on DNA and
XX      amino acid sequences. ABG00010-ABG30377 represent novel human
XX      diagnostic amino acid sequences of the invention.
XX      Note: The sequence data for this patent did not appear in the printed
XX      specification, but was obtained in electronic format directly from WIPO
XX      at ftp.wipo.int/pub/published_pct_sequences.
SQ      Sequence 877 AA:

```

Query Match 32.6%; Score 1544; DB 22; Length 877;
Best Local Similarity 41.0%; Pred. No. 1.3e-128;
Matches 387; Conservative 109; Mismatches 269; Indels 178; Gaps 30;

```

QY      7 GGEEGAALWVKSGAAAAAGGRGSGKMDVESGGR-----VLNSAAAGDGLL 60
Db      14 GGGDGGGG-----GGAANDPAGSDAAAAGDEERKVGAPGDVEQVTLALGADKDGILL 68
QY      61 LGTRATLGGGGGLRESRRGKOGAMNSLLGK-PLSTSSQSCRNNKYRRVQVLYNVL 119
Db      69 L-----EGGGRDEGGRRTPG--IGLAKTRPLSPRV--KNNAKYRRIOILLIDAL 115
QY      120 EPRRGMAFYHAFVFLVFGCLILSVSTIPEHTKASSCLLIEFYVIVGIEPTIRI 179
Db      116 EPRRGWALLYHAFVFLVILGCLLAVLTPEKEEYVSGDWLLETFPAIFFGAEFALRI 175
QY      180 WSAGCCCRGWRGGRFARFKPCVDTYVLINSINVAKSAGTGNIFATSLSRFLQI 239
Db      176 WAAGCCCRKWRGGRKFKARPKLMDIVYLINSVPPVAVAGNOCNVLATS-LRSLRFLOI 234
QY      240 LMRVR-MDRGGTWWKLLGSVYVAHSHKELITAMYTIFELVIESFLYVLEKDA----- 291
Db      235 LRLMDRGEGEGTWWKLLGSAICASHKELITAMYTIFELTLLSFLYVLEKDEPDAQ 294
QY      292 ----NKEFSTYADALMWGITLTITLTIGGDKTPLTWGLRLSAGFALIGSFALPAGILGS 348
Db      295 EEMKEEFETAYADALMWGITLTITLTIGGXTPKTWGRLIAAFSLIGVFPALPAGILGS 354
QY      349 GFALKVQEHQKHFEKRRNPAANLIQCVMSYAADEKSVS-IATWK-----PHLKA 399
Db      355 GLALKVQEHQKHFEKRRRPAELIQAMRYATNPNDIIVATWRSYEVSVSFPFPRK 414

```

QY 400 LHTCSPTNOKLSFEKERVMA SPRGOSIKRSQASVGD RSRPSDTITAGSPPTKQKMSFN 459
 DB 415 EOLEAASSOKLGLDRLVLSNPRGSNTK-----GKLEFPLNVDAIESSPSKEPKVGLN 468
 QY 460 DRTFRPSLRK-----SSQPKPVIDADTALGTDDVYDEKGCQCQDVSEDLPLPLKTVI 513
 DB 466 NKEFRFTRFRKAKAFWQSSSE-----DAGTG---DPMADRGYGNDFIEDMPTLKAAI 520
 QY 514 RAIRIMKFAVAKRKETLRPYDKVIEOYSAGHLDMLCRISLQTRVDQILKGQOITS 573
 DB 521 RAVRILOFRLYKKKKEKTELPRYDKVIEOYSAGHLDMLSRILQTRIDMIFTPGPSPST 580
 QY 574 DKRSREKITAETH-----ETTDLSMLGRVVK-VEKOVQSIESTK 610
 DB 581 PKHKEVFRKGGHFTFPSSQSSRGLNHMKARPSTSEIEDORHMKGVKFKSLKGVOGLGRK 640
 QY 611 LDCLDIYQOVLK-----KGSASALALASFOIPPECEQTSYQSPFSDKSL 658
 DB 641 LDPLVDMHMQHMERLQVOVTEYYPKRGTS-----PAEAKKEDNRYS-DLKTII 689
 QY 659 GSAQNSGLSKSTSNANISRGLOFILTPNEFSQOTFALSPMTMSQATQVPIQSODSAYA 718
 DB 690 CNYSETGPEPPYSPH-----QVTIDVSPYGFPAHP-----VNLPRGGPSGKVQ 736
 QY 719 ATNTIANQINTAPKPAAPTLOIPPLPAIKHLPRPETLHPNAGLOESISDVTTCIVAS 778
 DB 737 AT-----PSSATTYVERPYVPLITLILDSRVSCH-SQADLQGPST-----777
 QY 779 KENVOVAQSNLTKRDSMRKSFDMGGETLLSCPMVPRKDLKSLSYONLIRSTEELNIQLS 838
 DB 778 --RISPRQ-----RRSITRDSPTPLSL-----MSVNH-----EELERSPS 810
 QY 839 GSESGSGSGSDPYF---KMRSEKLFITDEVEYPEETENDTF 877
 DB 811 GFSISQDRDDYVFGPGSGSSMMREKRYLAE---GETDTIDTDPF 850

RESULT 29

ABG19734
 ID ABG19734 standard. Protein; 1375 AA.

AC ABG19734;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #19725.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS83921.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

PS Claim 20; SEQ ID No 50093; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful for treating
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

Sequence 1375 AA;

Query Match 32.6%; Score 1544; DB 22; Length 1375;
 Best local similarity 41.0%; Pred. No. 2,7e-128;

Matches 387; Conservative 109; Mismatches 269; Indels 178; Gaps 30;

QY 7 GGEEGAAGLWVKSAAAAAGGRLSGMKDVEGRGR-----VLNSAARGCGLL 60
 DB 83 GGGDGGGG-----GGAANPAGDAAAAGDEBERKGLAPGDEOVTIAGAGDKGCTLL 137
 QY 61 LGTRATITGGGGGGLRESRKGAGRMSLGK-PLSYTSSQSCRWVKRYRVOYNYLV 119
 DB 138 L-----EGGGRDEGGRTPDG--TGLAKTPLSPVK---RNNAKTRRIOTLIYDAL 184
 QY 120 ERPRGMATYHAFVELVAVGCLISVFTSTPETHKLASSCLLIEFMVVFGELEIRI 179
 DB 185 ERPRMALLYHVLVAVLIVAGCLILAVLTFFKEEYVSGDWLLELFAIRIFGAEFALRI 244
 QY 180 WSAGCCCRYRGMQGRILRFARPCVYDITVLIASIVASAKTQGNIFATASLSRLQI 239
 DB 245 WAAGCCCRKYGWRGLKFAKPLCMIDIFVLASVAVVAVANGNVLATS-LSLRLQI 303
 QY 240 LRMVR-MDRRGSTWKLGSVVAHSHKELTAWYIGFLVIFSEFLVYVEKDA----- 291
 DB 304 LRLMDGPEGGTWWKLSALCAHSHKELTAWYIGFLTLLSSFLVYLVKDPVENDAG 363
 QY 292 ---NKEFTYADALMMGTTLTITGYGDKTPTLWLGRLSAGFALLGISFPALPAGILGS 348
 DB 364 EEMKEFEFTYADALMMGLTITATIGYGDTPKTEWEGRLIATPSLIGVSFPALPAGILGS 423
 QY 349 GFALKVQEOHQHKEFRKRNPAANLIQCVRSTAADEKYS-IATWK-----PILKA 399
 DB 424 GLALKVQEOHQHKEFRKRNPAANLIQAARRYATNPRIDLVATWTFYSSVVSFPFRK 483
 QY 400 LHTCSPTNOKLSFEKERVMA SPRGOSIKRSQASVGD RSRPSDTITAGSPPTKQKMSFN 459
 DB 484 EOLEAASSOKLGLDRLVLSNPRGSNTK-----GKLEFPLNVDAIESSPSKEPKVGLN 537
 QY 460 DRTFRPSLRK-----SSQPKPVIDADTALGTDDVYDEKGCQCQDVSEDLPLPLKTVI 513
 DB 538 NKEFRFTRFRKAKAFWQSSSE-----DAGTG---DPMADRGYGNDFIEDMPTLKAAI 589
 QY 514 RAIRIMKFAVAKRKETLRPYDKVIEOYSAGHLDMLCRISLQTRVDQILKGQOITS 573
 DB 590 RAVRILOFRLYKKKKEKTELPRYDKVIEOYSAGHLDMLSRILQTRIDMIFTPGPSPST 649
 QY 574 DKRSREKITAETH-----ETTDLSMLGRVVK-VEKOVQSIESTK 610
 DB 650 PKHKEVFRKGGHFTFPSSQSSRGLNHMKARPSTSEIEDORHMKGVKFKSLKGVOGLGRK 709

QY 611 LDCILDIYQOVL-----KGSASALALASFOIPPECEOTSDYQSPVDSKLS 658
 Db 710 LDELVDHMOHMERLOVETVEYPTKGTSS-----PAEAKKEDNRK-DLKTII 758
 QY 659 GSAONSGCLSRSTSANISRGIOFLITPREFSAQTFYALSPTMHSGATVPISQSDGSAYA 718
 Db 759 CNISETGPEPPPSF-----QVTIDKSPYGFADP-----VMI.PRGSPSSGKVQ 805
 QY 719 ATNTIANQINTAPKPAFTLQIPPLPAIKHLPRPELHNPAGLOSISDVTCLVAS 778
 Db 806 AT-----PSSATTYVERTYVPIILLLSRVSC-HSQADLQGPYSD----- 846
 QY 779 KENVOYAQSNLTDRSMKRSFDMGGETLLSYCPWVPKDLGKLSVONLIRSTEELIQLS 838
 Db 847 -RISPRQ-----RSITRSDSPPLSL-----MSVNH-----EELERSPS 879
 QY 839 GSSSGSGSGSDPYF-----KWRSEKLTITDEVEPEETETPTF 877
 Db 880 GFSISODRDRDYVFPNGSSWMREKRYLAE---GETDITDPTF 919

RESULT 30

AAM25585
 ID AAM25585 standard; protein; 875 AA.
 AC AAM25585;

16-OCT-2001 (first entry)

Human protein sequence SEQ ID NO:1100.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus; anti-inflamatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; vitreous; anti-HIV; fungicide; antimutagen; cardiovascular; antihaemic; aneemia; dermatologic; haemostatic; vulnery; antilucer; osteopathic; eczema; neuroprotective; antiallergic; antistimatic; antidiabetic; cytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathologic disorder; cardiac anaphylaxis; autoimmunity; thrombocytopenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; asthma; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; neurological disorder.

Homo sapiens.

MO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000WO-US35017.

23-DEC-1999; 99US-0471275.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI: 2001-457603/49.

N-PSDB: AAH99526.

Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Claim 20; Page 224; 1217pp; English.

AAH99166 to AAH99904 encode the human proteins given in AAM25225 to

CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: anti-inflamatory; antirheumatic;
 CC antirheumatic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; vitreous; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antihaemic; antiagregant; haemostatic; vulnery;
 CC antilucer; osteopathic; dermatologic; antiallergic; antistimatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.

Seq Sequence 875 AA;

Query Match 32.5%; Score 1540; DB 22; Length 875;
 Best Local Similarity 41.2%; Pred. No. 2,9e-128;
 Matches 388; Conservative 111; Mismatches 266; Indels 176; Gaps 31;

QY 7 GGEBCGAGLWVSGAAAAAGGRLGSMKDVESGRG-----VLNSAARGDGLL 60
 Db 14 GGGDGGGG-----GGAANPAGDAAAGDEKRVGLARGVYALGAGADKDGDTLL 68
 QY 61 LGTRATLGGGGGGLRESRKGAGMSLIGK-PLSTYSQSGRRVYKRVQNYLYNV 119
 Db 69 L-----EGGGRBEGQRTYQ--IGLATTPLSRPVK---RNNAKRRRLQTLIYDAL 115
 QY 120 EPRGWAFYNAFVFLVFGCLLSVSTIPEHTKLSSCLLIEFVMIVFEGLEFIRI 179
 Db 116 EPRGMALLYHALVFLVGLCLLAVLTFFKEVEYVSGDWMLLETFALFIEGAERALRI 175
 QY 180 WSAGCCGVRGMOGLRFAKRPFCYIDTVLAASIAVSAKQGNIFATLSALSLFLDI 239
 Db 176 WAAGCCGVRGMOGLRFAKRPFCYIDTVLAASIAVSAKQGNIFATLSALSLFLDI 234
 QY 240 LRMVR-MDRRGVTWMLGIVYVAHSEKLTIVYIFLVIFSSFLVYVEKDA----- 291
 Db 235 LRMVRDGGEGGTWMLGIVYVAHSEKLTIVYIFLVIFSSFLVYVEKDA----- 294
 QY 292 ---NKEFTYADALMWGITITLTIGYCKTPTLWGLRSLGAGFALLGISFPALGILGS 348
 Db 295 EEMKEEFTYADALMWGITITLTIGYCKTPTLWGLRSLGAGFALLGISFPALGILGS 354
 QY 349 GFALKVOEHOHQRKFEKRRNPAANLQCVMSYADEKSVS-IATWK-----PHUKA 399
 Db 355 GLALKVOEHOHQRKFEKRRNPAANLQCVMSYADEKSVS-IATWK-----PHUKA 414
 QY 400 LHTCSPTNOKLSFEKRVMAASPRQSIKROASVDRSPSTDTAEQSPVKQKSWEN 459
 Db 415 EOLEAASSOKLGLDRVYLSNPRGSNTR-----GKLEFTPLNVAIDESPKEPRVGLN 468
 QY 460 DRTFRPSLRK-----SSQPKYIDADTALGDDVDYDEKGCOCVDEDLTPPLKTYI 513
 Db 469 NKEFRFAFRKAKAYAFMOSS-----DAGTG--DPMADBGYGDPIENMIPLYKAAI 520
 QY 514 RAIRIMKFAVAKRKEFTLRPYDVYDEQVYSAHLDMLCRKSLQTVQVDOILGQGLTS 573
 Db 521 RAVRILOFRLYKKKFKETLRPYDVYDEQVYSAHLDMLCRKSLQTVQVDOILGQGLTS 580
 QY 574 DK-KSRKETA-----EHEFTDLSMLGRVVK-VEKOVOSIESKID 612
 Db 581 PKHRSQKSAFTFPPSOOSPRNEPYVARPSTSEIDQHNKMGKFKSLKGOVGLGRKLD 640
 QY 613 CLDIYQOVL-----KGSASALALASFOIPPECEOTSDYQSPVDSKLSGS 660

Db 641 FLVDMHOMERLQOVTEYYPTKGTSS-----PAEAKEKEDNRY-S-DLKTIIION 689
 QY 661 AONSGLSRSTNSANISRLQFLIPNERSAOTFVALSPHMQAQVPIQSODGSVAAT 720
 Db 690 YSEGPPEPPYSEH-----QVITDKVSPYGEFAHP-----VNLPRGPPSSGRVQAT 736
 QY 721 NTIANQINTAPKPAAPTLQIIPPLPAIKHLPRPETLHPNPAOLOESIDVTTCIVASKE 780
 Db 737 -----PPSATITVERPVTYVPIITLILDSRVSC-HSQADLOGPYSD----- 775
 QY 781 NVOVAQSNLTKDRSMKSFDMGGETLLSCVCPVPRDLGKSLSVQNLIRSTEELINIQLSGS 840
 Db 776 RISRPQ-----RSITRSDSDPLSL-----MSVNH-----EELERSPSGF 810
 QY 841 ESSGSRGSDFP-----KWRESKLEPTDEVGPEETDTDF 877
 Db 811 SISODRDDYVYVPGNGSSMREKRYLAE---GETPTDIDPF 848

RESULT 31
 AAW14282
 ID AAW14282 standard; Protein: 393 AA.
 AC AAW14282;
 DT 09-JAN-1998 (first entry)
 XX Human K+ channel protein sequence.
 DE Human K+ channel protein sequence.
 KW Human; neuroblastoma; K+ channel; glioma; probe; diagnosis; detection;
 KM tumour.
 XX Homo sapiens.
 OS JP09191882-A.
 PN 29-JUL-1997.
 PD 16-JAN-1996; 96JP-0004726.
 PF 16-JAN-1996; 96JP-0004726.
 XX 16-JAN-1996; 96JP-0004726.
 PR 16-JAN-1996; 96JP-0004726.
 XX (NIBS) JAPAN TOBACCO INC.
 PA WPI: 1997-429182/40.
 DR N-PSDB; AAT85964.
 XX DNA encoding new human K+ channel protein - useful for detecting
 PT glioma(s) and tumours
 PS Claim 1; Page 10-12; 14pp; Japanese.
 XX This is the amino acid sequence of a novel human K+ channel protein
 CC which is expressed on human glioma cells. The encoding gene was isolated
 CC from a 3' directed cDNA library prepared from human neuroblastoma cell
 CC line CHP134. The screen isolated a clone designated GS008740 whose
 CC insert contained the coding sequence and the 5' and 3' sequences of the
 CC gene (AAT85964-6 respectively). Expression of the gene was detected in
 CC neuroblastoma cell lines. Oligonucleotides derived from the sequence of
 CC the K+ channel gene can be used as probes for diagnosing human gliomas,
 CC and in the detection of new tumours.
 CC
 XX Sequence 393 AA:
 SO

Query Match 25.9%; Score 1227.5; DB 18; Length 393;
 Best Local Similarity 64.8%; Pred. No. 7.7e-101;
 Matches 243; Conservative 37; Mismatches 72; Indels 23; Gaps 5;

QY 21 GAAAAAGCGRLGSGMKVYSGRGVNLNSAAARGDGLLITRAATLGGGGGLRESRR 80
 Db 9 GVPYPSGEKKTKLVFVGLDPGA-----PDSTRDGLALLIAGSEAK---RGSILSKPRA 59
 QY 81 GKGARMSLTKPLSYTSSQSCRNVKRYRVQNYLVLEPRGMFIYHAFVLLVFGC 140

Db 60 GGAGA-----GKP-----PKRNAFYRKLQNFYLVLEPRGMFIYHAFVLLVFGC 106
 QY 141 LILSVESTIEPHNTLASSCLLILFVFMIVVGLERTITINSAGCCCRRGNGRIREFARK 200
 Db 107 LVLSVFSTIKREKESBGALTLIEIVTLVGVGEFVRIAGACCCRRGMGRLEFARK 166
 QY 201 PFCVIDITVILASIAVYSAKTQGNIFATSAIRSLFELILNRVNRDRRGVTKLLGSVY 260
 Db 167 PFCVIDIMVLASIAVLAGSQGNVFAISRLFLIOLINIRDRRGVTKLLGSVY 226
 QY 261 AHSKELITAMVYIGFLVLIFFSFLVLYLEKDKANKREFTYADALIMWGTTITLTIGYDKPEL 320
 Db 227 AHSKELITAMVYIGFLVLIFFSFLVLYLEKDKANKREFTYADALIMWGTTITLTIGYDKPEL 286
 QY 321 TWIGRLISAGFALLIGSFALPAGILGSGFALQVOEOROKHFEKRRNPAALIQVARS 380
 Db 287 TWNGRLIAATFTLIGVSFFALPAGILGSGFALQVOEOROKHFEKRRNPAALIQVARS 346
 QY 381 YAADEKSVSI-ATWK 394
 Db 347 YATWLSRTDLHSTWQ 361

RESULT 32
 AAY08342
 ID AAY08342 standard; Protein: 807 AA.
 AC AAY08342;
 DT 22-JUL-1999 (first entry)
 XX Human nKQT1 protein.
 DE Human nKQT1 protein.
 KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KM benign familial neonatal epilepsy; BPNE; juvenile myotonic epilepsy;
 KM JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KM detection; gene therapy; drug screening; nKQT1.
 XX Homo sapiens.
 OS W09921875-A1.
 PN 06-MAY-1999.
 PD 23-OCT-1998; 98WO-US22375.
 PF 23-OCT-1998; 98WO-US22375.
 XX 24-OCT-1997; 97US-0063147.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Charlier C, Leppert MF, Singh NA;
 PI WPI: 1999-312938/26.
 XX Nucleic acid encoding potassium channels KCNQ2 and 3
 CC
 PS Disclosure: Page 125-128; 195pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement

CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.

XX Sequence 807 AA;

Query Match 25.1%; Score 1188; DB 20; Length 807;
 Best Local Similarity 37.7%; Pred. No. 8.7e-97;
 Matches 285; Conservative 118; Mismatches 186; Indels 166; Gaps 22;

```

QY 75 LRESRRGKOGARMSLGLKPLSTYSSOSCRNRYRVOYNTLVNLERPGW-AFTYHAFV 133
DB 77 LADSEGNR--KMSLGGKPLTY--KNYRDFORFRMRQNMKNHNLERPGWKAATYHNAV 131
QY 134 FLVVGCLLSVSTPEHTKCLASSCLLEFVMIIVVFGLEFIRMSAGCCRRYRNOG 193
DB 132 LFMVLMCLLSVSTPEHTKCLASSCLLEFVMIIVVFGLEFIRMSAGCCRRYRNOG 191
QY 194 RLRFARKEPCVIDITVLIASIAVVSATKGNIFATSRLSLRFLQILRMVMDRRGTWK 253
DB 192 RLRFARSAVCVIDITVLIASIAVVSATKGNIFATSRLSLRFLQILRMVMDRRGTWK 250
QY 254 LIGSVYVAHSEKELITAMTIGFLVLISSFLVYIYVENDANKFEETADALMGTTLTIG 313
DB 251 LIGSVYVAHSEKELITAMTIGFLVLISSFLVYIYVENDANKFEETADALMGTTLTIG 310
QY 314 YGDKTPLMFLGRLSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 373
DB 311 YGDKTPEHPGKIIAFCALLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 370
QY 374 IQCVRSYAADKSVSIATWKR--LKAHLTCSP--TNOKLSFKERVRMSAPRGOSIK 427
DB 371 IQCLMRHYSAPDESLATWIKHLABELPRIVKLTPLGNNATGLINLRQSTKRTPLNL 430
QY 428 SRQASVGRDRS-----PSTDT-----AEG-----SPTVQKWS 457
DB 431 NQMLAVNSQATSKNLSVPRVVRHDTISLSTDISIEIOLGALGFSLGWKSXSGSKK 490
QY 458 FND-----RFRFRPSL-----RLKSOGRPVDAADTALG-- 486
DB 491 ATDDSVLOSRLAPSAHLDMDMRSRRSASLCRYVNTGHLRLQDRSTLSDSDVITDY 550
QY 487 -----TDVYD-----EKGQC 498
DB 551 SLMAPIYOWCEOMYORNSTPGEQVWSQLSOLTTTCATRRREDISDGEBAVGYO- 609
QY 499 DVSVEDLPPKTYIRAIRIMKFNHAKRKPELTPVDVLEOYSAGHDMLCRTSL 558
DB 610 POTIEFTPALNCVRAIRIQLVARKKFKALKRPYDKVLEOYSAGHDMLCRTSL 669
QY 559 QTRVDOLIGQOITSDKSRREKITAHEETDLSMLGRVVKVEKOVOSIESKLCILDIDY 618
DB 670 QAKIDFIG-----KNIETIEPK-----ISMFRITLLETTVYKMKDKLDMVML 715
QY 619 QOVLKGSASALALASFOITPECEQTSOYQSPVDSKLSGSAONSCLSRSTANSIRG 678
DB 716 M-----GQASQGRVFSQNTSP-----RGEFSEPTSAQO-----DLFRSRMSVSTD 756
QY 679 LOFILPNEFSQTFYALSPTMHSQATQYPISSD 713
DB 757 MEM-----YIARSH-----SPGYHGDARPI-IAQID 781

```

RESULT 33
 AAB82236 ID AAB82236 standard: Protein: 676 AA.

XX AAB82236;
 XX 21-JUN-2001 (first entry)
 XX Human KVLQ1 mutant S566F.
 XX DE

KW KVLQ1: Long QT syndrome; LQTS: cardiovascular disease;
 KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
 KW diagnosis; prognosis; therapy; drug screening; mutant; mutenl.

XX Homo sapiens.

PN W0200124681-A2.

PD 12-APR-2001.

PF 09-AUG-2000; 2000WO-0521660.

PR 09-AUG-1999; 99US-0147488.

PR 17-MAR-2000; 2000US-0190057.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

PI WPI; 2001-290564/30.

PT New KVLQ1 and SCN5A genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome -

PS Claim 6; Page -; 76pp; English.

CC The present sequence is that of the claimed S566F mutant of the
 CC human KVLQ1 protein. The mutant is encoded by a KVLQ1 mutant
 CC gene in which a C/T mutation alters codon 566 from TCC to TTC.
 CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:
 CC V110I, E160K, R174H, G179S, A194P, R243C, W248R, I266P, V307S,
 CC V310I, S349W, Q356V, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX Sequence 676 AA;

Query Match 23.3%; Score 1104; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.2e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

```

QY 98 SSQSCRNRNRYR-RVQNTLVNLERPGW-AFTYHAFVLLVFGCLLSVSTIDEHRL 155
DB 92 SITSTRPPLARHVOGRVYVNFLEPRMGKCFYVHFAVLLVLCVLSVSTIQYAL 151
QY 156 ASSCLLIEFVMTVVEGLEFIRMSAGCCCRRYGWCGRLEAFARKEPCVIDITVLIASIA 215
DB 152 ATGTLMEVLELVVFGTEYVRLMSAGCRKYVGLMRLRFPARRPISITIDLVVAVSV 211
QY 216 VVSATKGNIFATSRLSLRFLQILRMVMDRRGTWKLSVYVAHSEKELITAMTIGFL 275
DB 212 VLVGSKGVFAISALRIGIRFLQILRLMLHNDROGTWRLSSVYFIHQELTTLTYIGFL 271
QY 276 VLISSFLVYLVKDA-----NKESTYADALMGTTLTIGYGDKTPFLWGLRLSAG 330
DB 272 GLIFSSYFVYLAEKDAVNESGRVFEYSADALMGVTVITIGYDQVPTWVGKTIASC 331
QY 331 FALGISEFALPAGILGSGFALKVQBOHROKHFEKRRRPAANLIQCVRSYAADKSVSI 390
DB 332 FSVFAISFALPAGILGSGFALKVQBOHROKHFEKRRRPAANLIQCVRSYAADKSVSI 390

```


QY 391 ATWKPHLAL---HT-CSPFNOKLSFRERYRMASPRGOSIKSROASVGDRRSPSTDTITAE 446
 DB 391 -TWKIYIRKAPRSHLTLSPPKP---KSYVYVKKKKFKLDKNDGVTPGEKMLTYPHTICD 446
 QY 447 GSPTRVQKQMS---FNDRTFRPSLRKSSQPKPVIDADATGDDVYDEKGCOCDSVE 503
 DB 447 PPEERLDHFSDVDGYSSVAKSPPTL-LEVSMFH-----FMRINSFAD---LDLEGE 494
 QY 504 DLTPLP-----KTVIRAIRIMKFNHAKRKFKETLRPYDKVDEYSGAGHLMIC 553
 DB 495 TLTPTTHISOLREHHRATIKVIRRMQYFAKKKFOQARRPYDVEDYIEQYSGHLMV 554
 QY 554 RIKSLQTRVDQILGKQ---ITSDKSRREKTTAHEHTTDSMLGRVYVKEKOVOSIESKL 611
 DB 555 RIKEIQRRLDQSGISLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDLQRL 606
 QY 612 DCLLDIYQGVL-----RKGS-----SALALASFOIPEE 641
 DB 607 ALITDMLHQLLSHGSGTPGSGPPREGGAHITQPCGSGGSVDPDLPLPSNTLPTYE 663

RESULT 34

AAB82229

ID AAB82229 standard; Protein; 676 AA.

AC AAB82229;

DT 21-JUN-2001 (first entry)

DE Human KVLQ1 mutant V310I.

KM KVLQ1; Long QT syndrome; LQTS; cardiovascular disease;

KM Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

KM diagnosis; prognosis; therapy; drug screening; mutant; mutain.

OS Homo sapiens.

PN WO200124681-A2.

PD 12-APR-2001.

PF 09-AUG-2000; 2000MO-US21660.

PR 09-AUG-1999; 99US-0147488.

PR 17-MAR-2000; 2000US-0190057.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

DR WPI; 2001-290564/30.

XX

XX Claim 6; Page -: 76pp; English.

CC The present sequence is that of the claimed V310I mutant of the
 CC human KVLQ1 protein. The mutant is encoded by a KVLQ1 mutant
 CC gene in which a G/A mutation alters codon 310 from GTC to ATC.

CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:

CC V310I, S349W, Q356R, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human

CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the sequence listing
 CC (see AAB82220).

SQ Sequence 676 AA;

Query Match 23.3%; Score 1103; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2,7e-69;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSQSCRNVKVR-RVQNYLYNVLPRPGW-AETIYHAFVLLVFGCLLSVSTIPEHTKL 155
 DB 92 SYSTRFRPVLARTHWQGRVYNELERPTGMCFYHNAVFLIVAVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLILFEVMIVYGLFEITIRIMSGACCCRRGMGRIRFARKPCVIDTIVLISIA 215
 DB 152 ATGTLEFMEIVLVEFGTEYVRLWSAGCSKTVGLMGRIRFARKPISITDLVAVASV 211
 QY 216 VVSATQGNIFATSALESRLFLQILRMVMDRRGTWKLISVYVYAHSKELITAMYIGFL 275
 DB 212 VLVGSKGVFATSAIRGIRFLQILMHLMDRGGTWKLISVYVYHROELITLTYIGFL 271
 QY 276 VLISSFLVYVVEKDA----NKESTYADALMGITITITIGYDKTPLTWIGRLISAG 330
 DB 272 GLIFSSYFVYLAEKDAVNESGRVEFSYADALMVGVTITITIGYDKTPLTWIGRTASC 331
 QY 331 FALGIFPALPAGILGSGFALKVQEOHQHKEKRNPAANLIQCWRSTADDEKSVSI 390
 DB 332 FSVFALSPFALPAGILGSGFALKVQOKOROKHNRROIIPAASLIQTMARCYAAENPDS- 390
 QY 391 ATWKPHLAL---HT-CSPFNOKLSFRERYRMASPRGOSIKSROASVGDRRSPSTDTITAE 446
 DB 391 -TWKIYIRKAPRSHLTLSPPKP---KSYVYVKKKKFKLDKNDGVTPGEKMLTYPHTICD 446
 QY 447 GSPTRVQKQMS---FNDRTFRPSLRKSSQPKPVIDADATGDDVYDEKGCOCDSVE 503
 DB 447 PPEERLDHFSDVDGYSSVAKSPPTL-LEVSMFH-----FMRINSFAD---LDLEGE 494
 QY 504 DLTPLP-----KTVIRAIRIMKFNHAKRKFKETLRPYDKVDEYSGAGHLMIC 553
 DB 495 TLTPTTHISOLREHHRATIKVIRRMQYFAKKKFOQARRPYDVEDYIEQYSGHLMV 554
 QY 554 RIKSLQTRVDQILGKQ---ITSDKSRREKTTAHEHTTDSMLGRVYVKEKOVOSIESKL 611
 DB 555 RIKEIQRRLDQSGISLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDLQRL 606
 QY 612 DCLLDIYQGVL-----RKGS-----SALALASFOIPEE 641
 DB 607 ALITDMLHQLLSHGSGTPGSGPPREGGAHITQPCGSGGSVDPDLPLPSNTLPTYE 663

RESULT 35

AAV57368

ID AAV57368 standard; Protein; 676 AA.

AC AAV57368;

DT 19-JUN-2000 (first entry)

DE Human KVLQ1 protein.

KM KVLQ1; KCNE1; Long QT syndrome; LQT syndrome; minK protein;

KM antiarrhythmic; gene therapy; human.

OS Homo sapiens.

PN WO200006600-A1.

PD 10-FEB-2000.

PF 06-OCT-1998; 98WO-US17838.

XX


```

Db      272 GLIFSSYFYVLAEKDAVNESGRVEFGSADALMVGVTVTITIGYGDVPGQTMVGKTIASC 331
QY      331 FALIGSFFALPAGILSGFALKVOEQRHOKHEKRRNPANLIOCVRSTAADKSVSI 390
Db      332 FSVFAISFFALPAGILSGFALKVOEQRHOKHEKRRNPANLIOCVRSTAADKSVSI 390
QY      391 ATKRPHLKAL---HT-CSPFMOKLSFKERVMAASPRGOSISRSQASVGDRLSPSDITAE 446
Db      391 -TWKTIYIRKAPRSHHTLSPSPKP---KRSVYVKKKKFKLDKNGVTPGEKMLTVPHITCD 446
QY      447 GSPTKVKQSWMS---FNDTRFRPRLRLKSQPKPYIDATLGDVYDEKQCQDVSVE 503
Db      447 PPEERRLDHFSDVGDSSVRKSPYL-LEVSMPH-----FMRTNSFAD-----LDLEE 494
QY      504 DLTPPL-----KTVIRAIRIMKFNHAKRKFKETLRPYDVADVIEQYSAGHLDMIC 553
Db      495 TLLPPIITHISQLRHHRATIKIVIRMOYFVAKKKQARKPYDADVIEQYSAGHLDMY 554
QY      554 RIKSLQTRVQOILGKGQ--ITSDDKSREKITAHEHTTDLMLGVRVYKVKQVOSIESKL 611
Db      555 RIKELORLDDOSIGKPSLFISSVEKSKDR-----GSNTIGARLNRYEDKVTQLDORL 606
QY      612 DCLLDIYQOVL-----RKGA-----SALALASFOIPPE 641
Db      607 ALITDMLHQLLSHGSGTPSGGPPREGGAHITQPCGSGSVDPPELFLPSNLTPTYE 663

```

RESULT 37
AAB82220 standard; Protein: 676 AA.

AAB82220:

21-JUN-2001 (first entry)

Human KVLQTL protein.

KVLQTL: Long QT syndrome; LQTS; cardiovascular disease;

Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

diagnosis; prognosis; therapy; drug screening.

Homo sapiens.

MO200124681-A2.

12-Apr-2001.

09-AUG-2000; 2000WO-US21660.

09-AUG-1999; 99US-0147488.

17-MAR-2000; 2000US-0190057.

(UTAH) UNIV UTAH RES FOUND.

Keating MT, Splawski I;

WPI: 2001-290564/30.

N-PSDB: AAF30824.

New KVLQTL and SCN5A genes, which contains alterations or mutations,

useful in diagnostic/prognostic or drug screening methods, particularly

in mutational analyses for screening individuals with or at risk for

long QT syndrome -

Claim 6; Page 59-61; 76pp; English.

The present sequence is that of the protein encoded by the human

KVLQTL gene. This gene is implicated in Romano-Ward syndrome, the

autosomal dominant form of long QT syndrome (LQTS), and in Jervell

and Lange-Nielsen syndrome, a form of LQTS associated with deafness,

a phenotype abnormality inherited in an autosomal recessive fashion.

Novel mutations have been identified in the gene using single strand

conformation polymorphism analysis. These result in the following

CC amino acid alterations: Y111C, E160K, R174H, G179S, A194P, R243C,
CC W248R, I266P, V307SP, V310I, S349W, Q356X, R366Q, T391I, P448R,
CC Q530X, S566F, R583C and R594Q. Isolated human polypeptides
CC comprising such a mutation (see AAB82221-38) are claimed.
CC Knowledge of the mutations provides means for assessing a risk
CC in a human subject for LQTS, for diagnosing a mutation which
CC causes LQTS, and for screening for drugs useful in treating a
CC human having a mutation in the KVLQTL gene.

Sequence 676 AA;

Query Match 23.3%; Score 1102; DB 22; Length 676;

Best Local Similarity 41.9%; Pred. No. 3.3e-89;

Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

```

QY      98 SSOSCRNNVYR-RVQNTLVNVERPRGW-AFIYHAPFLVFPGLITVSPSTPEHRL 155
Db      92 SYSTRBPVLAIRHVGVRVYNERPFGWKCEYHFAVELVLVCLIFSVLSTIEQVAL 151
QY      156 ASSCLITLFEVMIVFGLFETIRMSAGCCCRYGMOGRLEFARKPCVIDITVLASIA 215
Db      152 ATGTFEMELIVLVFETEVYRLMSAGCRSKYVGLMGRLEFARKPISIIDIVVASVY 211
QY      216 VSAKTQGNIPANSALSLRFLQILRMVMDRGGTAKLSSVYVASHKELITAVYIGFL 275
Db      212 VLCVSGKQVFATSAIRGIRFLQILRMVMDRGGTAKLSSVYVASHKELITAVYIGFL 271
QY      276 VLFSSFLVYLVEKDA-----NKEFSYADALMVGVTITITIGYGDTPFLMGLRLSAG 330
Db      272 GLIFSSYFYVLAEKDAVNESGRVEFGSADALMVGVTVTITIGYGDTPQTMVGKTIASC 331
QY      331 FALIGSFFALPAGILSGFALKVOEQRHOKHEKRRNPANLIOCVRSTAADKSVSI 390
Db      332 FSVFAISFFALPAGILSGFALKVOEQRHOKHEKRRNPANLIOCVRSTAADKSVSI 390
QY      391 ATKRPHLKAL---HT-CSPFMOKLSFKERVMAASPRGOSISRSQASVGDRLSPSDITAE 446
Db      391 -TWKTIYIRKAPRSHHTLSPSPKP---KRSVYVKKKKFKLDKNGVTPGEKMLTVPHITCD 446
QY      447 GSPTKVKQSWMS---FNDTRFRPRLRLKSQPKPYIDATLGDVYDEKQCQDVSVE 503
Db      447 PPEERRLDHFSDVGDSSVRKSPYL-LEVSMPH-----FMRTNSFAD-----LDLEE 494
QY      504 DLTPPL-----KTVIRAIRIMKFNHAKRKFKETLRPYDVADVIEQYSAGHLDMIC 553
Db      495 TLLPPIITHISQLRHHRATIKIVIRMOYFVAKKKQARKPYDADVIEQYSAGHLDMY 554
QY      554 RIKSLQTRVQOILGKGQ--ITSDDKSREKITAHEHTTDLMLGVRVYKVKQVOSIESKL 611
Db      555 RIKELORLDDOSIGKPSLFISSVEKSKDR-----GSNTIGARLNRYEDKVTQLDORL 606
QY      612 DCLLDIYQOVL-----RKGA-----SALALASFOIPPE 641
Db      607 ALITDMLHQLLSHGSGTPSGGPPREGGAHITQPCGSGSVDPPELFLPSNLTPTYE 663

```

RESULT 38

AAB82234 standard; Protein: 676 AA.

AAB82234:

21-JUN-2001 (first entry)

Human KVLQTL mutant P448R.

KVLQTL: Long QT syndrome; LQTS; cardiovascular disease;

Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

diagnosis; prognosis; therapy; drug screening; mutant; mutein.

Homo sapiens.

WO200124681-A2.

XX 12-APR-2001.
 PD 09-AUG-2000; 2000MO-US21660.
 PF 09-AUG-1999; 99US-0147488.
 PR 17-MAR-2000; 2000US-0190057.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA Keating MT, Splawski I;
 PI MPI: 2001-290564/30.
 DR
 XX
 XX New KVLQT1 and SCN5A genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome -
 XX
 XX
 PS Claim 6; Page -: 76pp; English.
 CC
 CC The present sequence is that of the claimed P488R mutant of the
 CC human KVLQT1 protein. The mutant is encoded by a KVLQT1 mutant
 CC gene in which a C/G mutation alters codon 488 from CCA to CGA.
 CC Mutations of the KVLQT1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of Long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormally inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQT1 gene
 CC lead to the following amino acid alterations in the KVLQT1 protein:
 CC Y111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307SP,
 CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQT1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQT1 sequence given in the Sequence Listing
 CC (see AAB82220).
 CC
 XX
 SO Sequence 676 AA;
 Query Match 23.3%; Score 1102; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 3,3e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
 QY 98 SSOSCRNVKVR-RVONTLYNVLPRGW-AFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
 DB 92 SIYSTRRVLARTHVQGRVYNLEPRTGKCEYHRAVFLIVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLLLEFVMIYVVEGFEIIRIMSAGCCCRYRGMOGRLEFRARKPCVITIVLASIA 215
 DB 152 ATGTLFMEIYLVVEFGTEYVRLMSAGCRSKYVGLMGRLEFRARKPCVITIVLASIA 211
 QY 216 VSAKTGGINFATSAIRLRLQILRMVMDRGRGKWLKSGVYVHAKSKELLTAWIYGL 275
 DB 212 VLCVSGSGQVFAIRKIRFLQILRMVMDRGRGKWLKSGVYVHAKSKELLTAWIYGL 271
 QY 276 VLIFFSFLVLEKDA-----NKEFSTYADALMWGITITITIGYGDRTPLTWLGRLLSAG 330
 DB 272 GLIFFSYFYVLAEKDAVNESGRVEGVSADALMWGVITITITIGYGDRTPLTWLGRLLSAG 331
 QY 331 FALLGISFFALPAGILSGFALVKVOEHRKHFEKRRNPANLIQCVMRSYADEKSVST 390
 DB 332 FSVFAISFFALPAGILSGFALVKVOEHRKHFEKRRNPANLIQCVMRSYADEKSVST 390
 QY 391 ATWPKPHKAL---HT-CSPTNOKLSFKERVRVRSAPRGOSIKRQASVGRRSSTDTITAE 446
 DB 391 -TWKIYIRKAPRSTITLSPSPK---KTSVYVKKKKFKLDKNGVTPGKMLTVPHITCD 446
 QY 447 GSPRTKYOKSMS---FNDTRFRPSLRKSSQPKPIVADTALGTDDVYDEKGCQCQDVSE 503
 DB 447 PREERIRLDHFSVDGYDSSVRSKPSPL-LEVSMPH-----FWRITNSFAD-----LDLEGE 494

QY 504 DLTPPL-----KTVIRAIRMKFPAKRRKEPLLRPYDVKVIOEYSGAHLMLC 553
 DB 495 TLTPPIRHISQLRHHRRATIVIRMOYFVAKKFKQARKPYDVQVIOEYSGHNLNW 554
 QY 554 RIKSLQTRVDIOLGKQ--ITSDDKSREKITAHEHTTDLISMAGRVYKEKQVQSTIESKL 611
 DB 555 RIKELQRRLDQSIGKPSLFIYSEKSKDR-----GSNTIGARLNREDKVTQDQRL 606
 QY 612 DCLLDIYQOYL-----RKSA-----SALALASFOIPPE 641
 DB 607 ALITDMLHLLSLGSGTPSGGPPREGAHITOPCGSGSVDPPELFLPSNTLPYE 663
 RESULT 39
 AAB49494
 ID AAB49494 standard; Protein; 676 AA.
 XX
 XX AAB49494;
 AC
 XX
 XX 08-MAR-2001 (first entry)
 DT
 XX
 XX Human KVLQT1.
 DE
 XX Human; KVLQT1; antiarrhythmic; cardiact; gene therapy;
 KW cardiac potassium channel; Jervell and Lange-Nielsen syndrome; JLN;
 KW chromosome 11p15.5; long QT syndrome.
 XX
 OS Homo sapiens.
 XX
 XX US6150104-A.
 PN
 XX 21-NOV-2000.
 PD
 XX
 PF 17-AUG-1998; 98US-0135021.
 PR 29-JUL-1998; 98US-0094477.
 PR 13-JUN-1997; 97US-0874655.
 XX
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Keating MT, Splawski I;
 PI MPI: 2001-060013/07.
 DR N-PSDB; AAC89911.
 XX
 XX DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
 PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
 PT or diagnosing or prognosing JLN -
 XX
 XX Example 4; Columns 59-64; 58pp; English.
 PS
 CC The present sequence is wild-type human KVLQT1. KVLQT1 is a cardiac
 CC potassium channel and mutations in the KVLQT1 gene cause Jervell and
 CC Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome 11p15.5. The
 CC present invention relates to a mutant KVLQT1 coding sequence (see
 CC AAC89914). The mutant KVLQT1 coding sequence is useful in the diagnosis
 CC of long QT syndrome and in screening humans for the presence of KVLQT1
 CC gene variants which cause JLN syndrome.
 CC
 XX
 SO Sequence 676 AA;
 Query Match 23.3%; Score 1102; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 3,3e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
 QY 98 SSOSCRNVKVR-RVONTLYNVLPRGW-AFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
 DB 92 SIYSTRRVLARTHVQGRVYNLEPRTGKCEYHRAVFLIVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLLLEFVMIYVVEGFEIIRIMSAGCCCRYRGMOGRLEFRARKPCVITIVLASIA 215
 DB 152 ATGTLFMEIYLVVEFGTEYVRLMSAGCRSKYVGLMGRLEFRARKPCVITIVLASIA 211

```

QY 216 VSAKTGQNFATSAKSLRFLQILRWVRMDRGSTWKLSSVVAHSEKELTAMWIGL 275
D 212 VLVGSFVLYLVEKDA-----NKESTYADALMVGITLTITGYGDKPTLWLGRLLSAG 330
QY 276 VLVGSFVLYLVEKDA-----NKESTYADALMVGITLTITGYGDKPTLWLGRLLSAG 330
D 272 GLTFSITVYLAEKDAVNESGRVEGSIADALMVGIVYTTIGYGDKNPQTWVGKTIASC 331
QY 331 FALGISFPALPAGILSGFALKVOEOROKHFEKRRNPANLLOCWMSYADEKSVSI 390
D 332 FSVFAISFPALPAGILSGFALKVOEOROKHFEKRRNPANLLOCWMSYADEKSVSI 390
QY 391 ATWPHLAL---HT-CSPFNOKLSKREVRNAPRGOSIKRSQASVGDREPSDTITAE 446
D 391 -TWKIYIRKAPRSHLTLSPKPR--KRSVYVKKKKFKLDKONGVTPGKMLTPHITCD 446
QY 447 GSPTRVOKSWS---FNDRTFRPSLRLKSSOPKPVIDADTALGTDDVDEKGCQCQDVSE 503
D 447 PPEERLDHFSVDGDSVSRKSPYL-LEVSMPH-----FMRTNSPFAED---LDLEGE 494
QY 504 DLTPPL-----KTVIRAIRMKFHVAKRKEKTELPRYVDKVIDEYSGHLDMLC 553
D 495 TLLPTPIHISQLRHHRATIKVIRRMQYFVAKKFFQAKRPYDVRDVIDEYSGHILNLW 554
QY 554 RIKSLQTRVDOLLGQ--ITSDKRSREKITAHEHTDLSMLGRVYVKEKQVQSIESTKL 611
D 555 RIKELQRLDOSIGKPSLFTSVSEKSKDR-----GSNTIGARLNKRVEDKQTOLDORL 606
QY 612 DCLDIYQOVL-----RKGSA-----SALALASFOIPEPE 641
D 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGGSVDPELFLPSNTLPTYE 663

RESULT 40
AAEL16618
ID AAEL16618 standard; Protein; 676 AA.
XX
AC AAEL16618;
DT
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ1.
XX
DE Human potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
XX
DE Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
XX
DE dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
XX
DE ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
XX
DE anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
XX
DE addiction; myokymia; Alzheimer's disease; age-associated memory loss;
XX
DE learning deficiency; cognitive disorder; motor disease; neuron disease;
XX
DE neuropsychological disorder; neuropsychological disorder; asthma;
XX
DE neuron cell death; brain tumour; gene therapy; antisense therapy;
XX
DE synaptic transmission; electrical excitability; KCNQ1 protein;
XX
DE cardiac arrhythmia.
XX
OS Homo sapiens.
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US17314.
XX
PR 26-MAY-2000; 2000US-207389P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworeszky SI, Ramanathan CS, Trojacek JT, Boissard CG;
XX
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding

```

```

PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neuropsychological and neuropsychological
PT diseases
PS Disclosure; Fig 5; 128pp; English.
XX
XX The invention relates to potassium channel polypeptides referred to
XX as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
XX polypeptides are useful for identifying compounds that modulate their
XX biological activity. The compounds identified and KCNQ5 polynucleotides
XX are useful for treating acute and chronic pain, migraine, acute stroke,
XX dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
XX (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
XX disorders, depression, bipolar disorder, sleep disorders, eating
XX disorders, addiction, myokymia, Alzheimer's disease, age-associated
XX memory loss, learning deficiencies, cognitive disorders and motor
XX neuron diseases. The nucleic acid molecules of the invention are
XX further useful for treating neuropsychological, neuropsychological
XX disorders, asthma, neuron cell death and brain tumours. They are also
XX used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
XX synaptic transmission and electrical excitability in the brain and are
XX useful for generating antibodies. They are also useful to affinity
XX purify biological effectors from biological materials e.g. disease
XX tissues or cells. The present sequence is human KCNQ1 protein.
XX Mutations in this protein is associated with particular disease
XX e.g. cardiac arrhythmias.
SQ Sequence 676 AA;
QY Query Match 23.3%; Score 1102; DB 23; Length 676;
QY Best Local Similarity 41.9%; Pred. No. 3,3e-89;
QY Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
D 98 SSQCRNRVKKR-RNONTLVNLEPRGM-AIYHAFVLAEGCLISFETPETHL 155
D 92 SIYSTRPVLAARTHOGRVNELEKPCVHPFAVLIVCLIFSVLTIDYAL 151
D 156 ASSCLILEFYMIIVFGEFTIRISAGCCCRYRMOGRPARRPFVDTIVLASIA 215
D 152 ATGTLFWMEIYLVFEGTEYVRLMSAGCRSKYVGLMGRLPARKRISITDILVVAAMV 211
QY 216 VSAKTGQNFATSAKSLRFLQILRWVRMDRGSTWKLSSVVAHSEKELTAMWIGL 275
D 212 VLVGSFVLYLVEKDA-----NKESTYADALMVGITLTITGYGDKPTLWLGRLLSAG 330
QY 276 VLVGSFVLYLVEKDA-----NKESTYADALMVGITLTITGYGDKPTLWLGRLLSAG 330
D 272 GLTFSITVYLAEKDAVNESGRVEGSIADALMVGIVYTTIGYGDKNPQTWVGKTIASC 331
QY 331 FALGISFPALPAGILSGFALKVOEOROKHFEKRRNPANLLOCWMSYADEKSVSI 390
D 332 FSVFAISFPALPAGILSGFALKVOEOROKHFEKRRNPANLLOCWMSYADEKSVSI 390
QY 391 ATWPHLAL---HT-CSPFNOKLSKREVRNAPRGOSIKRSQASVGDREPSDTITAE 446
D 391 -TWKIYIRKAPRSHLTLSPKPR--KRSVYVKKKKFKLDKONGVTPGKMLTPHITCD 446
QY 447 GSPTRVOKSWS---FNDRTFRPSLRLKSSOPKPVIDADTALGTDDVDEKGCQCQDVSE 503
D 447 PPEERLDHFSVDGDSVSRKSPYL-LEVSMPH-----FMRTNSPFAED---LDLEGE 494
QY 504 DLTPPL-----KTVIRAIRMKFHVAKRKEKTELPRYVDKVIDEYSGHLDMLC 553
D 495 TLLPTPIHISQLRHHRATIKVIRRMQYFVAKKFFQAKRPYDVRDVIDEYSGHILNLW 554
QY 554 RIKSLQTRVDOLLGQ--ITSDKRSREKITAHEHTDLSMLGRVYVKEKQVQSIESTKL 611
D 555 RIKELQRLDOSIGKPSLFTSVSEKSKDR-----GSNTIGARLNKRVEDKQTOLDORL 606
QY 612 DCLDIYQOVL-----RKGSA-----SALALASFOIPEPE 641
D 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGGSVDPELFLPSNTLPTYE 663

```



```

QY 98 SSQSCRNNKYR-RVONYLYNVLERPRGM-AFIYHAFVELLVFGCLLSVFSTIPEHTKL 155
DB 92 SIYSTRRPVLARHVGGRVYVNFLEPRGKCFYVHFVFLVLCILSVSTIEQYAL 151
QY 156 ASSCLLLEFVMIVVGLFEITIRMSAGCCCRYRGOGRLFPARKPCFVIDITVILASTA 215
DB 152 AGTLEFMETIVLVFEGTEYVRLMSAGCSKRYVGLMGRLFPARKPISIIDILIVVASAV 211
QY 216 VVSATQGNIFATLSALRSLEFLOILRMVNRDRGRTWKLGSVYVAHSELTAVYIGTL 275
DB 212 VLCVSGKGVFATSAIRGIFLOILRLNHDROGRTWKLGSVYVHNOELITLYIGTL 271
QY 276 VLIFSSFLVYLVKDA-----NKEFSYADALMGWITLTITGYGDKTPTLWGLRLSAG 330
DB 272 GLIFSSFYVYLAEKDAVNESGRVEFGSYDALMGVYVTTITGYGDKVPTWVGKRTIASC 331
QY 331 FALGISFPALPAGILSGFALVQEOHROKHFEKRNPANLIQCVRSYAADKSVSI 390
DB 332 FSVFAISFPALPAGILSGFALVQOKOROKHNRQIPAAASLIQTAWRCYAAENPDSS- 390
QY 391 ATWKPHLKLAL---HT-CSPTNOKLSFERVMAASPRGOSIKSRQASVGDERSPTDITAE 446
DB 391 -TWKITIRKAPRSHLTLLSPSPK---KKSYYVKKKKRKLKDNQVTEGKMLTVPHITCD 446
QY 447 GSPTVQKMS---FNDRTFRPSRLKSSQPKFVIDADTALGTDVYDEKGCQCDVSE 503
DB 447 PEERRLDHFVSDGVSVAKSPTL-LEVSMPH-----FMRTNSFAD-----LDLGE 494
QY 504 DLTPPL-----KTVIRAIRIMKEHVAKRREKTELRYDYDKVDEQYSAHLDMLC 553
DB 495 TLTPITHTISOLREHNRATIKVIRMOYFAKKRFOQARKPYDADVIEQYSGHNLNAV 554
QY 554 RIKSLQTRVDOILGKQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEQVOSIESKL 611
DB 555 RIKELQRLDQSIGKPSLFSVSEKSKDR-----GSNTIGARLNKRVEDKAVQGLDRL 606
QY 612 DCLLDYQOVL-----RKGS-----SALALASQIPEE 641
DB 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGSVDEPLFLPSNTLPTYE 663

```

RESULT 47
AAB82223
ID AAB82223 standard: Protein; 676 AA.

AC AAB82223;
XX
XX 21-JUN-2001 (first entry)
XX
XX Human KVLQTL mutant R174H.
XX
XX KVLQTL; Long QT syndrome; LQTS; cardiovascular disease;
XX Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
XX diagnosis; prognosis; therapy; drug screening; mutant; muten.
XX
XX Homo sapiens.
XX
XX MO200124681-A2.
XX
XX 12-APR-2001.
XX
XX PD 09-AUG-2000; 2000WO-US21660.
XX
XX PE 09-AUG-1999; 99US-0147488.
XX PR 17-MAR-2000; 2000US-0190057.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Keating MT, Splawski I;
XX WPI; 2001-290564/30.
XX
XX New KVLQTL and SCN5A genes, which contains alterations or mutations,
XX
XX

PT useful in diagnostic/prognostic or drug screening methods, particularly
PT in mutational analyses for screening individuals with or at risk for
PT long QT syndrome -

PS Claim 6; Page -; 76pp; English.

CC The present sequence is that of the claimed R174H mutant of the
CC human KVLQTL protein. The mutant is encoded by a KVLQTL mutant
CC gene in which a G/A mutation alters codon 174 from CGC to CAC.
CC Mutations of the KVLQTL gene are implicated in Romano-Ward syndrome,
CC the autosomal dominant form of Long QT syndrome (LQTS), and in
CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
CC deafness, a phenotype abnormality inherited in an autosomal
CC recessive fashion. Mutations newly discovered in the KVLQTL gene
CC lead to the following amino acid alterations in the KVLQTL protein:
CC V111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307S,
CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S565F, R583C and
CC R594Q. Knowledge of the mutations provides means for assessing a
CC risk in a human subject for LQTS, for diagnosing a mutation which
CC causes LQTS, and for screening for drugs useful in treating a human
CC having a mutation in the KVLQTL gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQTL-1 sequence given in the Sequence Listing
CC (see AAB82220).

CC Sequence 676 AA;

Query Match 23.2%; Score 1097; DB 22; Length 676;
Best Local Similarity 41.7%; Pred. No. 9.2e-89;
Matches 249; Conservative 105; Mismatches 165; Indels 78; Gaps 16;

```

QY 98 SSQSCRNNKYR-RVONYLYNVLERPRGM-AFIYHAFVELLVFGCLLSVFSTIPEHTKL 155
DB 92 SIYSTRRPVLARHVGGRVYVNFLEPRGKCFYVHFVFLVLCILSVSTIEQYAL 151
QY 156 ASSCLLLEFVMIVVGLFEITIRMSAGCCCRYRGOGRLFPARKPCFVIDITVILASTA 215
DB 152 AGTLEFMETIVLVFEGTEYVRLMSAGCSKRYVGLMGRLFPARKPISIIDILIVVASAV 211
QY 216 VVSATQGNIFATLSALRSLEFLOILRMVNRDRGRTWKLGSVYVAHSELTAVYIGTL 275
DB 212 VLCVSGKGVFATSAIRGIFLOILRLNHDROGRTWKLGSVYVHNOELITLYIGTL 271
QY 276 VLIFSSFLVYLVKDA-----NKEFSYADALMGWITLTITGYGDKTPTLWGLRLSAG 330
DB 272 GLIFSSFYVYLAEKDAVNESGRVEFGSYADALMGVYVTTITGYGDKVPTWVGKRTIASC 331
QY 331 FALGISFPALPAGILSGFALVQEOHROKHFEKRNPANLIQCVRSYAADKSVSI 390
DB 332 FSVFAISFPALPAGILSGFALVQOKOROKHNRQIPAAASLIQTAWRCYAAENPDSS- 390
QY 391 ATWKPHLKLAL---HT-CSPTNOKLSFERVMAASPRGOSIKSRQASVGDERSPTDITAE 446
DB 391 -TWKITIRKAPRSHLTLLSPSPK---KKSYYVKKKKRKLKDNQVTEGKMLTVPHITCD 446
QY 447 GSPTVQKMS---FNDRTFRPSRLKSSQPKFVIDADTALGTDVYDEKGCQCDVSE 503
DB 447 PEERRLDHFVSDGVSVAKSPTL-LEVSMPH-----FMRTNSFAD-----LDLGE 494
QY 504 DLTPPL-----KTVIRAIRIMKEHVAKRREKTELRYDYDKVDEQYSAHLDMLC 553
DB 495 TLTPITHTISOLREHNRATIKVIRMOYFAKKRFOQARKPYDADVIEQYSGHNLNAV 554
QY 554 RIKSLQTRVDOILGKQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEQVOSIESKL 611
DB 555 RIKELQRLDQSIGKPSLFSVSEKSKDR-----GSNTIGARLNKRVEDKAVQGLDRL 606
QY 612 DCLLDYQOVL-----RKGS-----SALALASQIPEE 641
DB 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGSVDEPLFLPSNTLPTYE 663

```

RESULT 48

CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQT1 gene
 CC lead to the following amino acid alterations in the KVLQT1 protein:
 CC V111C, E160K, R174H, G179S, A194P, R243C, W248R, I266P, V307SP,
 CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566P, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQT1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQT-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX Sequence 676 AA:

Query Match 23.2%; Score 1096; DB 22; Length 676;
 Best Local Similarity 41.7%; Pred. No. 1.4e-88;
 Matches 249; Conservative 105; Mismatches 165; Indels 78; Gaps 16;

```

QY 98 SSOSCRNRYKR-RVQNYLYNVLEPRGW-AFIYHAFVLLVFGCLITSVSTPEHRL 155
DB 92 SIYSTRRPPLARHTVQGRVYNLEPRTGKCFYHFAVFLVLCILFVSITTEQYAL 151
QY 156 ASSCLLIEFVMIIVVEGLEFIIRWSAGCCCRYRGMOGRLEFARKPCVIDITVILASIA 215
DB 152 ATGTLFMEIIVLVFEGTEYVVRILMSAGCSKRYVGLMGRLFAFKPISIIDLIYVVASMV 211
QY 216 VVSATOGNIFATSLRSLRFLQILMVRDRGGMKLLGSVYVANSKEILITMYIGFL 275
DB 212 VLVGSKGQVFAITSARIGIRFLQILMHLVDRGGMKLLGSVYVFIHQEILITLYIGFL 271
QY 276 VLISSFLVLYVEKDA-----NKEFSYADALMMGTITLTIGYDGTPLTLCRLLSAG 330
DB 272 GLIFSSYFYVLAEKDAVNESGRVEFSYADALMMGVTVTTIGDVPOTWVKTTASC 331
QY 331 FALIGISFALPAGILGSGFALKVQOQKHEKRNRPANLITQCYWRYADEXSYSI 390
DB 332 FSVFAISFPALPAGILGSGFALKVQOKOKKHNRQIPAAASLIQTAMRCYAANPDSS- 390
QY 391 ATWKPHLAL---HT-CSPITNOKLSFKERYRMAASPRGOSIKSROASVGDERSPSTDITAE 446
DB 391 -TWIYIKARSHSLSPSP---KRSVYVAKKFKLKDNGCVTPGEKMLIVPHITCD 446
QY 447 GSPTRKQVQWS---ENDTRRPRSLRLKSSQRPVADATLGTDDYDEKCCOCDSVE 503
DB 447 PPEERRLDHFVSVDSSVRSKSPTL-LEVSMFH-----FMRTNSPAED---LDLEGE 494
QY 504 DLTPPL-----KTVIRAIRIMKEHVAKRKEKETLRYVYKDYIEQYSAGHLMCL 553
DB 495 TLLPPIHISQREHRAITIKVIRKQYFVAKKFOQARKPYVRDIEQYSOGHLMV 554
QY 554 RIKSLQTRVQDILGQO---ITSDDKSREKITAHEHETDLSMLGRVVKVQVOSIESKL 611
DB 555 RIKELQRLDQSIGKPSLFISSSEKSDR-----GSNTIGARLNRYEDKTYQDQRL 606
QY 612 DCLLDIYQVU-----RKSGA-----SALASFOIPPEF 641
DB 607 ALITDMLHQLLSLHGSGTPGSGGPPREGAHITPOCGSGSVDPPELPSNTLPTYE 663

```

RESULT 50
 AAB82230
 ID AAB82230 standard; Protein: 676 AA.

XX AAB82230;
 AC
 XX 21-JUN-2001 (first entry)
 DT Human KVLQT1 mutant S349W.
 DE
 XX KVLQT1; Long QT syndrome; LQTS; cardiovascular disease;
 KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

KW diagnosis; prognosis; therapy; drug screening; mutant; mutein.

XX Homo sapiens.

XX WO200124681-A2.

XX 12-APR-2001.

XX 09-AUG-2000; 2000WO-US21660.

XX 09-AUG-1999; 99US-0147488.

XX 17-MAR-2000; 2000US-0190057.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX WPI; 2001-290564/30.

XX New KVLQT1 and SCN5A genes, which contains alterations or mutations,
 XX useful in diagnostic/prognostic or drug screening methods, particularly
 XX in mutational analyses for screening individuals with or at risk for
 XX long QT syndrome

XX Claim 6; Page -: 76pp; English.

The present sequence is that of the claimed S349W mutant of the
 human KVLQT1 protein. The mutant is encoded by a KVLQT1 mutant
 gene in which a C/G mutation alters codon 349 from TCG to TGG.
 Mutations of the KVLQT1 gene are implicated in Romano-Ward syndrome,
 the autosomal dominant form of long QT syndrome (LQTS), and in
 Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 deafness, a phenotype abnormality inherited in an autosomal
 recessive fashion. Mutations newly discovered in the KVLQT1 gene
 lead to the following amino acid alterations in the KVLQT1 protein:
 V111C, E160K, R174H, G179S, A194P, R243C, W248R, I266P, V307SP,
 V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566P, R583C and
 R594Q. Knowledge of the mutations provides means for assessing a
 risk in a human subject for LQTS, for diagnosing a mutation which
 causes LQTS, and for screening for drugs useful in treating a human
 having a mutation in the KVLQT1 gene.
 Note: The present sequence is not shown in the specification but is
 derived from the KVLQT-1 sequence given in the Sequence Listing
 (see AAB82220).

XX Sequence 676 AA:

Query Match 23.1%; Score 1095; DB 22; Length 676;
 Best Local Similarity 41.7%; Pred. No. 1.4e-88;
 Matches 249; Conservative 105; Mismatches 165; Indels 78; Gaps 16;

```

QY 98 SSOSCRNRYKR-RVQNYLYNVLEPRGW-AFIYHAFVLLVFGCLITSVSTPEHRL 155
DB 92 SIYSTRRPPLARHTVQGRVYNLEPRTGKCFYHFAVFLVLCILFVSITTEQYAL 151
QY 156 ASSCLLIEFVMIIVVEGLEFIIRWSAGCCCRYRGMOGRLEFARKPCVIDITVILASIA 215
DB 152 ATGTLFMEIIVLVFEGTEYVVRILMSAGCSKRYVGLMGRLFAFKPISIIDLIYVVASMV 211
QY 216 VVSATOGNIFATSLRSLRFLQILMVRDRGGMKLLGSVYVANSKEILITMYIGFL 275
DB 212 VLVGSKGQVFAITSARIGIRFLQILMHLVDRGGMKLLGSVYVFIHQEILITLYIGFL 271
QY 276 VLISSFLVLYVEKDA-----NKEFSYADALMMGTITLTIGYDGTPLTLCRLLSAG 330
DB 272 GLIFSSYFYVLAEKDAVNESGRVEFSYADALMMGVTVTTIGDVPOTWVKTTASC 331
QY 331 FALIGISFALPAGILGSGFALKVQOQKHEKRNRPANLITQCYWRYADEXSYSI 390
DB 332 FSVFAISFPALPAGILGSGFALKVQOKOKKHNRQIPAAASLIQTAMRCYAANPDSS- 390
QY 391 ATWKPHLAL---HT-CSPITNOKLSFKERYRMAASPRGOSIKSROASVGDERSPSTDITAE 446

```

```

Db      391 -TWKIYIRKAPRSHHTLSPSPKP---KKSvvvkkkkfkldkngvtpgkmltvphtcd 446
QY      447 GSPTKVOKSWS--FNDRTFRPPLSLKKSOPKPYIDATALGTDDVDYDEKGCQCDVSYE 503
Db      447 PPEERLDHFESVDGVDSSVRKSPTL-LEVSMH-----FMRTNSFAD---LDLEGE 494
QY      504 DLTPPL-----KTVIRAIRIMKFFHAKRKFETLRPYDVKDVIEQYSAGHLMYC 553
Db      495 TLLPTPIHISOLREHHRATIVIRRMQYFVAKKFFQAKRPYDVRDVIQYSGHLMYV 554
QY      554 RIKSLQTRVDOILGKQ--ITSDDKSREKITAHEHTDDLSMLGRVVKVEKQVQSIESTKL 611
Db      555 RIKELQRRLDOSTIGKPSLFIYSVEKSKDR-----GSNTIGARLNREDEKVTQLDQRL 606
QY      612 DCLLDIYQOVL-----RKGSa-----SALALASFOIPEPE 641
Db      607 ALITDMLHQLSLHSGSPGSGGPPREGGAHITOPCGSGGSVDPPELFLPSNTLPTYE 663

```

Search completed: June 14, 2003, 17:42:35
 Job time : 87 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:31 ; Search time 48 Seconds
(without alignments)
1848.585 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHHAGGEGGAAGLVWKS.....SICKAGESTDALSPHVKLK 923

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1227.5	25.9	393	2	J05275 voltage-gated pota
2	1226	25.9	744	2	T34116 voltage-gated pota
3	950	20.1	645	2	T27186 hypothetical prote
4	423.5	8.9	664	2	T28852 probable potassium
5	291.5	6.2	858	2	S31761 potassium channel
6	289	6.1	853	1	CHRTD1 potassium channel
7	279	5.9	857	2	I56529 potassium channel
8	272	5.7	802	2	JH0595 potassium channel
9	251	5.3	769	2	I56546 Shaw type potassium
10	248.5	5.3	528	2	T34417 delayed rectifier
11	248.5	5.3	924	2	B41359 potassium channel
12	245	5.2	484	2	T24238 potassium channel
13	245	5.2	581	2	S17150 potassium channel
14	243.5	5.1	679	2	A42073 potassium channel
15	242.5	5.1	490	2	T26983 potassium channel
16	242	5.1	613	2	A39402 potassium channel
17	242	5.1	624	2	S22703 voltage-gated pota
18	241.5	5.1	625	2	E90564 potassium channel
19	241.5	5.1	644	2	S13919 potassium channel
20	241	5.1	263	2	A12384 hypothetical prote
21	238	5.0	654	2	S11049 potassium channel
22	237	5.0	523	2	A38101 potassium channel
23	237	5.0	525	2	A43531 potassium channel
24	235.5	5.0	660	2	S24125 potassium channel
25	235	5.0	624	2	S12746 potassium channel
26	234	4.9	643	2	S00480 potassium channel
27	234	4.9	653	2	A39922 potassium channel
28	233.5	4.9	656	2	JH0193 potassium channel
29	232	4.9	528	2	I84205 potassium channel

30	230	4.9	280	2	E75470 probable ion trans
31	230	4.9	495	2	B39113 potassium channel
32	230	4.9	511	2	A46020 potassium channel
33	230	4.9	511	2	S07095 potassium channel
34	229.5	4.8	495	2	I57680 potassium channel
35	228	4.8	651	2	A39372 potassium channel
36	227.5	4.8	630	2	JU0271 voltage-sensitive
37	227	4.8	585	2	A39395 delayed rectifier
38	226.5	4.8	558	2	T23991 hypothetical prote
39	225	4.8	495	2	A40090 potassium channel
40	223.5	4.7	602	2	JH0166 potassium voltage-
41	222.5	4.7	490	2	A35312 potassium channel
42	221.5	4.7	295	2	C72692 probable potassium
43	220.5	4.6	597	2	S51212 BAK5 protein - bov
44	219	4.6	361	2	S19552 potassium channel
45	215.5	4.6	460	2	T27759 hypothetical prote
46	214.5	4.5	280	2	C62490 probable potassium
47	214.5	4.5	455	2	A70461 potassium channel
48	214.5	4.5	489	2	I51532 potassium channel
49	214.5	4.5	602	2	A49507 potassium channel
50	214	4.5	489	2	JC4787 shaw protein - Cal
51	213	4.5	598	2	S66669 potassium channel
52	212.5	4.5	499	2	I77466 potassium channel
53	212.5	4.5	499	2	A48672 delayed rectifier
54	212.5	4.5	499	2	I84204 potassium channel
55	212.5	4.5	499	2	A33814 potassium channel
56	211.5	4.5	476	2	S21144 potassium channel
57	211.5	4.5	613	2	A56031 potassium channel
58	211	4.5	278	2	AD0651 probable membrane
59	211	4.5	498	2	A41359 potassium channel
60	211	4.5	776	2	T20896 hypothetical prote
61	207	4.4	514	2	C49507 potassium channel
62	207	4.4	530	2	JH0167 potassium channel
63	206.5	4.4	494	2	JC5919 potassium channel
64	203	4.3	482	2	T15829 hypothetical prote
65	200.5	4.2	499	2	JH0313 potassium channel
66	199.5	4.2	513	2	JC5920 potassium channel
67	199	4.2	529	2	S12787 potassium channel
68	198.5	4.2	491	2	T19635 hypothetical prote
69	196	4.1	297	2	A82682 ion transporter XF
70	193	4.1	491	2	JE0276 voltage-gated pota
71	191.5	4.0	236	2	I57681 potassium channel
72	184.5	3.9	247	2	AC1332 voltage-gated pota
73	184.5	3.9	497	2	JE0275 probable potassium
74	181.5	3.8	283	2	B83459 hypothetical prote
75	180	3.8	209	2	C64317 potassium channel
76	176.5	3.7	247	2	AC1703 potassium channel
77	168	3.5	160	2	S60172 potassium channel
78	167.5	3.5	428	2	A82873 potassium channel
79	162.5	3.4	256	2	C97062 potassium channel
80	162.5	3.4	731	2	T09172 probable calcium-a
81	159.5	3.4	2271	2	F90073 hypothetical prote
82	158	3.3	421	2	T29789 hypothetical prote
83	157	3.3	265	2	C95885 probable ionic voi
84	151.5	3.2	5327	2	T13564 microtubule-associ
85	146.5	3.1	338	2	D84067 potassium channel
86	145.5	3.1	1390	2	T18883 hypothetical prote
87	145.5	3.1	1910	2	H88124 protein T12C9.3 f1
88	144.5	3.1	985	2	T27083 hypothetical prote
89	144	3.0	1539	2	T30037 hypothetical prote
90	144	3.0	2206	2	JC5280 voltage-dependent
91	142.5	3.0	1891	2	T43262 calcium channel at
92	142	3.0	2212	2	A41098 conserved hypothet
93	141.5	3.0	256	2	E69166 calcium channel al
94	141	3.0	2161	2	JH0564 calcium channel pr
95	140.5	3.0	2223	2	A47447 hypothetical prote
96	140	3.0	815	2	T08450 voltage-dependent
97	139	2.9	2251	2	B54972 omega-conotoxin-se
98	139	2.9	2336	2	A45386 calcium channel al
99	138.5	2.9	2262	2	T30890 voltage-dependent
100	136.5	2.9	2272	2	C54972 probable calcium-a
101	135.5	2.9	1112	2	T43383 voltage-dependent
102	135	2.9	1610	2	A46227


```

Db      305  FLVAVLGIAETFOAANTQISVGLTLMMEENKNQOTNRILNLANSTIQCMWRHYHA -- 362
QY      386  KSVSIATMKP---HLKALHTC-----SPTNQKLSFKERVRNARSRGOSIKRSQASVCD 435
      363  -----TNKKPPRRRYTFVHVCCKLYTEERIRIQNRVLAKLREKLEKKRPRIKAK--SLTH 415
QY      436  RRSPTDITTAEG---SPTKYKQSWMSFNDRTRFRSRLKSSQPKPEVIDADTALGTDDVY 491
      416  QNSVYAEILKGFGEKGMAKPMLEKQDSF--DKAEIKISLR--RTRKVLFLFEAR--NSSVE 469
QY      492  DEKGQGVQSVEDLPPPLKTVIRAIRIMKFVYAKKRFKET-----LRPYDKVDYEQY 544
Db      470  TSMSSSVDSV-----ELETOPEITNFFQANDVEDSSKQNSQGRSLILMKPQGSTLAQTOR 523
QY      545  SAGHLMDL-----CRKISLQTRVDDIILGKGQITSDPKSREKIKTIAHEHTDDLS 592
      524  IAGGLIMTEAETAEERONORQMKKELEAAILLETGKPTVSPFDDSQK-----LS 573
QY      593  MLGRVYVKEKQVOSTESKLDCLDDI 617
      574  IIERLEFECKEMEDLERKTDALNEL 598
Db

```

RESULT 5

potassium channel protein DRK1 - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C/Accession: S31761
R/Albrecht, B.; Lörta, C.; Stocker, K.; Pongs, O.
submitted to the EMBL Data Library, September 1992
A/Description: Cloning, expression and chromosomal localization of the delayed rectifier
A/Reference number: S31761
A/Accession: S31761
A/Molecule type: DNA
A/Residues: 1-858 <ALB>
A/Cross-references: EMBL:X68302; NID:g30892; PIDN:CAA48374.1; PID:g30893
C/Genetics:
A/Gene: GDB:KCNB1; KV2.1; DRK1
A/Cross-references: GDB:128081; OMIM:600397
A/Map position: 20q13.2-20q13.2
C/Superfamily: potassium channel protein drk1

Query Match

Best Local Similarity 20.2%; Pred. No. 3e-11;
Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33

```

QY 115 LYNNLEBRGNA---FYTHAVFLVPECLLSVSTIPEHKL-----ASSCLLIE 164
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LMDLEKPNSSVAAKILALISIMEVISTALST--NLPELOSLDEFGOSTDNPOLAHVE 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 FVMVIVGLEFIIRIMSAGCCCRFRGMQGRIRFNAKPPCVIDITVLLASINAVSAKTQCN 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 AVCIAMFTMEYLKFLSSP-----KKW-----KFEFGPINALDILALPYYV-----T 276
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 IFATSAISSL-----RFLQILIRAVRMDRRCGTWKLGSVYAAHSEL--ITAM 270
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 IFLSEKSASYVQONVRRVQVIFIMRLIKLILAKHSTGLOSLFTLRIRSTNEIGLTL 336
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 YIGFLVLIFSSFLVYVEKDA--NKEFSYADALMWGITTLTIGIGDKTPLWLGRLISA 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 FLAMGINIFSS--LVFAEKEDDDTKFISIPASFWMATITMTTVGGLDIYKLLKQIVGG 395
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 GFALLGISFALPAGILGSGFALVQDOHRQKHEKRRNPANLIQCVWRSYAADKSYS 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 LCCIAGLVIALPLPIIVNNSEFYKQKQREKAIKR-----EALERRAKRNGS 444
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 IATWPKPLKALHHCSPYNOKLISFEERYRM---ASPRQGISKSROASVGDRRSPSTDTITA 445
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 445 IVS-----NMKDAEFARSIEEMDIYVEKNGENGMKKDKVQDNHLSPKMKWT 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 446 EGSPITKQWSMFNDKTRFRPSLAKSSQRPVYIDADTALGTDDVYDEKGCOCADVSEDL 505
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db	492	KRTISETSSSKFEITKEQSSPEKARSSSSPHL-----	NNQOLEDMYNKMA-----	537
QY	506	TPPLKTVIRALIKMFHNAKKRKFETLRDYDKVDVLEQY	SAGHLMICRIKISQTRVDQI	565
Db	538	-----KTQSOPILNTESSAQSPPKEELEMESIPS-----	-----PVAPLPTRTTEGV	579
QY	566	LKGQITSDPKSREKRTIAEHETFTDLSMGRVVKVEKOV	OSIESKLDCLDIYQOVLKRG	625
Db	580	I-----DMRS-----	-----MSIDSFTISCATD-PPEATRFS	605
QY	626	SASALALASFOIIPPECEQTSDYQSBVDSKDLSGSAQNS	GCSSRSTSANISRGLOFTLIP	685
Db	606	HSPLTSLPS-----KTGGSTAP-EVGNRGALGAGG-	GREVEANPS-----P	644
QY	686	NEFSAQTFYALSP-----TMHSAQTPVPLISOQD-	-----GSAVVA	719
Db	645	DASQHSFFIESPKSMKMTNPDLKIRALVLNFMESG	PSPLLRYLGMYHDLRNRRGAAAA	704
QY	720	T-----NTIANQINTAPRAAFTTLOIPPLPAIKHL	PRPETLHPN-----PAGLOESIS	769
Db	705	VAGLECATILLDKAVLSPSSSIYTTASAKTP-----	PRSPREKHTAIANFENAGVHQYI-	756
QY	770	DVTTCLVASKENVAQAQSNLTGDBRMKRSFDMGGETL	SYSCFVAPVRDQKSLSYVUNLIRS	829
Db	757	DADT-----	-----DDEGOLLVSVDSPKSLGTSIPK-----	785
QY	830	TEELINOLSGSESSGSGSGODEFYPKMRRESKLFIT	DEBEVPELETETPTFPAAPAREAAAF	889
Db	786	-----FSTQTRSEKNHF-----	-----ESSPLTSPRFLRQNCI	814
QY	890	ASDSLRTGRSRSSQISCKAGE-----STDALSLP	918	
Db	815	YSTALTKGSGGQCKLENNHISDPVRVLP	845	

RESULT 6

potassium channel protein drkl - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S05448; A44838
R:Frech, G.C.; Vandongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A:Title: A novel potassium channel with delayed rectifier properties isolated from rat
A:Reference number: S05448; M0ID:89365157; PMID:2770868
A:Accession: S05448
A:Molecule type: mRNA
A:Residues: 1-853 <PRE>
A:Cross-references: EMBL:X16476; NID:957785; PIRN:CAA34497.1; PID:957786
A:Note: It is uncertain whether Met-1 or Met-17 is the Initiator
R:Drewe, J.A.; Verna, S.; Frech, G.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A:Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from d
A:Reference number: A44838; M0ID:92156897; PMID:1740690
A:Accession: A44838
A>Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'MPAG'1-571 <DRE>
A:Cross-references: GB:M01783; NID:9205038
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:81768)
C:Genetics:
A:Gene: drkl
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembra
F:1182/Domain: Intracellular #Status predicted <INT1>
F:183-204/Domain: transmembrane #status predicted <TM1>
F:225-245/Domain: transmembrane #status predicted <TM2>
F:256-276/Domain: transmembrane #status predicted <TM3>
F:291-312/Domain: transmembrane #status predicted <TM4>
F:327-348/Domain: transmembrane #status predicted <TM5>
F:389-410/Domain: transmembrane #status predicted <TM6>
F:411-853/Domain: intracellular #status predicted <INT2>

F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 289; DB 1; Length 853;
Best Local Similarity 19.7%; Pred. No. 4,4e-11;
Matches 176; Conservative 134; Mismatches 269; Indels 316; Gaps 37;

```

115 LYNVLEPRGMA--FIYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLILE 164
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
171 LMDLLEKPNSSVAKILAIISIMFIVSTALSL-NILPELOSIDERGOSTDNPOLAHVE 229
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
165 FVMIVVGEFTIRISAGCCCRYGWGLRFARKPCVDTIVLASIAVSAKTQGN 224
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
230 AVCIAMFTMEYLRLFLSSP-----KKW---KEFKGPLNAIDLAILPYV-----T 272
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
225 IFATSLARSL-----RFLOILRMVRMDRGGTKLLGSVYVAHAKEL-ITAW 270
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
273 IFLETESKSVLQONVRRVVOIFRIMRLRLKLARHSTGLQSGFTLRSYNELGLLIL 332
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
271 YIGFVLIVFSSFLVYLVKDA-NKEFSTYADALMNGITTLTIGYDKTPTLWGLRLISA 329
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
333 FLAMGIMIFSS-LVFEAKEDDDTKFKSIPASFMAITTTMTVGDIYPTLLGKIYGG 391
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
330 GFALLGISFPALPAGILGSPALKVQOHROKHEKRRNPANLILQCVWRSTADEKSVS 389
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
392 LCCIAGLVIALPLPIIVNNESEFYKQKROEKAIKRR----- 429
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
390 IATWKPRLKALHNCSPINOKLSFKERVRMASPRQSIKRSQASVGRDRSPSDITAEGSP 449
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
430 -----EALERAKRNGSIV----- 442
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
450 TKVQKSWSPNDRTRFRPSRLKSSQPKVIDADATLGDVYDEKGCOCOVSVEDLTPL 509
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
443 -----SMMKDAFARSIEH-----MDIYVEKNG----- 465
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
510 KTVIRAIRIMKFNVAKKRKETLAPYDKVIEQYSAGHLDMLCRISLQTRVDOILGK 569
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
466 ESIAKKKQKVDNHLSPNKKMT-----KRALSETSS-----KSPETK----- 503
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
570 QITSDKRSREKITAHEHTDLSMLGRVYKVEKQVQSIKSLDCLDIYQVLRKGSASA 629
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
504 EGSGPEKARSSSSPOH-----LNVQOLE-----DMYSKAKQOSQPI 540
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
630 L---ALASFOIPPECEGTSQSPVDSKDLGSAONSGLSRSTANISRLQITLTPN 686
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
541 LNTKEMAPQSKPPELEMS-MPSVAPL---PARTGVIDMRSSSID---SFTSCAT 592
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
687 EFSAGTYALSP---TMSQATQVPLSQ-----SDGSAVAATNTIANQINT---AP 731
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
593 DFPATRFSSHPLASLSSKAGSSTAPEVGMGALGASGRLETNPIDETSRSGFEVESP 652
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
732 KPAAPPTLQIP-----PLPAIKHLPRPETLHPNP-----AGLOESIS 769
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
653 RSSKATNNPLKRLALKVNFVEGDDPTPLPSL---GLYHDLPLRNKGAAVAAGL-ECAS 707
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
770 DVTTCVLASKENVOVQNSLTKDRSMRK-----SFDMG-----GETLISVCP 811
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
708 LLDKPVLSPESSIIYTTASARTPPRSPEKHTAIAFNFEAGVHHYIDTDEGQLTYSVS 767
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
812 MVRPDLGKSLVONLIRSTELNLTQSGSESGSRGSDQFPKWRSKSLFTIDEVGPPE 871
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
768 SPKPSLHGSTSPK-----FSTGAR----- 786
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
872 TETPTFDAPOPAPAR-----EAAFAASDLRTGRSRSSQISCKAGEST---DALSLP 918
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
787 TEKNHFESSPLPTSKFLRPNCVYSSEGL-TGCKPGAQCKKCLNENTPPDVHMLP 840
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 7

156529

potassium channel protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 20-Aug-1999

C:Accession: I56529

R: Pak, M.D.; Covarrubias, M.; Ratcliffe, A.; Salkoff, L.

J. Neurosci. 11, 869-880, 1991

A:Title: A mouse brain homolog of the Drosophila Shab K⁺ channel with conserved delay

A:Reference number: I56529; MID:91162315; PMID:2002364

A:Accession: I56529

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-857 <RES>

A:Cross-references: GB:M64228; NID:g200975; PIDN:AAA0112.1; PID:g200976

C:Genetics:

A:Gene: Shab

C:Superfamily: potassium channel protein drkl

Query Match 5.9%; Score 279; DB 2; Length 857;

Best Local Similarity 20.4%; Pred. No. 2.1e-10;

Matches 181; Conservative 124; Mismatches 280; Indels 304; Gaps 37;

```

115 LYNVLEPRGMA--FIYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLILE 164
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
175 LMDLLEKPNSSVAKILAIISIMFIVSTALSL-NILPELOSIDERGOSTDNPOLAHVE 233
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
165 FVMIVVGEFTIRISAGCCCRYGWGLRFARKPCVDTIVLASIAVSAKTQGN 224
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
234 AVCIAMFTMEYLRLFLSSP-----KKW---KEFKGPLNAIDLAILPYV-----T 276
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
225 IFATSLARSL-----RFLOILRMVRMDRGGTKLLGSVYVAHAKEL-ITAW 270
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
277 IFLETESKSVLQONVRRVVOIFRIMRLRLKLARHSTGLQSGFTLRSYNELGLLIL 336
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
271 YIGFVLIVFSSFLVYLVKDA-NKEFSTYADALMNGITTLTIGYDKTPTLWGLRLISA 329
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
337 FLAMGIMIFSS-LVFEAKEDDDTKFKSIPASFMAITTTMTVGDIYPTLLGKIYGG 395
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
330 GFALLGISFPALPAGILGSPALKVQOHROKHEKRRNPANLILQCVWRSTADEKSVS 389
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
396 LCCIAGLVIALPLPIIVNNESEFYKQKROEKAIKRR-----EALERAKRNGS 444
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
390 IATWKPRLKALHNCSPINOKLSFKERVRM---ASPRQSIKRSQASVGRDRSPSDITA 445
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
445 IYS-----NMKDAFARSIEHMDIYVEKNGEYAKKQKVDNHLSPNKKMT 491
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
446 EGSPTKVQKSWSPNDRTRFRPSRLKSSQPKVIDADATLGDVYDEKGCOCOVSVEDL 505
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
492 KRALSETSSSKSPETKEGSEKARSSSPHL---NVQOLQDYK---NAKTQS 541
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
506 TPPLKTVIRAIRIMKFNVAKKRKETLAPYDKVIEQYSAGHLDMLCRISLQTRVDO 565
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
542 QPILNT-----KEMAPQSQPELEMS---MPSVAPLPTRTGCV 579
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
566 LGKQITSDKRSREKITAHEHTDLSMLGRVYKVEKQVQSIKSLDCLDIYQVLRKG 625
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
580 I-----DMRS-----MSSIDSFISCATDF----- 598
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
626 SASALALASFOIPPECEGTSQSPVDSKDLGSAONSGLSRSTANISR 677
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
599 -----PEATRFSSHPLAS---LSGSGSSTAPEVGMGALGASGGR--- 636
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
678 GIQFTLTPN---EFSAGTYALSP---TMSQATQVPLSQSDGSAVAATNTIANQ 726
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
637 LMEINPLPEASRSRSGFEVESRSSKMTNNPKMLRLALKVFLGSD----- 679
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
727 INTAPKPAAPPTLQIPPLPAIKHLPRPETLHPNP-----AGLOESISDVTTCL 775
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
680 -----PT---PLPAL-----GLYHDLPLRNKGAAVAAGL-ECASLDRKV 717
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
776 VASKENVOVQNSLTKDRSMRK-----SFDMG-----GETLISVCPMPKDL 817
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
718 LSPSSIIYTTASARTPPRSPEKHTAIAFNFEAGVHHYIDTDEGQLTYSVSIPKSL 777
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
818 GKSLSVONLIRSTELNLTQSGSESGSRGSDQFPKWRSKSLFTIDEVGPPEETDTDF 877
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
778 HGSTSPK-----FSTGAR-----TEKNHF 796
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```


QY 70 GGGGGLRESRRGKOGARMSL-----LGKPLSTYSSOSCRNKKYRVQNTLYNLERP-- 122
 Db 176 GDDPDDEDLGGK---RLGIEDAAGLGGPDG-----KSGRWKRLQPRMALLPEDEYS 224
 QY 123 -RGMAFIYAFVFLVFG-----CL-----ILSVSTPEHKLKSSCLLI 162
 Db 225 SRAARFIAPASLFEILVSTTFTCLETHEAPENIVKNKTEPVINGTSAVLQYELETPALTY 284
 QY 163 LEFVNIIVVGLFEIIRIMSAGCCCRYRGWOGRLFAKRPFCVIDITIVL-----ASIVV 217
 Db 285 VEGCVVWMTFEFLVIVFS-----PNKLEFIKNLNIIDFVAILPFYLVKGLSG 335
 QY 218 SAKTGNIFATSAISSLRLQILIRVMYMDRGGTGWLLGSVVAHSKE-LITAWYIGFLV 276
 Db 336 SSKAAKDVLT--GFLRVVRFRVIRILFKLTHFVGLRVGLHTRASTNEFLLIIFALGV 393
 QY 277 LIFSFLVLYVER-----DANKFSTYADALMWGTTITLTIGYGDTPLTWLCRL 326
 Db 394 LIFAT-MIYYAERVGAQPNPDSASEHTQFNIPDIGFWMAVVTMTLTGYDMYPTWISGML 452
 QY 327 LSAGFALLGISFPFALPAGIL---GSGFALKVOEQ---HROKHF-----EKR 366
 Db 453 VGALCALAGVLIITAMPVPIYVNNFGMYISLAMAOKLPKRKKHIIPAPLASSPTFCKTE 512
 QY 367 RNPAANLIQ---CVMRSYADEKSVSIATWKPPLKALHTCSPT 406
 Db 513 LNMACNSTQSDYCLCKENRLLEHNRSVAS---TLEPMESTSQ 552

RESULT 14

A:Accession: A42073
 A:Species: Mus musculus (house mouse)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Feb-2001
 C:Accession: A42073; S22046
 R:Ghanshani, S.; Pak, M.; McPherson, J.D.; Strong, M.; Dethlefs, B.; Wasmuth, J.J.; Salik
 A:Title: Genomic organization, nucleotide sequence, and cellular distribution of a Shaw
 A:Reference number: A42073; MUID:92155707; PMID:1740329
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-679 <GNA>
 A:Cross-references: GB:X60796; NID:953759; PIDN:CAA43209.1; PID:9817994; GB:X60797
 C:Superfamily: potassium channel protein drkl

Query Match 5.1%; Score 243.5; DB 2; Length 679;
 Best Local Similarity 23.2%; Pred. No. 3.4e-08;
 Matches 96; Conservative 66; Mismatches 160; Indels 91; Gaps 14;

QY 3 RHNAEGEBGAAGLWVKSAAAAAGGRLGSGMKDYESGRGVLLNSAARGDGLILLG 62
 Db 114 RQHRDAEALDSFEAPDSSANNANANNAAGHADGLD--EAGAG-----GGGLDAG 162
 QY 63 TRATL-----GGGGGLRESRRGKOGARMSLGRKLSTSSOSCRNKKYRVQNTLYN 117
 Db 163 GELKRLCFQDAGGAGGLPGARAA--GATW-----WRRQPRVMA 200
 QY 118 VLERP---RGMAFIYAFVFLVFCCLISV-----FTIPEHKLKSS----- 158
 Db 201 LFEDPYSSRARAYAFALFLILISITTFCLTHEFHIHSNTYQASIPGAPPENIT 260
 QY 159 -----CLILFEVMIYVGLFEIIRIMSAGCCCRYRGWOGRLFAKRPFCVIDITVL 210
 Db 261 NVEVETEFLLYVGVGVWMTFEFLMRV---TFC-----PDKVEFLKSLNIIDCVAI 311
 QY 211 I-----ASIVVSAKTGQINIFATSLRSLRFLQILIRVMYMDRGGTGWLLGSVVAHSKE 265
 Db 312 LPTFLEVLGLSLSSKAANDVL--GFLRVVRFRVIRILFKLTHFVGLRVGLHTRASTNE 369
 QY 266 -LITAWYIGFLVLIIFSFLVLYVLEKDANKE-----FSTYADALMWGTTITLTIGYG 315
 Db 370 FLILITFLALGVLIIFATMIYYAERIGADPDGLISNHTYFKNIPIGFWMAVVTMTLTIGYG 429

QY 316 DKTPITWLGRLSAGFALLGISFPFALPAGILGSGFALKVOEQHROKHFERRN 368
 Db 430 DMTPTKWSGMLVGLCALAGVLTITAMPVPIYVNNFGMYISLAMAOKLPKRKN 482

RESULT 15

A:Accession: T26983
 A:Species: hypothetical protein Y48A6B.6 - Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
 C:Accession: T26983
 R:Gardner, A.
 A:Submitted to the EMBL Data Library, June 1998
 A:Reference number: Z20295

A:Accession: T26983
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-490 <WIL>
 A:Cross-references: EMBL:AL023844; PIDN:CAA19530.1; GSPDB:GN00021; CESP:Y48A6B.6
 A:Experimental source: clone Y48A6B
 A:Genetics:
 A:Gene: CESP:Y48A6B.6
 A:Map position: 3
 A:Introns: 34/2; 94/1; 138/1; 175/3; 256/1; 282/1; 365/3; 410/2; 419/1; 429/1; 452/3
 C:Superfamily: potassium channel protein drkl

Query Match 5.1%; Score 242.5; DB 2; Length 490;
 Best Local Similarity 27.1%; Pred. No. 2.4e-08;
 Matches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

QY 104 RNKYRVQNTLYNLERP---RGMAFIYAFVFLV-FGLISVSTPEHKLKSS 158
 Db 192 KTLRFGEIRRCVWNITIEPPASSGKAQFAVCSVFLVLSIGLVLSLPELQVATKQRKN 251

QY 159 -----CLILFEVMIYVGLFEIIRIMSAGCCCRYRGWOGRLR---FARKP 201
 Db 252 LNGEFTFEMPMPILGIYEVCIWFMVEYGLKMLVS--ADRSKTFRLNITIDLLALIP 309

QY 202 FCVIDITIVLIASIAVVASAKQGNIFALSRLFLQILIRVMYMDRGGTGWLLGSVVA 261
 Db 310 F-IIEMLLIFGISTEQLRLKGAFL--VRIILVLRIRVRLKGRYSSGLQMFCKTLKA 366

QY 262 HSKELITAWYIGFLVLIIFSFLVLYVLEKD--ANKFSTYADALMWGTTITLTIGYDQHR 319
 Db 367 SFRQLGMAMVWVTGVIFESTVLYVLEKDEASK-FHSIPAAKWCIVTMTTIVGIGDLP 425

QY 320 LTMGLRLSAGFALLGISFPFALPAGILGSGFALKVOEQHR 359
 Db 426 VTVPGKLVATGAIACGVLVLPITLITVDNF-MKVAETER 464

RESULT 16

A:Accession: A39402
 A:Species: potassium channel protein IIA form 1, shaker-type - rat
 C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Feb-2001
 C:Accession: A39402
 R:McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
 A:Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
 A:Reference number: A39402; MUID:91219512; PMID:2023956

A:Contents: eriatum
 A:Accession: A39402
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-613 <MCC>
 A:Cross-references: GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914
 C:Superfamily: potassium channel protein drkl

Query Match 5.1%; Score 242; DB 2; Length 613;
 Best Local Similarity 24.1%; Pred. No. 3.6e-08;
 Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY	70	GGGGGRRSRNRKQGRMSL-----LCKPLSTYSSQSRNKKYRVQNYLVNERP--	122
Db	176	GGDDDEDDLGK---RLGIEDAAGLGPGD-----KSGRRKKLPQRMALFEDPDS	224
QY	123	-RGMAFIHAFVELLVFG---CL-----ILVESTIEHTKLASCLLI	162
Db	225	SRAAFINAFSLFELIVSITTFPLETHFHEAFINVKNKTEPVIINGTSAVLQYELIETDPA	284
QY	163	LEFVNIIVFGLEFIIRIMSGCCCRKRGWGRLEFRAPKPFECVIDTIVLI-----	217
Db	285	VEGCVVWTFPEFELIVRIFS-----PNKLEFIKLNLIIDFVALIPFYLEVGLSGL	335
QY	218	SAKTQGNIFATSAKSLRFLQIILRMVMDRGRGKMWKLGSVYVAHSKE-LITAMVIGFLV	276
Db	336	SSKAAKDYV--GFLRVRRFVRIIRIEKLTIRHFVGLRVLYGHLRASTNEILLIIIFALGV	393
QY	277	LIEESFLIVLVK-----DANKEFSYADALIMWGTLITLTIGYGDKPPLTWGLRL	326
Db	394	LIEAF-mIYAEVEVGAQPNPDSASEHTQFNKPIGFWMAVAVMTLTIGYGDMPQIWSGML	452
QY	327	LSAGFALLGISFFALPAGIL-----GSGFALKVQEO-----HROKH	362
Db	453	VGALCALAGVLTITAMPVPIVYVNNFGMTYSLAMAOQKPRKKKH	496

RESULT 17

voltage-gated potassium channel protein Raw1 - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-2001
 C.Accession: S22703; A45292; S19099
 C.Retting, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Beckh, S.; Rues
 EMO J. 11, 2473-2486, 1992
 A.Title: Characterization of a shaw-related potassium channel family in rat brain.
 A.Reference number: S22702; MUID:92331599; PMID:1378392
 A.Accession: S22703
 A.Status: nucleic acid sequence not shown
 A.Molecule type: mRNA
 A.Residues: 1-624 <RET>
 A.Cross-references: EMBL:X62839; NID:g57650; PIND:CAA4643.1; PID:g57651
 R.Rudy, B.; Kentros, C.; Weisler, M.; Frituhling, D.; Serodio, P.; Vega-Saenz de Miera, E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
 A.Title: Region-specific expression of a K⁺ channel gene in brain.
 A.Reference number: A45292; MUID:92262488; PMID:1374908
 A.Accession: A45292
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 594-624 <RND>
 A.Note: sequence extracted from NCBI backbone (NCBIN:102300, NCBIIP:102305)
 C.Superfamily: potassium channel protein drkl
 C.Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
 F.230-246/Domain: transmembrane #status predicted <TM1>
 F.282-303/Domain: transmembrane #status predicted <TM2>
 F.315-335/Domain: transmembrane #status predicted <TM3>
 F.347-365/Domain: transmembrane #status predicted <TM4>
 F.382-401/Domain: transmembrane #status predicted <TM5>
 F.452-473/Domain: transmembrane #status predicted <TM6>

Query Match	5.1%	Score 242;	DB 2;	Length 624;
Best Local Similarity	24.1%	Pred. NO. 3.7e-08;		
Matches 83; Conservative	70;	Mismatches 117;	Indels 74;	Gaps 14;

```

QY 70 GGGGGLREERNRKQAGRMML-----LGKPLSTYSOSSCRNNVYRRVQVNLVAVLRP--122
    || || || || || || || || || || || || || || || || || || || || || ||
Db 176 GGDPPDDELGLGK---RLGIEDPAAGLGPDG-----KSGWRKLTQPMMLALFDPDYS 224
    || || || || || || || || || || || || || || || || || || || || || ||

QY 123 -RGMAFIYHAFVLLVFG-----CL-----ILSYESRIPEHTKLASSCLL 162
    || || || || || || || || || || || || || || || || || || || || || ||
Db 225 SNAARFIARASLFILVSTTTCLEHNEAFNYKNTKEVYINQTSAVLOYEIEDRALTY 264
    || || || || || || || || || || || || || || || || || || || || || ||

QY 163 LEFVMIYVGLIEIIRIMSAGCCCRKRYRQMOGRIRFARKRPECVDTIVL-----ASTAVV 217
    || || || || || || || || || || || || || || || || || || || || || ||
Db 285 VGVGVCMVPTFEFLVIVS-----PNKLEIFKNLNIIDPAALFEYILEVGSIGL 335
    || || || || || || || || || || || || || || || || || || || || || ||

```

```
QY      218 SAKOQGNIFEARISALBSLEFLOLIRAVRMDRGCKWKLIGSVYAHKE--LITAMYGFLV 276
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       336 SSKAKDVL--GELEVRFRVRLIRLFKLRHFEGLREGLHTLRASINELLLLIFALGV 393
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      277 LIFSSELYVEVK-----DNKERSTYADALMVGITLTITTGCGDKPLTWLGRL 326
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       394 LIFFAT-MIYYERVAQAQRPDPSASEHTQKNPIGFWMAVVMTITLIGYGDMPQTWSGM 452
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      327 LSAGFAILGISFFALPAGIL-----GGSGFALVOEQ---HRÖKH 362
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       453 VGALCALAGVLIAMPVPVIYNVFCGYYSLAAMAKÖLPRKRKKH 496
```

RESULT 18

potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C.Accession: E90564
R.Chemband, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A.Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma P
A.Reference number: A93512; M01D:21267165; PMID:11353084
A.Accession: E90564
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-344 <NUR>
A.Cross-References: GB:AL44556; PID:g14089835; PIDN:CAC13594.1; GSPDE:GN00153
A.Experimental source: strain UAB CTIP
C.Genetics:
A.Gene: MPPU_4210
A.Genetic code: SGC3

Query Match	5.1%;	Score 241.5;	DB 2;	Length 344;
Best Local Similarity	26.3%;	Pred. No. 1.6e-08;		
Matches 81;	Conservative 69;	Mismatches 109;	Indels 45	

Best Local Similarity 26.3%; Pred. No. 1.6e-08;
Matches 81; Conservative 69; Mismatches 109; Indels 49; Gaps 12.

QY 105 NVKRYRVQNYLYNVL-----ERPRGMAF--IYHAFVFLVFGCLISVESTPEHTK 154

Db 9 NÖKYLNIAKHLNNVAINEKSEKEDÖPKVNLIVDYLRKIMFIVVLSFIILSFLLIDKKE 68

155 LAS--SCLLLEFWMIVFGLFIIRIWSAGCCCPYRGWQGBLRFARKPCVIDITVLA 212

Db 69 IASNSFEFLVIELTIFVLLVDF--LMTFTYPIKNG--KLISMIIEFF-TFTGILVS 1233

QY 213 SIAB-----VSAKTQGNIF-----ATISALRSLRFLQILRMVRMDRGGT 25

Db 124 SFVPSIWLAEFTENKDINVESQNNKVPKTFEISQVLSFLRSLVFLRGGVLMLLQVFEF 183

252 WKLGSVYAHSKELITAW-YIGFLVLTFSSFLVIVE---KDNKESFYADALMNGTI 307

184 PKILYRAFKNKKILLISLFFVFIILLILLF-SLIISVETIGENANPNIKNYWDALVFTTI 244

QY 308 TLTTTIGYDKPTLWLGRLLSAGFALLGISFALPAGILGSCFALKVQEQ-----HRQK 36

Db 243 SMTTIGIGDISPVTNGKIILVTSITGATLFAISGVIAAGFLAEIQKINNQNNEEE 302

QY 362 HEKRRNP 369 .
 . I I . I I

Db 303 NFFKKLNP 310

RESULT 10

potassium channel protein Raw3 - rat

C.Species: *Rattus norvegicus* (Norway rat)
 C.Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 16-Feb-2001

C/Accession: SI3919; S22702
R:Schroeter, K.H.; Rumpersberg, J.P.; Wunster, F.; Rettig, J.; Stocker, M.; Pot

A: Title: Cloning and functional expression of a TEA-sensitive A-type potassium

A; Reference number: S13919; MUID:91122287; PMID:1840526

11

A:Accession: S13919
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-625 <SCH>
 A:Cross-references: EMBL:X62841; NID:g57648; PIDN:CAA44645.1; PID:g57649
 R:Retley, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Beckh, S.; Kues, E.M.B.O. J. 11, 2473-2486, 1992
 A:Title: Characterization of a shaw-related potassium channel family in rat brain.
 A:Reference number: S22702; MUID:92331599; PMID:1378392
 A:Accession: S22702
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-625 <RET>
 A:Cross-references: EMBL:X62841; NID:g57648; PIDN:CAA44645.1; PID:g57649
 C:Superfamily: potassium channel protein drk1
 C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
 F:228-246/Domain: transmembrane #status predicted <TM1>
 F:282-303/Domain: transmembrane #status predicted <TM2>
 F:315-335/Domain: transmembrane #status predicted <TM3>
 F:347-365/Domain: transmembrane #status predicted <TM4>
 F:382-401/Domain: transmembrane #status predicted <TM5>
 F:452-473/Domain: transmembrane #status predicted <TM6>
 F:257-266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 241.5; DB 2; Length 625;
 Best Local Similarity 21.9%; Pred. No. 4.1e-08;
 Matches 113; Conservative 75; Mismatches 194; Indels 133; Gaps 19;

OY 3 RHNAGGE-----GGAAGLWVKSAAAAAGGRLGSGMKDVGSGRGLNSA 51
 DB 150 RQHDAEALDIFESPDGGGAGPGDEGDDERELALRLGH-----EGSGP----- 199
 OY 52 AARDDGLLLGTRAAITLGGGGGLRESRRKQCARNSLLGKPLSYSSQCRNRYRY 111
 DB 200 -----GAGSGG-----RGQPRMMLFEDPYSSRA----- 226
 OY 112 QNLYLVNERPGMAFIYHAFVLLVFCGL-----ILSVSTPEHKLAS----- 157
 DB 227 -----RYVAERSLFFILVSTTF-CLTHEAFNIDRNVEIHRVGNITSVRRREV 276
 OY 158 ---SCLILEFVMIVFGLFIRIWSAGCCCRYGQGLRFAKPKFCVDTIVLI--- 211
 DB 277 ETEPLIYIEGVCMWFFLEFLVRI-----VCC-----PRLDGVKLNINIDVAILPFY 327
 OY 212 --ASIANVSAKTQGNIFATSLRSIRFQITLMVRMDRRGGTWKLGSVVAHAKS-LIT 268
 DB 328 LEVGLSGLSSKAARDVL--GFLRVRFVRLIRFKLTHFVGLRVGHTLRASINTELL 385
 OY 269 AWYIGFVLFSSFLVYLVK-----DANKEFSYADALMWGTTITLTIGGDKT 318
 DB 386 ITFLALGVLLFAT-MIYAEIRIGARPSPPRGMDHTDFKNIPGFVMAVVTMTLGGDMY 444
 OY 319 PLTWGLRLSAGFALLGISFPALPAGILGSGFALVKV--EOHQKHKKRRNPAANLIQCV 377
 DB 445 PKTWSGLVGCALGVLITAMPVPIVNNNGMYISLAMAQKLPKRRKKHVRPPPLE 504
 OY 378 WRSYADDEKSVSTATWPKHALHTCSPFNOKLSKERVRMAVSPRGQSIKRSQASVDDR 437
 DB 505 SPLIKSEER-----SPRSTYSYDTSPPAREEGVEKRRADSKON-----GDAN 548
 OY 438 SPSTDTIAEG-----SPTRVOKSWSPNDTRFR 465
 DB 549 AVLSDEBAGLTOPLASAPTPPEERRALRRSGTRDR 583

RESULT 20
 A12384
 Hypothetical protein all4633 (imported) - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: A12384
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguhi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: A12384
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076332.1; PID:g17133770; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all4633

Query Match 5.1%; Score 241; DB 2; Length 263;
 Best Local Similarity 27.1%; Pred. No. 1.2e-08;
 Matches 65; Conservative 55; Mismatches 94; Indels 26; Gaps 6;

OY 109 RRYQNYLVNERPGMAFIYHAFVLLVFCGLILSVSTPEHKLASCLLLEFYMI 168
 DB 5 RQTEFYLVNDELPLGKALNLTAVLVLLSSGIFVAQYALPDSIRLQ--LDQIDYVIL 61
 OY 169 VYFGLFIRIWSAGCCCRKRGQRLRFAKPKFCVDTIVLIASIAVSAKTQGNIFAT 228
 DB 62 VIFAEVYVLRMSA-----ENKLYFSEFAIIDLALTEPLL-----GLVNI 104
 OY 229 SALRSIRFQILMVR-MDRRGTWKLGSGVVAHAKSKEITPAWYIGFVLFSSFLVYLV 287
 DB 105 SFIRILMRIRLIRLIFIDK-----FLFGSISSDGIIFIRLITFLITFIYVSSLIQV 160
 OY 288 EKDANKE-RSTYADALMWGTTITLTIGYGKTPPLTWKRLLSAGFALLGISFPALPACIL 346
 DB 161 EHPVNAQVSTFLDAEFVSVMVTWVGFGDVPISLGRLLTVMILTGVAIIPQVQDL 220

RESULT 21

S11049
 potassium channel protein - rat
 N:Alternate names: potassium channel RK3; shaker-related potassium channel RCK4
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
 C:Accession: S11049; E39113; S06710
 R:Tseeng-Crark, J.C.L.; Tseeng, G.N.; Schwartz, A.; Tanouye, M.A.
 FEBS Lett. 268, 63-68, 1990
 A:Title: Molecular cloning and functional expression of a potassium channel cDNA iso1
 A:Reference number: S11049; MUID:90346174; PMID:2384173
 A:Accession: S11049

A:Molecule type: mRNA
 A:Residues: 1-654 <TSE>
 A:Cross-references: GB:M32867; NID:g205042; PIDN:AAA41469.1; PID:g205043
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan
 A:Reference number: A39113; MUID:91156654; PMID:1705709
 A:Accession: E39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-41, 'A', '43-83, 'G', '310-654 <ROB>
 R:Stuehmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,
 E.M.B.O. J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
 A:Reference number: S06708; MUID:90059914; PMID:2555158
 A:Accession: S06710

A:Molecule type: mRNA
 A:Residues: 1-41, 'A', '43-83, 'EEAT', '89-94, 'K', '95-308, 'G', '310-654 <STU>
 A:Cross-references: EMBL:X16002; NID:g57036; PIDN:CAA34133.1; PID:g57037
 C:Superfamily: potassium channel protein drk1
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:309-327/Domain: transmembrane #status predicted <TM1>
 F:372-393/Domain: transmembrane #status predicted <TM2>
 F:405-424/Domain: transmembrane #status predicted <TM3>
 F:425-462/Domain: transmembrane #status predicted <TM4>
 F:479-498/Domain: transmembrane #status predicted <TM5>
 F:514-523/Domain: transmembrane beta strand #status predicted <TM6>

F:524-532/Domain: transmembrane beta strand #status predicted <TMb2>
 F:540-562/Domain: transmembrane #status predicted <TM6>
 F:553/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:600/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 5.0%; Score 238; DB 2; Length 654;
 Best Local Similarity 21.5%; Pred. No. 7,4e-08;
 Matches 74; Conservative 62; Mismatches 116; Indels 92; Gaps 10;

QY 135 LVFGCLILSVSTFPE-----HTKLASSC-----LTL 163
 Db 136 LVILISIVFCLFLEPFRRDRLIMALSAGHSRLNDTSAPHLNENGHITFNDPFIV 375
 QY 164 EFMIYVFGLEFIIRMSAGCCCRVGRMGRLRFARPCVITVLI---ASIAVVSXK 220
 Db 376 EYICVIFWSEFVYRCFAC-----PSQALFFKINIMNIDIVSILPYFTLTGLDIAQ 426
 QY 221 TQC-----NIFATSLRSLRFLQILRMVMDRRKGTWKLGSVYVAHSEKLTAWYIG 273
 Db 427 QQGGNGQQQQAAMFALIRIRLVRFIRFKLSRSGKQLQILGHFLRASMRELGLIFPL 486
 QY 274 FLVLISSFLVLYVEKD-ANKKESTYADALMMGTTLTITIGYDKTPLTWGRLLSAGFA 332
 Db 487 FIGVILFSSAVYFAEADPTTHFQSIDPAFWAVVMTVTGVDKMKPTVGGKIVGSLCA 546
 QY 333 LIGSFFALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCVWRSYVADEKSVSIAT 392
 Db 547 IAGVLTALPVPVIVSNF---FYHRETEDEOTQLQONAVSC----- 587
 QY 393 WKPHLKALHTCSPTNOKLSFKERVMSAPRGOSIKSROASVGR 436
 Db 588 --PVL-----PSNLKKFR-----SSTSSSLGDK 609

RESULT 22

A38101
 potassium channel KCNA3 - human

N:Alternate names: potassium channel HLK3; potassium channel PCN3; shaker-related potass
 C:Species: Homo sapiens (man)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 01-Dec-2000

A:Accession: A38101; B38556; I52990
 R:Altali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ricar
 J. Biol. Chem. 267, 8650-8657, 1992
 A:Title: Cloning, functional expression, and regulation of two K(+) channels in human T
 A:Reference number: A38101; MUID:92235098; PMID:1373731

A:Accession: A38101
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-523 <ATT>
 A:Cross-references: GB:M55217; NID:q186664; PID:AAA59457.1; PID:q186665
 R:Phillipson, L.H.; Hice, R.E.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Nelson, D.J.; St
 Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
 A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and
 A:Reference number: A38556; MUID:91095456; PMID:1986582

A:Accession: B38556
 A:Molecule type: DNA
 A:Residues: 1-19, 'G', 21-36, 'V', 38-60, 'U', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS', 4
 R:Gal, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
 DNA Cell Biol. 11, 163-172, 1992
 A:Title: Characterization and functional expression of genomic DNA encoding the human 1y
 A:Reference number: I52990; MUID:92189730; PMID:1547020

A:Accession: I52990
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-60, 'U', 62-523 <RES>

A:Cross-references: GB:M38217; NID:q186670; PID:AA88073.1; PID:q186671
 C:Genetics:

A:Gene: GDB:KCNA3; HGK5
 A:Cross-references: GDB:128079; OMIM:176263
 A:Map position: 1p21-1p13.3
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; vola

Query Match 5.0%; Score 237; DB 2; Length 523;
 Best Local Similarity 22.2%; Pred. No. 6,2e-08;
 Matches 68; Conservative 64; Mismatches 114; Indels 60; Gaps 8;

QY 104 RNKRYRVOYLYNVLERP-----KGMATYNAFVLVFGCLILSVSTFPEH----- 152
 Db 157 RPLPRDFQWVLMFLFEPSSGPARIAIV---SVLVILISIVFCLFLEPFRRDKD 212
 QY 153 -----TKLASSCLILFVMIYVFGLEFIIRMSAGCCCR 189
 Db 213 YPASTQDSPEAAGNSTSGSRAGASSPSDFVEVETCLTFSEFLRFPAC----- 265
 QY 190 GMGRLRFARPCVITVLI---ASIAVVSXKTCGN---IFATSLRSLRFLQILRMV 243
 Db 266 --PSKATFSNINMLDIVALIIPFTLTGLTELAROGNGQQAAMFALIRLVRFIRF 323
 QY 244 RMDRGGTWKLGSVYVAHSEKLTAWYIGFLVLISSFLVLYVEKDANKFSTYDAL 302
 Db 324 KLSRHSKGLQILGOTLKASMELEGLIFLEFVIGVILFSSAVYFAEADPTSGFSIPDAF 383
 QY 303 WMGTTLTITIGYDKTPLTWGRLLSAGFALGISFPLPAGILGSGF-----ALKVOE 356
 Db 384 WMAVVTMTVTGVDKMKPTVGGKIVGSLCATAGVLTALPVPVIVSNFYHRETEDE 443
 QY 357 QHROKH 362
 Db 444 QSQYMH 449

RESULT 23

A43531
 potassium channel Kv1.3 - rat

N:Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel R
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 17-Nov-2000

A:Accession: A43531; JH0168; S06708
 R:Douglass, J.; Osborne, P.B.; Cai, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P
 J. Immunol. 144, 4841-4850, 1990
 A:Title: Characterization and functional expression of a rat genomic DNA clone encodi
 A:Reference number: A43531; MUID:90278098; PMID:2351830

A:Accession: A43531
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-525 <DOU>

A:Cross-references: GB:M30312
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Polander, K.;
 Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec
 A:Reference number: JH0166; MUID:90297965; PMID:2361015

A:Accession: JH0168
 A:Molecule type: DNA
 A:Residues: 1-180, 'G', 182-525 <SMA>
 A:Cross-references: GB:M31744; NID:9205104; PID:AAA41500.1; PID:9205105

A:Experimental source: brain
 A:Note: only a list of differences from sequence S06708 is given
 R:Stuehrmer, W.; Ruppertsberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,
 EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
 A:Reference number: S06708; MUID:90059914; PMID:2555158

A:Accession: S06708
 A:Molecule type: mRNA
 A:Residues: 1-105, 'U', 107-180, 'G', 182-525 <STU>
 A:Cross-references: EMBL:X16001; NID:957034; PID:CAA34132.1; PID:957035
 C:Superfamily: potassium channel protein drkl

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:185-203/Domain: transmembrane #status predicted <TM1>
 F:245-266/Domain: transmembrane #status predicted <TM2>
 F:278-298/Domain: transmembrane #status predicted <TM3>
 F:313-331/Domain: transmembrane #status predicted <TM4>
 F:348-367/Domain: transmembrane #status predicted <TM5>
 F:383-392/Domain: transmembrane beta strand #status predicted <TMb1>
 F:393-401/Domain: transmembrane beta strand #status predicted <TMb2>

A:Accession: S01111
A:Molecule type: mRNA
A:Residues: 1-643 <SCS>
A>Note: the clone is designated as SHD1
R:Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 332, 740, 1988
A:Reference number: S01113
A:Contents: annotation; erratum
C:Genetics:
A:Gene: Shaker
A:Cross-references: FlyBase:FBgn0003380
C:Superfamily: potassium channel protein drk1
C:Keywords: alternative splicing; transmembrane protein

Query Match 4.9%; Score 234; DB 2; Length 643;
Best Local Similarity 22.4%; Pred. No. 1,3e-07;
Matches 87; Conservative 61; Mismatches 150; Indels 90; Gaps 11;

QY 128 IYHAFVFL-VEGCL-----ILSVSTIPEHTKL-----ASSCLILEFYMIWV 171
Db IISVFIILSIYFICLETLPPEFKHYKVFNTTNGTKIEDEVPDITDPFLETLIIWF 278
QY 172 GLEFIIRMSACCCCYRQGRLEFRARKPCVDTIVL--ASIAVYSA----- 219
Db 279 TFEITV-----RFLACPKNLFCRDYMNVTIDTIIIPYFTIATVAEEDTLNLP 329
QY 220 -----KTQGNIFATSLRLSLFQILRLMVRMDRSGTWKLIGSVYVAHSEK-ITAM 270
Db 330 KAPVSPQKSSNQAMSLALRLVRLVRVFRILFKLSRSGQLIIGRTLKASMRLEGLIF 389
QY 271 YIGFLVLIFFSFLVLYVEKDANKFESTYADALMWGTTTLTTITIGDGKTPPLMLGRLISG 330
Db 390 FLFIQVLIFFSAVYFEAGSESENFSPKSIDPAFWAVVTMTTVGDMTPVGVWGKIVGSL 449
QY 331 FALIGSEFPAALGILGSGFALVKQEQHRQKHFEKRRNPANLLOCVRSYAADKSVSI 390
Db 450 CALAGVLTALTPVPYIVSNFN---YFYHRETDQEMQSQNNHV----- 490
QY 391 ATWKPHLKLALHCTSPNOKLSFKERVRMASPRGOSISRSQASVGDGRSPSTDTIEGSGPT 450
Db 491 -TSCPYL-----PGTLGGHMKKSSLESSSSDMMDLDDGVESTPG 528
QY 451 KVKQSWSFNDRTFRFRLRLKSSOPKPV 478
Db 529 LTFE---THPRGSVAPEFLGAQDQDQDQPV 553

RESULT 27
A39922 potassium channel KCNA4 - human
N:Alternate names: potassium channel HK1; potassium channel PCN2; shaker-related potassium
C:Species: Homo sapiens (man)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Nov-2000
C:Accession: A39922; S12630; I77465
R:Tamkun, M.M.; Knoch, K.M.; Walbridge, J.A.; Kroemer, H.; Roden, D.M.; Glover, D.M.
FASEB J. 5, 331-337, 1991
A:Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs
A:Reference number: A39922; MUID:91160866; PMID:2001794
A:Accession: A39922
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-653 <TAM>
A:Cross-references: GB:M60450; NID:q308762; PIDN:AAA61275.1; PID:q308763
R:Phillipson, L.H.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Steiner, D.F.
Nucleic Acids Res. 18, 7160, 1990
A:Title: Sequence of a human fetal skeletal muscle potassium channel cDNA related to RCK
A:Reference number: S12630; MUID:91088321; PMID:2263489
A:Accession: S12630
A:Molecule type: mRNA
A:Residues: 1-37,'R',39-41,'R',43-83,'EEEAR',89-303,'D',305-541,'V',543-630,'A',632-653
A:Cross-references: EMBL:M55514; NID:9189659; PIDN:AAA60034.1; PID:q189660
R:Ramshwami, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990

[illegible]

Db 75 TWVFADYLLRLGCA-----RRPLRYALSPFGLVDLLTLPSTLSPFGTOYLL- 124
 QY 227 AHSALSLRFLQLRMVRMRRCGTWKLGSVVAHSEKELITANYIGL--VLIFSSPLV 284
 Db 125 ---VVRALRLRVRFRFKIARYSDQALIEALQA-SREKLIFFISVLSMVIYFGT-LL 179
 QY 285 YLVEKANKRFESFYADLWMGTITLTITIGYGDPTPLWGLSLGAGFALLGISFPALPAG 344
 Db 180 YME-GESEFTIIPSTIYAVVITVIGIDISPKIGLGFATLMLSGAIIAYVPTG 238
 QY 345 ILGSGFALKVQEQHR 359
 Db 239 IYTVVGLQ-QAQEAR 252

RESULT 31

B39113
 potassium channel KV1.1 - rat
 N:Alternate names: potassium channel A; potassium channel RK1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Aug-1991 #sequence, revision 30-Aug-1991 #text, change 17-Nov-2000
 C:Accession: B39113; A41353; S01161
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
 A:Reference number: A39113; MUID:91156694; PMID:1705709
 A:Accession: B39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-495 <ROB>
 R:Christie, M.J.; Adelman, J.P.; Douglass, J.; North, R.A.
 Science 244, 221-224, 1989
 A:Title: Expression of a cloned rat brain potassium channel in Xenopus oocytes.
 A:Reference number: A41353; MUID:85203264; PMID:2539643
 A:Accession: A41353
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <CHR>
 A:Cross-references: GB:M26161; NID:g206490; PIDN:AAA1982.1; PID:g206491
 R:Baumann, A.; Grube, A.; Ackermann, A.; Pongs, O.
 EMBO J. 7, 2457-2463, 1988
 A:Title: Structure of the voltage-dependent potassium channel is highly conserved from D
 A:Reference number: S01161; MUID:89052659; PMID:3191911
 A:Accession: S01161
 A:Molecule type: mRNA
 A:Residues: 1-495 <BAU>
 A:Cross-references: EMBL:X12589; NID:g55957; PIDN:CAA31102.1; PID:g55958
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane bet
 F:361-370/Domain: transmembrane beta strand #status predicted <TM81>
 F:371-379/Domain: transmembrane beta strand #status predicted <TM82>
 F:207/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 4.9%; Score 230; DB 2; Length 495;
 Best Local Similarity 19.6%; Pred. No. 1.7e-07;
 Matches 75; Conservative 80; Mismatches 142; Indels 86; Gaps 10;
 QY 104 RNKRYRYQNTLYNLEPR--GMAFIYHAFVLLVFGCLISVSTIRE----- 151
 Db 142 RPLPEKEQROVWMLFEYRPSGPARVIAIVSMVILISIVFCLTEPELKDCKDPGTG 201
 QY 152 -----HTKASSCLLIEFVMIYVFGLEFIIRIMSAGCCCRYGWQGRLEFPARK 200
 Db 202 IHRDNTVTIYTSNFTDPPEFIVETLCIWSFELVVRFC-----PSKTFPEKN 252
 QY 201 PFCVIDITVLI---ASIAVSAKTOGN-----IFATSALRSRLFLQILRMVRMDRGGTW 252
 Db 253 IMNFIDYAIIPYFTLIGETAEAGNKGQATSLAIRVIRLVAVFRFLKSRHSGKL 312
 QY 253 KLGSSVVAHSEKEL-ITANYIGFVLVIRSSFLYVEKANKRFESFYADALWMGTITLT 311
 Db 313 QILGOTLKAAMEGLILFLIFIGVILFSSAVYFAAEAEASHSSIPDAFMVAVVSMT 372

QY 312 IGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGFALKVQEQHRQHFEKRNPA 371
 Db 373 VCGDMPYPTIGKIKYSLCAINGVLTALPVPYIYVSNEN---YFHRRETEGEQ----- 424
 QY 372 NLIQCVSRSTADEKSVSIATWKPRLKALTCSP-----TNOKLSFRKRVNMA 420
 Db 425 -----QOLLHVSSPNLASDLSRRSSSTISSEYMETEE 459
 QY 421 PRGQSIKS--ROASVGRSPSTD 442
 Db 460 DMNNSIAHYRQANIRTGNCYATD 482

RESULT 32

A46020
 potassium channel KCNC1 - human
 N:Alternate names: potassium channel NGK2-KV4; Shaw-related potassium channel KV3.1
 C:Species: Homo sapiens (hmn)
 C:Date: 21-Sep-1993 #sequence, revision 19-May-1994 #text, change 08-Dec-2000
 C:Accession: A46020; A45072
 R:Ried, T.; Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.
 Genomics 15, 405-411, 1993
 A:Title: Localization of a highly conserved human potassium channel gene (NGK2-KV4; K
 A:Reference number: A46020; MUID:93194190; PMID:8449507
 A:Accession: A46020
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-511 <RIE>
 A:Cross-references: GB:S56770; NID:g298602; PIDN:AB25764.1; PID:g298603
 A:Note: sequence extracted from NCBI backbone (NCBI:127271, NCBI:127272)
 R:Grissmer, S.; Chanshanh, S.; DeHlefs, B.; McPherson, J.D.; Wasmuth, J.J.; Gutman,
 J. Biol. Chem. 267, 20971-20979, 1992
 A:Title: The Shaw-related potassium channel gene, Kv3.1, on human chromosome 11, enco
 A:Reference number: A45072; MUID:93016011; PMID:1400413
 A:Accession: A45072
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 244-475 <GR1>
 A:Cross-references: GB:M96747; NID:g186672; PIDN:AAA59458.1; PID:g186673
 A:Experimental source: Louckes lymphoma cells
 A:Note: sequence extracted from NCBI backbone (NCBI:116151)
 C:Genetics:
 A:Gene: GDB:KCNC1
 A:Cross-references: GDB:128082; OMIM:176258
 A:Map position: 11p15.1-11p15.1
 C:Superfamily: potassium channel protein drkl
 C:Keywords: alternative splicing; glycoprotein; potassium channel; transmembrane prot

Query Match 4.9%; Score 230; DB 2; Length 511;
 Best Local Similarity 21.8%; Pred. No. 1.7e-07;
 Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;
 QY 3 RHRAEGEGGANGIMVSGAAAAAGGRLSGMKDVESGKRVLLNSAAAGDGLLLG 62
 Db 110 RQHRDAEE-----ALDSFGAPLDSAD-----ADAGPG----- 140
 QY 63 TRATLGGGGGLRESRKGQARMSLLGKPLSYTSOSCRNNKYRYQNTLYNLEPR 122
 Db 141 -----DSGGEDELEMT---KRLALSDSDGRGCGWRMRQPRIMALFEDP 183
 QY 123 RGMAFI-YHAFVFLVFGCLISV-----ESTIPEHTKL----- 155
 Db 184 YSSRAYRVAVASLFF--LIVSITPCLTEHERNPVINKTEIENVRNGTOVRYRAE 240
 QY 156 ASSCLLIEFVMIYVFGLEFIIRIMSAGCCCRYRMOGRRLRARKPFCVIDITVLI 211
 Db 241 TEAFLYIEGVCAVWTFEFLMRV---IFC-----PKNVERIKNSLTIIDVALIPYL 291
 QY 212 -ASIAVSAKTOGNIFATSRLRFLQILRMVRMDRGGTWKLGSVVAHSEKEL-LITA 269
 Db 292 EVGLSGSSKRAKAVL--GFLRVYFVRIILRIKFLRHVGVGRVGLHTRASTNEFLLI 349
 QY 270 WYIGFLVLISSFLYVYVK-----DANKFESTYADALWMGTITLTITIGYDGTIP 319

Db 350 IFLLALGVLLFAT-MIYAEIRIGAPNDPSASETHFKNIPIGFWMAVVTTLTGDMYP 408
 QY 320 LTMWGLRLSAGFALLGISFFALPAGILSGFALKVO-EQHROKHFEKRRNPANLIGCW 378
 Db 409 QTMGMLTALCALAGVLTAPVPVIVNNFGMYSLAMAKOLPKKKKHIPRPOLGS 468
 QY 379 RSYADEKSVSIATWPKHKLHTCSPTNOKLSFKERVRMASPRGOSI 426
 Db 469 PNCK-----SVNSPHSTQSDTCLPAQELLETIRAKRKLPGMSI 511

RESULT 33

potassium channel protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Dec-2000

C:Accession: S07095

R:Tokoyama, S.; Imoto, K.; Kawamura, T.; Higashida, H.; Iwabe, N.; Miyata, T.; Numa, S.

FEBS Lett. 259, 37-42, 1989

A:Title: Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells. Primary str

A:Reference number: S07095; MUID:90092535; PMID:2599109

A:Accession: S07095

A:Molecule type: mRNA

A:Residues: 1-511 <YOK>

A:Cross-references: EMBL:Y07521; NID:953997; PIDN:CAA68814.1; PID:953998

C:Superfamily: potassium channel protein drkl

C:Keywords: alternative splicing; membrane protein

Query Match 4.9%; Score 230; DB 2; Length 511;

Best Local Similarity 21.8%; Pred. No. 1.7e-07;

Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

QY 3 RHAGGEGGAGLWVSGAAAAAGGRLSGMKDVESGRGVLLNSAARDGILLG 62
 Db 110 RGRDAE-----ALDSFGAPLNSAD-----ADAGPG----- 140
 QY 63 TRATLGGGGGGLRESRRGQAGANSLGKPLSYTSSQCRNNVYRVVNTLYNLERP 122
 Db 141 -----DSDGDELEMT---KRLALSDSPDGRGFGFRWQPRIMALEEDP 183
 QY 123 RGMAFI-YHAFVFLVFGCLLSV-----FSTLPEHKL----- 155
 Db 184 YSRRYRYVAFASLFF---LIVSITTCLEHERNPNVKNKLEINRNGTQVRYREAE 240
 QY 156 ASSCLLLEFVMTVFGLEFLIRIMSAGCCCRNMGQRLREARPCVITIVL---- 211
 Db 241 TEAFLEYIEGVYVWFEEFLRV---VFC-----PKVERIKNSLNIIDVAILPEYL 291
 QY 212 -ASIAVSAKTOGNIFATLSRLFLQIILMVRMDRGGTCKLLGSVYVANSKE-LITA 269
 Db 292 EVGLSGLSKAAKQVL--GFLRVRFVRLIRIFKLTFRHVGILRVGLHRLASTNEFLDI 349
 QY 270 WYIGFVLILFSSFLVLYVER-----DANKEFSYADALMGITLITLIGYDKRP 319
 Db 350 IFLLAGVLLFAT-MIYAEIRIGAPNDPSASETHFKNIPIGFWMAVVTTLTGDMYP 408
 QY 320 LTMWGLRLSAGFALLGISFFALPAGILSGFALKVO-EQHROKHFEKRRNPANLIGCW 378
 Db 409 QTMGMLTALCALAGVLTAPVPVIVNNFGMYSLAMAKOLPKKKKHIPRPOLGS 468
 QY 379 RSYADEKSVSIATWPKHKLHTCSPTNOKLSFKERVRMASPRGOSI 426
 Db 469 PNCK-----SVNSPHSTQSDTCLPAQELLETIRAKRKLPGMSI 511

RESULT 34

157680

potassium channel KCNA1 - human

N:Alternate names: potassium channel protein HKC-1

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001

C:Accession: I57680; A60173

R:Ramshaw, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
 Mol. Cell. Neurosci. 1, 214-223, 1990

A:Title: Human potassium channel genes: molecular cloning and functional expression.

A:Reference number: I57680

A:Accession: I57680

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-495 <RAM>

A:Cross-references: GB:I02750; NID:9186662; PIDN:AAA36139.1; PID:9186663

R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Brammar, W.J.

Biochem. Soc. Trans. 18, 891, 1990

A:Title: Cloning and characterization of a cDNA encoding a human brain potassium chan

A:Reference number: A60173; MUID:91192386; PMID:2128063

A:Accession: A60173

A:Molecule type: mRNA

A:Residues: 263-264,266-314,'R' <PRE>

C:Genetics:

A:Gene: GDB:KCNA1; RBK1; HUK1; MBK1; AEMK; KVL.1

A:Cross-references: GDB:127903; OMIM:176260

A:Map position: 12p13-12p13

C:Superfamily: potassium channel protein drkl

Query Match 4.8%; Score 229.5; DB 2; Length 495;

Best Local Similarity 19.9%; Pred. No. 1.8e-07;

Matches 73; Conservative 82; Mismatches 142; Indels 69; Gaps 9;

QY 104 RNVRKRRQNTLYNLERP--GMATYHAFVFLVFGCLLSVSTIPE----- 151
 Db 142 RPLPERKYORQWMLFEYDESSGPARYVIVSVVILISIVICLTPLEKDKDFGT 201
 QY 152 -----HTKLASCLLIEFVMTVFGLEFLIRIMSAGCCCRNMGQRLREARPC 200
 Db 202 VHRIDNTVIVNSLFTDFFVETICTIMFSELYVRFAC-----PSKTDFKN 252
 QY 201 PCVIDITVLI--ASIAVSAKTOGN-----IFATSLRLSRLFLQIILMVRMDRGGTW 252
 Db 253 IMNFIDVAILIIFYFTLGTETIEAEQGNQGEQATSLALIVRLVRFKLSRHSKGL 312
 QY 253 KLGSVYVANSKE-LITMYIGFVILFSSFLVLYVEKQNKRFSTYADALMGITLIT 311
 Db 313 QILGOTLKSARELLILFELTIGVLFSSAVYFAEAESEHSSTIPDAFWMAVSMTP 372
 QY 312 IGYGDKPLTLMWGLRLSAGFALLGISFFALPAGILSGFALKVOEQHROKHFEKRRPAA 371
 Db 373 VGYGDMYPVTIGKIVSGICALAGVLTALPVPVIVSNR--YFHRTEGEEO-----A 425
 QY 372 NLIOCVMSYAAD-----EKVSATATWPKHKLHTCSPTNOKL 410
 Db 426 OLHVSSPNLASDLSRRSSSTMSKYEYMETEDMNNISIAHYROVINRTANCTTANQC 485
 QY 411 SFKERV 416
 Db 486 VNKSRL 491

RESULT 35

A39372

potassium channel protein Shal1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999

C:Accession: A39372

R:Park, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salikoff, L.

Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991

A:Title: mshal, a subfamily of A-type K(+) channel cloned from mammalian brain.

A:Reference number: A39372; MUID:91239573; PMID:2034678

A:Accession: A39372

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-651 <PAK>

A:Cross-references: GB:M64226; NID:9199812; PIDN:AAA39745.1; PID:9199813

Query Match

Best Local Similarity 4.8%; Score 228; DB 2; Length 651;

Matches 21.1%; Pred. No. 3.4e-07;


```

Db 110 KOHRAE-----ALDSFGAPLDNSAD-----ADADGP----- 140
QY 63 TRATILGGGGGLRESRRGOGARMSLGLKPLSTSSOSCRNRYRVQVLYNVLERP 122
Db 141 -----DSGDEDELEMT-----KRLALSDSPDGRPGGFWRWOPRIMALFBDP 183
QY 123 RGMAFI-YHAFVFLVFGCLLSV-----FSTIPHTKL----- 155
Db 184 YSSRYARVAFASLFE---ILVSTTEFLETHREFNFIVKTELEENRNGQVRYRAE 240
QY 156 ASSCLLIEFVIVVGLFEFIRIMSAGCCCRGMRGRLFRANKPCVIDITVLI----- 211
Db 241 TEALFTYLEGVCVWTFEFLMKV---VFC-----PNKVEFINSLNIDFVALPFLYL 291
QY 212 -ASIAVSAKTGNIATFATSLRFLQILRMVMDRGGTWKLLGVVYAHKE-LITA 269
Db 292 EVGLISGLSKAKADVL--GFLRVYRVRILIRIKLTHFVGLRVLGHLRASTNDFLLI 349
QY 270 WYIGFLVLIFFSFLVLYVER-----DANKFSTYADALMWGTTTLTITIGYDKTP 319
Db 350 IFLAGVLIFAT-MIYVAFRIGAQPNDPSASEHTHEKNIPIGFWMAVVTTLTGCDMP 408
QY 320 LFWIGRLSAGFALLGISFFALPAGIL---GSGFALKVQDQ---HROKHFEK 365
Db 409 QTWGSMVLGALCALAGVLTITAMPVPVIVNNFMYSILAMAKOKLPPKKKHIPR 462

```

RESULT 38

```

T23991
hypothetical protein R07M4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C:Accession: T23991; T24278
R:Coltage, A.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z19827
A:Accession: T23991
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-558 <MI>
A:Cross-references: EMBL:Z67756; PIDN:CAA91765.1; GSPDB:GN00028; CESP:R07M4.1
A:Experimental source: clone R07M4
R:Lennard, N.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z19868
A:Accession: T24278
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-558 <MI>
A:Cross-references: EMBL:Z68010; PIDN:CAA92011.1; GSPDB:GN00028; CESP:R07M4.1
A:Experimental source: clone T01C1
C:Genetics:
A:Gene: CESP:R07M4.1
A:Map position: X
A:Insertions: 32/1; 65/2; 91/3; 138/2; 177/3; 242/2; 439/3; 470/3; 507/1; 528/1
C:Superfamily: potassium channel protein drkl

```

```

Query Match. 4.8%; Score 226.5; DB 2; Length 558;
Best Local Similarity 21.6%; Pred. No. 3.4e-07;
Matches 83; Conservative 67; Mismatches 166; Indels 69; Gaps 11;
QY 104 RNWYRVQNVLYNVLERP-RGMAFIYHAFVFLVFGCLLSVFSSTI-----PEHTKLASS 158
Db 179 KRTVMKMLKPDQMSLFDLP-----YSSQAKLINGSIVLFIPTISFSCCLKTHQSRRLP 232
QY 159 CLILIEFV-----IVFGL-LEFIRIR-SAGCCCRYGMRGRLRPARK 200
Db 233 VILGQNTMREGVQPSIERVSTELPITFGQIEMCNWTFELILIRFVCPSKIRFFKS 292
QY 201 PFCVIDITVLI-----SIAVSAKTGNIATFATSLRFLQILRMVMDRGGTWKL 254
Db 293 PLMWIDVATLISFADAMKAVVEDEPK-----DVEFLSMIRIFRLFKLTOHQGLQI 346

```

```

QY 255 LGSVVAHAKSELIDAWYIGFLVLIFFSFLVLYVER---DANKFSTYADALMWGTTTLT 311
Db 347 LITFRASAKELLILVFLILIGIVFALVYAEKMEANPNQFOSIPGLMWAICTMTT 406
QY 312 IGYGDKTPTLWGLRLSAGFALLGISFFALPAGILGSGFALKVQDQHRQKHFEKRRN--- 368
Db 407 VGYGDMTPHTSFGLVGSLSACVMGVLTALTLPVIVSNFAMFYSHNQARDKLPKRRRVL 466
QY 369 PAANLIQCVKRSVAADKSVSIATW-----KPHUKALHTCSPTNQLSEKERVBM 418
Db 467 PVEQIRLQARRHAAVLEPPSASQGGIGGQAIRRMPTLIDQNCDEENHNHRE---- 522
QY 419 ASPRGQISKSQASGDRSPSTDI 443
Db 523 -----KSENDEGTINSSSTTV 539

```

RESULT 39

```

A40090
potassium channel KVL1 protein - mouse
N:Alternate names: potassium channel A; potassium channel MK1
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Nov-2000
C:Accession: A40090; S06378; I60746
R:Chandry, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanshani, S.; Tempel,
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regio
A:Reference number: A40090; MUID:9016196; PMID:2305265
A:Accession: A40090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHA>
A:Cross-references: GB:M30439; NID:q199702; PIDN:AAA39711.1; PID:q199703
R:Tempel, B.L.; Jan, Y.N.; Jan, L.Y.
Nature 332, 837-839, 1988
A:Title: Cloning of a probable potassium channel gene from mouse brain.
A:Reference number: S06378; MUID:88189348; PMID:2451788
A:Accession: S06378
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-495 <TEM>
A:Cross-references: GB:Y00305; GB:M36456; NID:q53605; PIDN:CAA68408.1; PID:q53606
A:Note: it is uncertain whether Met-1 or Met-4 is the initiator
C:Genetics:
A:Gene: MK1; MK1
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
E:361-370/Domain: transmembrane beta strand #status predicted <TM81>
E:371-379/Domain: transmembrane beta strand #status predicted <TM82>
E:207/Binding site: carbonylate (Asn) (covalent) #status predicted

```

```

Query Match 4.8%; Score 226; DB 2; Length 495;
Best Local Similarity 21.1%; Pred. No. 3.1e-07;
Matches 66; Conservative 74; Mismatches 125; Indels 48; Gaps 8;
QY 104 RNWYRVQNVLYNVLERP--GMAFIYHAFVFLVFGCLLSVFSSTI----- 151
Db 142 RLPEKEIYQVWMLFEYESSGPARYIAVSWVILISVIFCLELPELKDQDPTGT 201
QY 152 -----HTKLASSCLLIEFVIVVGLFEFIRIMSAGCCCRYGMRGRLRPARK 200
Db 202 IHRIDNTVITYINSIPTDFEIVETLCIWFSELVVRFAC-----PSKTDFFKN 252
QY 201 PFCVIDITVLI---ASIAVSAKTGQ-----IFATSLASLRLFLQILRMVMDRGGTW 252
Db 253 IMNFIDVIAIIPYITLIGTEIAEQEONQGEQATSLAILRVIRLVRFRIKLSRHSKGL 312
QY 253 KLIGSVVAHAKSEL-ITAYIGFLVLIFFSFLVLYVERDANKFSTYADALMWGTTTLT 311
Db 313 QILGTLASAKMELGILIFPLIGVILFSSAVFAEERESHSSIPDAFWMAVVSFTT 372
QY 312 IGYGDKTPTLWGLRLSAGFALLGISFFALPAGILGSGFALKVQDQHRQKHFEKRRPAA 371

```


Db 373 VGIQDMVPTIGKIVSLCAIAGVLTALPVIVSNFN---YYHETBEDEQ-----A 425
 QY 372 NLIOCVMSYAAD 384
 Db 426 QLLHVSFNPILASD 438

RESULT 40

JH0166
 potassium voltage-gated channel - rat
 N:Alternate names: potassium channel KV1; potassium channel RK4; shaker-related potassium
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
 C:Accession: JH0166; D39113; 155392
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunt
 Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed recti
 A:Reference number: JH0166; MUID:90297965; PMID:2361015
 A:Accession: JH0166
 A:Molecule type: mRNA
 A:Residues: 1-602 <SMA>
 A:Cross-references: GB:M27158; NID:9205100; PIDN:AAA41498.1; PID:9205101
 A:Experimental source: Brain
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
 A:Reference number: A39113; MUID:91156694; PMID:1705709
 A:Accession: D39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-552, 'S', 554-602 <ROB>
 R:Morl, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
 J. Biol. Chem. 268, 26482-26493, 1993
 A:Title: The transcription of a mammalian voltage-gated potassium channel is regulated b
 A:Reference number: 155392; MUID:94075338; PMID:8253777
 A:Accession: 155392
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-15 <RES>
 A:Cross-references: GB:L23434; NID:9443766; PIDN:AAA42337.1; PID:9443767
 A:Experimental source: Sprague-Dawley
 C:Genetics:
 A:Gene: KV1.5
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt
 F:242-260/Domain: transmembrane #status predicted <TM1>
 F:346-356/Domain: transmembrane #status predicted <TM2>
 F:347-368/Domain: transmembrane #status predicted <TM3>
 F:387-408/Domain: transmembrane #status predicted <TM4>
 F:423-444/Domain: transmembrane #status predicted <TM5>
 F:484-505/Domain: transmembrane #status predicted <TM6>
 F:510-44,116,181,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:81,535,546,569/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.7%; Score 223.5; DB 2; Length 602;
 Best Local Similarity 24.9%; Pred. No. 6, 1e-07;
 Matches 68; Conservative 49; Mismatches 111; Indels 45; Gaps 8;

QY 162 ILLEPMIVFGLFETIRMSAGCCCRKRGWGRRLRARRPCVYDITVL---IASIVVS 218
 Db 317 IVECTVIMFTEFLVRFAC-----PSKAEFSRNTMNIIDVAIFPPEITLCTEL 367
 QY 219 AKTO-----GNIFATSLRLPFLQILRMVRMDRGRTWKLGSVVAHSKELITAW 270
 Db 368 AEQDGGGQNGQQAAMSLAILKIVIRLVRFIRFKLSRHSKGLQILGKTLASMRGLLI 427
 QY 271 YIGFLVLFFSFLVLYLVKENDAN-KEESTYADALMWGTTITLTIGYGDPTLWGLRLLA 329
 Db 428 PFLFVIGLIFSSAVYFAEADNHSRHSIPDAFMVAIVMTITVGYGDMRPIVGGKIVGS 487
 QY 330 GALLGISFPAIPAGILSGF-----ALKVOEQRHQRKFEKRRNPANLIIQ 375

Db 488 LCAIAGVLTALPVIVSNFNYYHRETDHEEQALK-EEQGNQRRSGIDTGQORVKS 546
 QY 376 CVMRSYAAD-----EKSVSIATW-----KPHIKA 399
 Db 547 CSKASFCKTGSGLESDSIRRGSCPLERCHLKA 579

RESULT 41

A35312
 potassium channel protein Shal2 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 08-Dec-2000
 C:Accession: A35312; S12747
 R:Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salkoff, L.
 Science 248, 599-603, 1990
 A:Title: K⁺ current diversity is produced by an extended gene family conserved in Dro
 A:Reference number: A35312; MUID:90239553; PMID:2335511
 A:Accession: A35312
 A:Molecule type: mRNA
 A:Residues: 1-490 <WEI>
 A:Cross-references: GB:M32660; NID:9158456; PID:9158457
 R:Butler, A.; Wei, A.; Salkoff, L.
 Nucleic Acids Res. 18, 2173-2174, 1990
 A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.
 A:Reference number: S12746; MUID:90245668; PMID:2336395
 A:Accession: S12747
 A:Molecule type: mRNA
 A:Residues: 1-490 <BUT>
 A:Cross-references: EMBL:M32660; NID:9158456; PID:9158457
 C:Genetics:
 A:Gene: shal2
 A:Cross-references: Flybase:FBgn000564
 C:Superfamily: potassium channel protein drkl
 C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane prote

Query Match 4.7%; Score 222.5; DB 2; Length 490;
 Best Local Similarity 23.4%; Pred. No. 5, 2e-07;
 Matches 78; Conservative 65; Mismatches 136; Indels 55; Gaps 13;

QY 89 LIGKPLSTSSQSRKRVRYQNYLYNVERPR-----GNAFIYHAFVLLFGCLIS 144
 Db 148 LMDKLSBNGDONQQLTNMFO---KMRARENPPTSISALVFTYTGFIIV--SVMAN 202
 QY 145 VFSTIP-----BHTKLASSCLLLEFVMIVFGLFETIRMSAGCCCRNG 190
 Db 203 VVEIVPCGHRBAGRTLPCGERKIVFC---LDPAQVIMFAETILRLFAA----- 251
 QY 191 WQGRLEARRKPCVYDITVLASTIVVSAKTGNIPTAISALSLRFLQLRMVRMDRGG 250
 Db 252 -PDCKEFKRSWMSIIDVAIMP--YYIGLITDNDVSGAFYTLRFRVFRIFKFSRSQ 308
 QY 251 TWKLGSVVAHSKELTAWYIGFLV-----LIFSSFLVLYVENDAN-KEESTYADAL 302
 Db 309 GLRILGTLKSCASEL-----GLVFSIAMAIIIFATVMEY-AENNVGNTFTSIPAF 361
 QY 303 WMGTTITLTIGYGDPTLWGLRLLSAGPALLGISFPAIPAGILSGFA-LKVOEQRHQR 361
 Db 362 WYTIYMTTLTGCGDMVPEPIAGKIVGCSLGVIALPVIVSNFESRIYHQNORADK 421
 QY 362 HFEKRRNPANLIIQCVMSYAA--DEKSVSIATW 393
 Db 422 RKAQRKARLARIRIAKASSGAFAVSKKAAEARW 455

RESULT 42

C72692
 Probable potassium channel APE0955 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: C72692
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
 DNA Res. 6, 83-101, 1999


```

QY 152 ---HTKLASSCLLIEFVMIIVGELPIIRIMSGACCCRYRGOGRLRFARKPREVIDTI 208
Db 204 VFKYNIFDPFVETLITIMFSFELVAFPA--CSKDEFFKNNIMF-----IDIV 254
QY 209 VLI---ASIAVVSAKTQG-----NIPATSLRSLRFLQILRMVMDRGCTWKLGSVYV 260
Db 255 AIIPEFILTGMABEQEPQKQATSLALRLVLRVFRIFRIFLSHRSKQLILGOTLK 314
QY 261 AHSKRL-ITAWTIGFLVLIFFSFLVYLVEKDANKERSTYADALMWGITTLTIGYDKTP 319
Db 315 ASMRGLGLIFELFGLVLIFFSSAVYFAEAEDESHFISIDAFWMAVAVSMITVGYGDMYF 374
QY 320 LTMWGLRLSAGFALLGISFFALPAGILSGFALKVQEOHROKHREKRRNPANLIQCWR 379
Db 375 VTIGKIVGSLCAINGVLTIALPVPYIVSNFN---YFHHETEGEO----- 418
QY 380 SYADEKSVSIATWPKPHKALHTCSP---TNOKLSFERVRMASPRGOSIKS----- 428
Db 419 -----ADLLHVSSPNLASNSDLSSRSSAMSKESEYMEIEDLNNSIDN 461
QY 429 -ROASV 433
Db 462 FREANI 467

RESULT 49
A49507
potassium channel Kv1.5 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Nov-2000
C:Accession: A49507; B49507
J:Altali, B.; Lesage, F.; Ziliant, P.; Guillemaire, E.; Honore, E.; Waldmann, R.; Hugnot,
R. Biol. Chem. 268, 24283-24289, 1993
A:Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1.5 delayed rectifier K(+)
A:Reference number: A49507; MUID:94043264; PMID:8226976
A:Accession: A49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-602 <ATP>
A:Cross-references: GB:L22218; NID:9435603; PIDN:AAA9365.1; PID:9435604
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 201-602 <ATP>
A:Cross-references: GB:L22218
C:Superfamily: potassium channel protein drkl
C:Keywords: alternative splicing

Query Match 4.5%; Score 214.5; DB 2; Length 602;
Best Local Similarity 24.1%; Pred. No. 2.4e-06;
Matches 58; Conservative 53; Mismatches 105; Indels 25; Gaps 6;

QY 139 GCLILVSFTI-PHRTKLASSCLLIEFVMIIVGELPIIRIMSGACCCRYRGOGRLRF 197
Db 293 GSGVLSSGTIVAPLRLPRLADPEFIVETTCVIMFTFELLVREFAC-----PSKAEF 343
QY 198 ARKPECVIDITVL---IASIAVVSAKTQ-----GNIFATSALRSLRFLQILRMWRMD 246
Db 344 SRNIMNIIIDYALIPYFITLCTELAEQPGGGGQNGQAMSLALIRVIRVRFRIKLS 403
QY 247 RRGCTWKLGSVVAHSKELTITAWTIGFLVLIFFSFLVYLVEKD-ANKERSTYADALMWG 305
Db 404 RHSKGLIILGTTQASMRGLLIFELFGLVLIFFSSAVYFAEADNQSOLSSIPDAFWMA 463
QY 306 TITLTIGYDKTPPLTWMLGRLSAGFALLGISFFALPAGILSGFALKVQEOHROKHFEK 365
Db 464 VVMTITVGYGDMRPTVYGVKIVGSLCAITAGVLTIALPVPYIVSNFN---YFHRETDEH 520
QY 366 R 366
Db 521 Q 521

```

```

RESULT 50
JC4787
shaw protein - California spiny lobster
C:Species: Panulirus interruptus (California spiny lobster)
C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 08-Dec-2000
C:Accession: JC4787
R:Baro, D.J.; Cole, C.L.; Harris-Warrick, R.M.
Gene 170, 267-270, 1996
A:Title: The lobster shaw gene: Cloning, sequence analysis and comparison to fly shaw
A:Reference number: JC4787; MUID:96235147; PMID:8666257
A:Accession: JC4787
A:Molecule type: mRNA
A:Residues: 1-489 <BAR>
A:Cross-references: GB:L48691; NID:g1100226; PID:g1100227
C:Comment: This protein is a voltage-dependent potassium (K+) channel protein.
C:Genetics:
A:Gene: shaw
C:Superfamily: potassium channel protein drkl
C:Keywords: membrane protein; phosphoprotein; transmembrane protein
F:171-190/Domain: transmembrane #status predicted <TM1>
F:226-248/Domain: transmembrane #status predicted <TM2>
F:260-280/Domain: transmembrane #status predicted <TM3>
F:291-311/Domain: transmembrane #status predicted <TM4>
F:324-342/Domain: transmembrane #status predicted <TM5>
F:387-410/Domain: transmembrane #status predicted <TM6>
F:18-190/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II)
F:19-41,48,86,140,163,228/Binding site: phosphate (Tyr) (covalent) #status predicted
F:22-66,116,475/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #statu
F:126,157,281,320/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #sta
F:320,483/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred

Query Match 4.5%; Score 214; DB 2; Length 489;
Best Local Similarity 23.3%; Pred. No. 1.9e-06;
Matches 61; Conservative 52; Mismatches 113; Indels 36; Gaps 6;

QY 111 VONYLVNLEPRPGMAFYHAFVLLVFGCLLSVFSTIPRHTKLASSCLLIEFVMIIV 170
Db 199 IGNITVQNTMENTAW-----TLDKKANHNAHFYIEVCYTW 236
QY 171 FGLFPIIRIMSGACCCRYRGOGRLRFARKPECVIDITVILIA-SIAVVSATQGNIFATS 229
Db 237 FTFEILIRLIAS-----PNKFMELKASVNMIDFATLSFYVDILQKFASHLENAD 287
QY 230 ALRSLRFLQILRMVRMDRGCTWKLGSVVAHSKEL-ITAWTIGFLVLIFFSFLVYL- 286
Db 288 ILFFSIIKIMLFLKTRHSSGKILQITRASAKELTLVFFLVLGIVIFASLVYAER 347
QY 287 VEKDANKERSTYADALMWGITTLTIGYDKTPPLTWMLGRLSAGFALLGISFFALPAGIL 346
Db 348 IQANPHNDNSIPLGLMMLVMTVGYGDMARPTVYGMVGALCALAGVLTIALPVPYI 407
QY 347 GSGFALKVQE-QHROKHFEKRR 367
Db 408 VSNFMYYSHTQARAKLPKRR 429

```

Search completed: June 14, 2003, 17:45:11
 Job time : 59 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:27 ; Search time 26 Seconds
(without alignments)
1472.410 Million cell updates/sec

Title: US-09-825-147-2

Perfect score: 4733
Sequence: 1 MPRHHAGGEEGGAALMWKS.....SICKAGESTALSLPHVKLK 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4527.5	95.7	897	1	Q9N822 homo sapien
2	4227.5	89.3	878	1	C105_HUMAN
3	1991	42.1	695	1	C104_HUMAN
4	1805.5	38.1	852	1	C102_RAT
5	1784	37.7	872	1	C102_HUMAN
6	1756	37.1	759	1	C102_MOUSE
7	1620.5	34.2	872	1	C103_HUMAN
8	1590.5	33.6	873	1	C103_BOVIN
9	1589.5	33.6	866	1	C103_BOVIN
10	1102	23.3	676	1	C101_HUMAN
11	1101	23.3	669	1	C101_RAT
12	1100.5	23.3	604	1	C101_MOUSE
13	1083.5	22.9	670	1	C101_SQUAC
14	899.5	19.0	377	1	C101_XENLA
15	647	13.7	276	1	C104_MOUSE
16	591.5	12.5	172	1	C101_FELCA
17	538.5	11.4	159	1	C101_CAVPO
18	486.5	9.4	168	1	C104_RAT
19	446.5	9.4	155	1	C101_RABIT
20	409.5	8.7	123	1	C101_PIG
21	291.5	6.2	854	1	C101_HUMAN
22	289	6.1	853	1	C101_HUMAN
23	282	6.0	806	1	C101_HUMAN
24	276.5	5.8	806	1	C101_HUMAN
25	272	5.7	802	1	C101_HUMAN
26	251	5.3	769	1	C101_HUMAN
27	250.5	5.3	582	1	C101_HUMAN
28	248	5.2	985	1	C101_HUMAN
29	247	5.2	757	1	C101_HUMAN
30	244	5.2	889	1	C101_HUMAN
31	242	5.1	638	1	C101_HUMAN
32	241.5	5.1	625	1	C101_HUMAN
33	240.5	5.1	654	1	C101_HUMAN
34	240.5	5.1	655	1	C101_HUMAN
35	237	5.0	523	1	C101_HUMAN
36	237	5.0	525	1	C101_HUMAN
37	235.5	5.0	660	1	C101_HUMAN
38	234	4.9	654	1	C101_HUMAN
39	233	4.9	653	1	C101_HUMAN
40	233	4.9	656	1	C101_HUMAN
41	232	4.9	528	1	C101_HUMAN
42	230	4.9	405	1	C101_HUMAN
43	230	4.9	511	1	C101_HUMAN
44	230	4.9	511	1	C101_HUMAN
45	229.5	4.8	495	1	C101_HUMAN
46	229.5	4.8	585	1	C101_HUMAN
47	226	4.8	601	1	C101_HUMAN
48	225.5	4.8	602	1	C101_HUMAN
49	223.5	4.7	602	1	C101_HUMAN
50	222.5	4.7	602	1	C101_HUMAN
51	214.5	4.5	602	1	C101_HUMAN
52	213	4.5	598	1	C101_HUMAN
53	212.5	4.5	499	1	C101_HUMAN
54	212.5	4.5	499	1	C101_HUMAN
55	212	4.5	498	1	C101_HUMAN
56	211.5	4.5	613	1	C101_HUMAN
57	210	4.4	530	1	C101_HUMAN
58	207.5	4.4	499	1	C101_HUMAN
59	199	4.2	529	1	C101_HUMAN
60	192.5	4.1	579	1	C101_HUMAN
61	192.5	4.1	580	1	C101_HUMAN
62	188.5	4.0	574	1	C101_HUMAN
63	180	3.8	209	1	C101_HUMAN
64	178.5	3.8	536	1	C101_HUMAN
65	176.5	3.7	580	1	C101_HUMAN
66	174	3.7	561	1	C101_HUMAN
67	168	3.5	160	1	C101_HUMAN
68	163.5	3.5	724	1	C101_HUMAN
69	163.5	3.5	736	1	C101_HUMAN
70	159.5	3.4	732	1	C101_HUMAN
71	153.5	3.2	731	1	C101_HUMAN
72	142.5	3.0	425	1	C101_HUMAN
73	142.5	3.0	425	1	C101_HUMAN
74	142	3.0	2161	1	C101_HUMAN
75	142	3.0	2212	1	C101_HUMAN
76	141	3.0	2516	1	C101_HUMAN
77	140.5	3.0	2223	1	C101_HUMAN
78	137.5	2.9	2327	1	C101_HUMAN
79	137.5	2.9	2373	1	C101_HUMAN
80	137	2.9	1966	1	C101_HUMAN
81	137	2.9	2164	1	C101_HUMAN
82	136.5	2.9	2272	1	C101_HUMAN
83	135	2.8	1610	1	C101_HUMAN
84	133	2.8	1835	1	C101_HUMAN
85	132.5	2.8	2336	1	C101_HUMAN
86	132.5	2.8	2378	1	C101_HUMAN
87	131.5	2.8	1547	1	C101_HUMAN
88	130	2.7	1156	1	C101_HUMAN
89	130	2.7	2312	1	C101_HUMAN
90	129.5	2.7	783	1	C101_HUMAN
91	129	2.7	528	1	C101_HUMAN
92	129	2.7	2688	1	C101_HUMAN
93	128.5	2.7	705	1	C101_HUMAN
94	128.5	2.7	1939	1	C101_HUMAN
95	128	2.7	411	1	C101_HUMAN
96	127.5	2.7	668	1	C101_HUMAN
97	127.5	2.7	2190	1	C101_HUMAN
98	127.5	2.7	2259	1	C101_HUMAN
99	127	2.7	793	1	C101_HUMAN
100	127	2.7	1938	1	C101_HUMAN
101	127	2.7	2365	1	C101_HUMAN
102	126.5	2.7	2505	1	C101_HUMAN
103	126	2.7	897	1	C101_HUMAN
104	125.5	2.7	1687	1	C101_HUMAN
105	125.5	2.7	1873	1	C101_HUMAN
106	125.5	2.7	1873	1	C101_HUMAN
107	125.5	2.7	1873	1	C101_HUMAN
108	125.5	2.7	1873	1	C101_HUMAN
109	125.5	2.7	1873	1	C101_HUMAN
110	125.5	2.7	1873	1	C101_HUMAN
111	125.5	2.7	1873	1	C101_HUMAN
112	125.5	2.7	1873	1	C101_HUMAN
113	125.5	2.7	1873	1	C101_HUMAN
114	125.5	2.7	1873	1	C101_HUMAN
115	125.5	2.7	1873	1	C101_HUMAN
116	125.5	2.7	1873	1	C101_HUMAN
117	125.5	2.7	1873	1	C101_HUMAN
118	125.5	2.7	1873	1	C101_HUMAN
119	125.5	2.7	1873	1	C101_HUMAN
120	125.5	2.7	1873	1	C101_HUMAN
121	125.5	2.7	1873	1	C101_HUMAN
122	125.5	2.7	1873	1	C101_HUMAN
123	125.5	2.7	1873	1	C101_HUMAN
124	125.5	2.7	1873	1	C101_HUMAN
125	125.5	2.7	1873	1	C101_HUMAN
126	125.5	2.7	1873	1	C101_HUMAN
127	125.5	2.7	1873	1	C101_HUMAN
128	125.5	2.7	1873	1	C101_HUMAN
129	125.5	2.7	1873	1	C101_HUMAN
130	125.5	2.7	1873	1	C101_HUMAN
131	125.5	2.7	1873	1	C101_HUMAN
132	125.5	2.7	1873	1	C101_HUMAN
133	125.5	2.7	1873	1	C101_HUMAN
134	125.5	2.7	1873	1	C101_HUMAN
135	125.5	2.7	1873	1	C101_HUMAN
136	125.5	2.7	1873	1	C101_HUMAN
137	125.5	2.7	1873	1	C101_HUMAN
138	125.5	2.7	1873	1	C101_HUMAN
139	125.5	2.7	1873	1	C101_HUMAN
140	125.5	2.7	1873	1	C101_HUMAN
141	125.5	2.7	1873	1	C101_HUMAN
142	125.5	2.7	1873	1	C101_HUMAN
143	125.5	2.7	1873	1	C101_HUMAN
144	125.5	2.7	1873	1	C101_HUMAN
145	125.5	2.7	1873	1	C101_HUMAN
146	125.5	2.7	1873	1	C101_HUMAN
147	125.5	2.7	1873	1	C101_HUMAN
148	125.5	2.7	1873	1	C101_HUMAN
149	125.5	2.7	1873	1	C101_HUMAN
150	125.5	2.7	1873	1	C101_HUMAN

107	125	2.6	985	1	NAHL_YEAST	099271	saccharomyc
108	125	2.6	2222	1	CCAE_RAT	007652	rattus norv
109	125	2.6	2339	1	CCAB_HUMAN	000975	homo sapien
110	124.5	2.6	1311	1	FM22_HUMAN	P51816	homo sapien
111	124.5	2.6	1852	1	CCAS_CYPCA	P22316	cypripus ca
112	124	2.6	1375	1	BNRI_YEAST	P40450	saccharomyc
113	124	2.6	1518	1	KMR1_YEAST	P34244	saccharomyc
114	123.5	2.6	1272	1	FM22_MOUSE	055112	mus musculu
115	123.5	2.6	1972	1	P531_HUMAN	012888	homo sapien
116	123.5	2.6	2339	1	CCAB_RABIT	005152	oryctolagus
117	123	2.6	707	1	Y39C_YEAST	P47166	saccharomyc
118	123	2.6	2169	1	CCAC_RAT	P22002	rattus norv
119	122	2.6	722	1	MEP1_TOBAC	09m714	nicotiana t
120	122	2.6	2359	1	CCAA_RAT	P27884	oryctolagus
121	122	2.6	2424	1	CCAA_RABIT	P46821	homo sapien
122	122	2.6	2468	1	YADP_HUMAN	058732	methanococ
123	121.5	2.6	343	1	MYR1_HUMAN	P12882	homo sapien
124	121.5	2.6	1939	1	PGCV_HUMAN	090953	gallus gall
125	121.5	2.6	3562	1	PGCV_CHICK	P31069	escherichia
126	121	2.6	417	1	KCH_ECOLI	062812	rattus norv
127	121	2.6	1961	1	MYH9_RAT	015554	homo sapien
128	120.5	2.5	427	1	HCN4_HUMAN	P02836	dirosophila
129	120.5	2.5	552	1	MSL1_DROME	P50353	dirosophila
130	120.5	2.5	1039	1	SHK2_HUMAN	Q9UPX8	homo sapien
131	120.5	2.5	1253	1	COT3_SCHPO	P41004	schizosacch
132	120.5	2.5	1324	1	MC3A_MOUSE	Q9WU99	mus musculu
133	120.5	2.5	1971	1	ANK3_HUMAN	012955	homo sapien
134	120.5	2.5	4377	1	ANK9_RABIT	028628	oryctolagus
135	120	2.5	1087	1	MAP2_MOUSE	P20357	mus musculu
136	119.5	2.5	1828	1	MAP2_DROME	P47855	dirosophila
137	119.5	2.5	921	1	HERG_HUMAN	Q12809	homo sapien
138	119.5	2.5	1159	1	TAHA_DICDI	P54633	dictyostell
139	118.5	2.5	2492	1	YM96_YEAST	P57789	homo sapien
140	118.5	2.5	538	1	NEST_HUMAN	040693	saccharomyc
141	118.5	2.5	1140	1	CCAC_MOUSE	001815	mus musculu
142	118.5	2.5	1618	1	HRX_HUMAN	003164	homo sapien
143	118.5	2.5	2139	1	N12A_SCHPO	Q09904	schizosacch
144	117.5	2.5	3969	1	CCAS_RABIT	P07293	oryctolagus
145	117.5	2.5	1159	1	APC_MOUSE	061315	mus musculu
146	117.5	2.5	1873	1	BOB1_YEAST	P38041	saccharomyc
147	116.5	2.5	2845	1	BIR1_SCHPO	014064	schizosacch
148	116.5	2.5	980	1	MAP2_RAT	P15146	rattus norv
149	116.5	2.5	997	1			
150	116.5	2.5	1861	1			

ALIGNMENTS

RESULT 1
C105_HUMAN STANDARD; PRT: 897 AA.
AC 09NR82; 09NR80; 09NR16;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein KQR-like 5.
GN KCNQ5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE-20357367; PubMed-10787416;
RA Lerche C., Scherer C.R., Seebach G., Derst C., Weil A.D., Busch A.E.,
RA Steinmeyer K.,
RT "Molecular cloning and functional expression of KCNQ5, a potassium
channel subunit that may contribute to neuronal M-current
diversity".
RU J. Biol. Chem. 275:22395-22400(2000).
RL [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain;
RX MEDLINE-20379054; PubMed-10816588;
RA Schroeder B.C., Hechenberger M., Weinreich F., Kudisch C.,
RA Jentsch T.J.;
RT "KCNQ5, a novel potassium channel broadly expressed in brain, mediates
M-type currents".
RU J. Biol. Chem. 275:24089-24095(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Kanamura C., Biervert B., Hechenberger M., Engels H., Steinlein O.K.;
RT "The new voltage gated potassium channel KCNQ5 and early infantile
convulsions".
RU Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Retina;
RA Kniazeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
is a candidate gene for retinal disorders".
RU Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE-21095345; PubMed-11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
mammalian cells".
RU Br. J. Pharmacol. 132:381-384(2001).
RN [6]
RP FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
WHICH CONTRIBUTES TO M-TYPE CURRENT, A SLOWLY ACTIVATING AND
DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS.
MAY CONTRIBUTE, WITH OTHER POTASSIUM CHANNELS, TO THE MOLECULAR
DIVERSITY OF AN HETEROGENEOUS POPULATION OF M-CHANNELS, VARYING IN
KINETIC AND PHARMACOLOGICAL PROPERTIES, WHICH UNDERLY THIS
PHYSIOLOGICALLY IMPORTANT CURRENT. INSENSITIVE TO
TETRAETHYLAMMONIUM, BUT INHIBITED BY BARIUM, LINDAPIDINE AND
XE991. ACTIVATED BY NIFEDIPINE ACID AND THE ANTI-CONVULSANT
RETIGABINE. MUSCARINIC SUPPRESSES KCNQ5 CURRENT IN XENOPUS OOCYTES
IN WHICH CLOVED KCNQ5 CHANNELS WERE COEXPRESSED WITH M(1)
MUSCARINIC RECEPTORS.
CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ISOFORM 1 (SHOWN HERE), 2 AND 3;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN AND SKELETAL
MUSCLE. IN BRAIN, EXPRESSED IN CEREBRAL CORTEX, OCCIPITAL POLE,
FRONTAL LOBE AND TEMPORAL LOBE. LOWER LEVELS IN HIPPOCAMPUS AND
PUTAMEN. LOW TO UNDETECTABLE LEVELS IN MEDULLA, CEREBELLUM AND
THALAMUS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
SUBFAMILY.
CC -----
CC THIS SWISS-PROT ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (See <http://www.isb-sib.ch/announce/>
CC OR SEND AN EMAIL TO license@sib-sib.ch).
CC -----
DR EMBL: AF249278; AAF91335.1; ALT_INIT.
DR EMBL: AF202977; AAF69797.1; -
DR EMBL: AJ272506; CAC88112.1; -
DR EMBL: AJ272507; CAC88112.1; JOINED.
DR EMBL: AJ272508; CAC88112.1; JOINED.
DR EMBL: AJ272509; CAC88112.1; JOINED.
DR EMBL: AJ272510; CAC88112.1; JOINED.
DR EMBL: AJ272511; CAC88112.1; JOINED.


```

CC      or send an email to license@lsb-sib.ch).
CC      -----
DR      EMBL; AF263836; AAF73447.1; -.
DR      HSSP; Q54397.1BL8.
DR      MGD; MGI:1924937; Kcnq5
DR      InterPro: IPR001622; K-channel_pore.
DR      InterPro: IPR003946; KCNQ1_channel.
DR      InterPro: IPR003091; K_channel.
DR      Pfam; PF00520; Ion_trans_1.
DR      Pfam; PF03520; Ion_trans_1.
DR      PRINTS; PR00169; KCANMNL.
KW      Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW      Multigene family.
FT      TRANSMEM 1
FT      TRANSMEM 72 92 SEGMENT S1 (POTENTIAL).
FT      TRANSMEM 103 123 SEGMENT S2 (POTENTIAL).
FT      TRANSMEM 147 167 SEGMENT S3 (POTENTIAL).
FT      TRANSMEM 176 198 SEGMENT S4 (POTENTIAL).
FT      TRANSMEM 213 233 SEGMENT S5 (POTENTIAL).
FT      DOMAIN 245 265 SEGMENT H5 (POTENTIAL).
FT      TRANSMEM 272 292 SEGMENT S6 (POTENTIAL).
SQ      SEQUENCE 878 AA; 97029 MW; 35779F9C7D630F55 CRC64;

Query Match      89.3%; Score 4227.5; DB 1; Length 878;
Best Local Similarity 94.3%; Pred. No. 1.5e-237;
Matches 827; Conservative 14; Mismatches 27; Indels 9; Gaps 1;

55 GDCILLGTRATGCGGGGGLRESRSGKOGAMSLGKPLSTSSGCRNRYRRVQNY 114
1 GDGILLGTRAAALGGGGGGLRESRSGKOGAMSLGKPLSTSSGCRNRYRRVQNY 60
115 LVNLEPRGMATYHAFVFLVFGCLLSVFSTIPHTKLASSCLILEFVIVFEGLE 174
61 LVNLEPRGMATYHAFVFLVFGCLLSVFSTIPHTKLASSCLILEFVIVFEGLE 120
175 FIIIRMSAGCCCRGRRGOGRRFARKPRCVDTYLIVASIVAVSAKTOGNIFATSLRSL 234
121 FIIIRMSAGCCCRGRRGOGRRFARKPRCVDTYLIVASIVAVSAKTOGNIFATSLRSL 180
235 RFLQILRMVMDRRGRTGKTLGSLVYVAHASKELITAMYGELVLFSSFFVYVERKANKE 294
181 RFLQILRMVMDRRGRTGKTLGSLVYVAHASKELITAMYGELVLFSSFFVYVERKANKE 240
295 FSTYDALMWTGTTLTITIGDCKPLTWLGRLLSAGFALLGISFPALPAGILGSGFALY 354
241 FSTYDALMWTGTTLTITIGDCKPLTWLGRLLSAGFALLGISFPALPAGILGSGFALY 300
355 QEOHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWPKLALHTCSPT----- 406
301 QEOHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWPKLALHTCSPTKKEGEAS 360
407 -NOKLSFEKRVMSAPRGOSIKRSQASVGDPRSPTDTAAGSPTRKYOKSWGFNDTRPR 465
361 SSOKLSFEKRVMSAPRGOSIKRSQASVGDPRSPTDTAAGSPTRKYOKSWGFNDTRPR 420
466 PSRLKSSQPKRYIDATGCTDGVYDEKGCOCVSVEDLTPLPKTVIRAIRIMKEHVAK 525
421 PSRLKSSQPKRYIDATGCTDGVYDEKGCOCVSVEDLTPLPKTVIRAIRIMKEHVAK 480
526 RRFKETLRKYDVADVEIYOSAGHLDMLCRISLQTRVDQILGKQOMTSDDKRSREKITAHEH 585
481 RRFKETLRKYDVADVEIYOSAGHLDMLCRISLQTRVDQILGKQOMTSDDKRSREKITAHEH 540
586 EFTTDLISMLGRVYKVKOVQIESKLDCLDIYQOVLARKGSASALALASFOIPRECEQOT 645
541 EFTTDLISMLGRVYKVKOVQIESKLDCLDIYQOVLARKGSASALALASFOIPRECEQOT 600
646 SDYQSPVDSKDISSGNSGCLSRSSANSRGIQFLTPREESAQTFYALSPTMHSQAT 705
601 SDYQSPVDSKDISSGNSGCLSRSSANSRGIQFLTPREESAQTFYALSPTMHSQAT 660
QY      706 QVPISQDGSAAVAATNTIANQINTAPKPAFTTLQIPPLPAIKHLRPRPETHPRADQL 765

```

```

DB      661 QVPMSONDSSSVATNTNINAIQISAPKPAFTTLQIPPLPAIKHLRPRPETHPRADQL 720
QY      766 ESISDVTTCLVASKENYVAQSNLTKDRSNRKSFDMGGETLLSYCPWPKDLGKSLSYON 825
DB      721 ESISDVTTCLVASKENYVAQSNLTKDRSNRKSFDMGGETLLSYCPWPKDLGKSLSYON 780
QY      826 LIRSTPEELNIQLSGSSSGSGSGSODFPKPKRESKLTFTDEVGEEETFTDFDAAPQPAR 885
DB      781 LIRSTPEELNIQLSGSSSGSGSGSODFPKPKRESKLTFTDEVGEEETFTDFDGTTPPAPG 840
QY      886 EAFASDSLRTGSRSSQSGICKAGESTDALSLPHVKL 922
DB      841 EAFASDSLRTGSRSSQSGICKAGESTDALSLPHVKL 877

RESULT 3
C104_HUMAN
ID      C104_HUMAN          STANDARD;          PRT;          695 AA.
AC      P56696; O96025;
DT      15-JUL-1999 (Rel. 38, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Voltage-gated potassium channel protein KCOT-like 4.
GN      KCNQ4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFN2 SER-285.
RC      TISSUE=Retina;
RX      MEDLINE=99148276; PubMed=10025409;
RA      Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
RA      El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
RT      "KCNQ4, a novel potassium channel expressed in sensory outer hair
RT      cells, is mutated in dominant deafness.";
RL      Cell 96:437-446(1999).
RN      [2]
RP      INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX      MEDLINE=20178300; PubMed=10713961;
RA      Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA      Brown D.A.;
RT      "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT      via M1 muscarinic acetylcholine receptors.";
RL      J. Physiol. (Lond) 522:349-355(2000).
RN      [3]
RP      PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.
RX      MEDLINE=21143874; PubMed=11245603;
RA      Soegaard R., Ljungstrom T., Pedersen K.A., Olesen S.-P.,
RA      Jensen B.S.;
RT      "KCNQ4 channels expressed in mammalian cells: functional
RT      characteristics and pharmacology.";
RL      Am. J. Physiol. 280:C859-C866(2001).
RN      [4]
RP      VARIANTS DFN2 SER-276; CVS-285 AND SER-321.
RX      MEDLINE=99299248; PubMed=10369879;
RA      Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattman I.,
RA      Van Velzen D., Meyers J., Ensink R.J., Verstrecken M., Declau F.,
RA      Marres H., Kastury K., Bhasin S., McGill W.T., Smith R.J.H.,
RA      Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
RT      "Mutations in the KCNQ4 gene are responsible for autosomal dominant
RT      deafness in four DFN2 families.";
RL      Hum. Mol. Genet. 8:1321-1328(1999).
RN      [5]
RP      VARIANT DFN2 SER-281.
RX      MEDLINE=20040027; PubMed=10571947;
RA      Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;
RT      "Novel mutation in the KCNQ4 gene in a large kindred with dominant
RT      progressive hearing loss.";
RL      Hum. Mutat. 14:493-501(1999).
RN      [6]

```


RP VARIANT DENA2, HIS-274.
 RX MEDLINE-2038752; PubMed-10925378;
 RA Van Hauwe P., Coucke P.J., Enslin R.J., Huygen P., Cremers C.W.R.J.,
 RA Van Camp G.;
 RT "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal
 RT dominant hearing loss, cluster in the channel pore region.";
 RL Am. J. Med. Genet. 93:184-187(2000).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 CC EXCITABILITY. MAY UNDERLIE A POTASSIUM CURRENT INVOLVED IN
 CC REGULATING THE EXCITABILITY OF SENSORY CELLS OF THE COCHLEA. KCNQ4
 CC CHANNELS ARE BLOCKED BY LINOPIRIDIN, XE991 AND BEPRIDIL, WHEREAS
 CC CLOFLOMORINE-H WITHOUT SIGNIFICANT EFFECT. MUSCARINIC AGONIST
 CC OXOTREMORINE-H STRONGLY SUPPRESS KCNQ4 CURRENT IN CHO CELLS IN
 CC WHICH CLONED KCNQ4 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINIC
 CC RECEPTORS.
 CC -1- SUBUNIT: MAY FORM HETEROMULTIMERS WITH KCNQ3.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SITUATED AT THE
 CC BASAL MEMBRANE OF COCHLEAR OUTER HAIR CELLS (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
 CC SENSORY HAIR CELLS OF THE COCHLEA. SLIGHTLY EXPRESSED IN HEART,
 CC BRAIN AND SKELETAL MUSCLE.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF NONSYNDROMIC
 CC SENSORINEURAL DEAFNESS TYPE 2 (DENA2), AN AUTOSOMAL DOMINANT FORM
 CC OF PROGRESSIVE HEARING LOSS.
 CC -1- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT BY
 CC EXPRESSING IN XENOPUS OOCYTES KCNQ4 MUTANTS EITHER INDIVIDUALLY
 CC (HOMOMULTIMERS) OR IN COMBINATION WITH WILD-TYPE KCNQ4 (MUT/WT
 CC HOMOMULTIMERS) IN A RATIO OF 1:1. TO MIMIC THE SITUATION IN A
 CC HETEROZYGOTIC DENA2 PATIENT.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -1- DATABASE: NAME-Hereditary hearing loss homepage;
 CC NOTE-Genes page:
 CC WWW-<http://www.uit.ac.be/dnablab/hhh/hhgenes.html>.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Multigene family; Disease mutation; Deafness; Alternative splicing.
 FT TRANSMEM 98 118 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 132 152 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 173 193 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 202 224 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 238 258 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 271 292 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 297 317 SEGMENT S6 (POTENTIAL).
 FT VARSPLIC 378 431 MISSING (IN ISOFORM 2).
 FT VARIANT 274 274 L -> H (IN DENA2).
 FT VARIANT 276 276 W -> S (IN DENA2).
 FT VARIANT 281 281 L -> S (IN DENA2).
 FT VARIANT 285 285 /FTID-VAR.010937.
 FT VARIANT 285 285 /FTID-VAR.008727.
 FT VARIANT 285 285 G -> S (IN DENA2).
 FT VARIANT 321 321 /FTID-VAR.001547.
 FT VARIANT 321 321 G -> S (IN DENA2).
 FT MUTAGEN 285 285 /FTID-VAR.008728.
 FT SEQUENCE 695 AA; 77091 MW; A58737BD845E1A3A CRC64;
 Query Match 42.1%; Score 1991; DB 1; Length 695;
 Best Local Similarity 57.8%; Pred. No. 4,1e-108;
 Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;
 25 AAAGGRLGSGMDVDSGRGVLLNSAARDGILLGTRATLTGGGGGGLRESNRKGG 84
 2 AEAPRRRLGSGPPGDAFRAELVALTAVOSRG-----EAGGGSPR----- 43
 85 ARMSLLGKPL-----SYSSSGCRNNKRYRQNTLYNLEPRGNAFTYH 130
 44 -RLGLLGSPLPGCAPLDPGSGSGSAGCGRSSAHRKRYRQNTLYNLEPRGNAFTYH 102
 131 AFPELVFGLLVSFTIPETIPETIASGCLLLEFVMLVGLFETIRMSAGCCRYRG 190
 103 VFPELVFSCVLVSSTIOHOLANCLLLEFVMLVGLFETIRMSAGCCRYRG 162
 191 MGRRLRFRKPFVYDITVLASTAVSAKTQGNIFATLSALSLFLOILRMVRMDRGG 250
 163 MGRFRFRKPFVYDITVLASTAVSAKTQGNIFATLSALSLFLOILRMVRMDRGG 222
 251 TWKLLGSVVAHAKSELITAMTIGFLVLIFFSFLVLYVERKDNKESTYADALMGITLT 310
 223 TWKLLGSVVAHAKSELITAMTIGFLVLIFFSFLVLYVERKDNKESTYADALMGITLT 282
 311 TIGYGDTPPLTWLGRLLSAGFALLGISFPALGIGSGFALKVGOEHOKHFERKRNPA 370
 283 TIGYGDTPPLTWLGRLLSAGFALLGISFPALGIGSGFALKVGOEHOKHFERKRNPA 342
 371 ANLTQCYWRSYAAD-EKVSISATW----- 393
 343 ANLTQCYWRSYAAD-EKVSISATW----- 402
 394 -----KHLKALHT-----CSPLNOKISFEKERYMASPPROGISTSRQ--ASVGR 436
 403 PVPDGPSPRPVATCHRRPGSTSPGSSRRGIDRIWSSQRRTGSSKQOLAPPTMP 462
 437 RSPNDITAEQ-SEPKVQKSMSEFNDRTFRPSLRKSSQKPEVIDADTALGTDVYDEKG 495
 463 TSPSEQGEATSPKVKQSMSEFNDRTFRPSLRKSSQKPEVIDADTALGTDVYDEKG 516
 496 CQCVSVEDLTPPELKTIVIRAIRIMKFFHAKKRFKELTRYDYKVDYEQSAGHDLMLCET 555
 517 YQCELTVDIMPAVATVIRISIRILKFLVAKRKFELTRYDYKVDYEQSAGHDLMLCET 576
 556 KSLQTRVQDILGKGITSDKRSR-----KTAHETTTDLSMLGRVYKVKOVQSIKSID 612

```

Db 577 KSLQTRVQIVRG--PGRRKAREKCDKGPDSAEVDEISMGMGRVYKQVQSIENKLD 634
QY 613 CLLDYQVQVLRKSGASALAFQIPPECEOTSDVSPDSDKSLSSAQNQSGLSRST 672
Db 635 LLGYSYSCLRSGTSA--SLGAVQVLEFDPDITSDHSPVDHEDISVSAQTLIS-ISRVS 691
QY 673 ANI 675
Db 692 TNN 694

RESULT 4
C102_RAT STANDARD: PRT: 852 AA.
AC 088943;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 2.
GN KCNQ2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE-Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RN Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE-Brain;
RA MEDLINE=20493350; PubMed=11038262;
RX Jow F., Wang K.-W.;
RT "Cloning and functional expression of rKCNQ2 K(+) channel from rat
brain.";
RN Brain Res. Mol. Brain Res. 80:269-278(2000).
[3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC TISSUE-Brain, and Sympathetic ganglion;
RA MEDLINE=21154288; PubMed=11230508;
RX Pan Z., Selyanko A.A., Hadley J.K., Brown D.A., Dixon J.E.,
RN McKinnon D.;
RT "Alternative splicing of KCNQ2 potassium channel transcripts
contributes to the functional diversity of M-currents.";
RN J. Physiol. (Lond) 531:347-358(2001).
[4]
RP TISSUE SPECIFICITY.
RA MEDLINE=99055398; PubMed=9836639;
RX Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RN Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
the M-channel.";
RN Science 282:1890-1893(1998).
-1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING
THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE
RESPONSES TO SYNAPTIC INPUTS. KCNQ2 CURRENT IS BLOCKED BY
BARITUM AND TETRAETHYLAMMONIUM WHEREAS 4-AMINOPIPERIDINE AND
CHARYBDOXIN HAVE NO EFFECT ON KCNQ2 CURRENT. TYROSINE KINASE
INHIBITORS GENSTEIN OR HERBIMYCIN A MARKEDLY DOWN-REGULATE KCNQ2
CURRENT. MUSCARINIC AGONIST OXOTREMORINE-M SUPPRESSED KCNQ2/KCNQ3
CURRENT IN CHO CELLS IN WHICH CLONED KCNQ2/KCNQ3 CHANNELS WERE
COEXPRESSED WITH HUMAN M1 MUSCARINIC RECEPTORS.
-1- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
-1- SUBCELLULAR LOCATION: Integral membrane protein. B, C, D, E, F,
G, H and I; are produced by alternative splicing. Splice isoforms
fell into three classes, those that contain an in frame exon 16

```

```

CC (Isoforms A-I) those that contain an out-of-frame exon 16 due to
CC an alternative splice junction in exon 14 and those that terminate
CC prematurely to exon 16. Only the forms containing an in frame exon
CC 16 are able to form functional channels. A similar splice pattern
CC is also produced for splice variants that contain an out-of-frame
CC exon 16. A wide variety of different truncated isoforms were
CC isolated for splice variants that terminate prematurely to exon
CC 16.
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SYMPATHETIC GANGLIA. IN
CC BRAIN, EXPRESSED IN CORTEX, HIPPOCAMPUS, AND CEREBELLUM. IN
CC SYMPATHETIC GANGLIA, EXPRESSED AT LOWER LEVELS IN CELIAC GANGLIA
CC AND SUPERIOR MESENTERIC GANGLIA THAN IN SUPERIOR CERVICAL GANGLIA.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1- MISCELLANEOUS: WHEN CO-EXPRESSED WITH KCNQ3 SUBUNIT IN CHO CELLS
CC OR XENOPUS OOCYTES, ISOFORM B WAS FOUND TO HAVE SIGNIFICANTLY
CC DIFFERENT DEACTIVATION-ACTIVATION KINETICS. THE KINETICS WAS 2.5
CC TIMES MORE SLOWLY THAN THE KINETICS OF OTHER ISOFORMS. THE
CC PRESENCE OF EXON 15A IN ISOFORM B ACCOUNTS FOR THE SLOW
CC DEACTIVATION-ACTIVATION KINETICS. ALTERNATIVE SPLICING OF THE
CC KCNQ2 GENE MAY CONTRIBUTE TO THE VARIATION IN M-CURRENT KINETICS
CC SEEN IN VIVO.
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
-----
DR EMBL: AF087453; AAC36722.1;
DR HSSP: 054397; 1BL8.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF03520; KCNQ1_channel_1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Multigene family; Phosphorylation; Alternative splicing.
FT TRANSMM 92 112 SEGMENT S1 (POTENTIAL).
FT TRANSMM 123 143 SEGMENT S2 (POTENTIAL).
FT TRANSMM 167 187 SEGMENT S3 (POTENTIAL).
FT TRANSMM 198 221 SEGMENT S4 (POTENTIAL).
FT TRANSMM 232 252 SEGMENT S5 (POTENTIAL).
FT DOMAIN 265 285 SEGMENT H5 (POTENTIAL).
FT TRANSMM 292 312 SEGMENT H6 (POTENTIAL).
FT MOD_RES 52 52 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT VARSPPLIC 373 382 MISSING (IN ISOFORM C, ISOFORM F AND
FT ISOFORM H).
FT VARSPPLIC 416 416 S -> SKRRPGCGICGRRGHS (IN ISOFORM D,
FT ISOFORM E, ISOFORM F AND ISOFORM H).
FT VARSPPLIC 417 428 MISSING (IN ISOFORM B).
FT VARSPPLIC 491 491 MISSING (IN ISOFORM D, ISOFORM F AND
FT ISOFORM I).
FT VARSPPLIC 571 571 R -> RIDMIVGPPPTSRHKYPTKGPAPRSPQYSP
FT R (IN ISOFORM B AND ISOFORM G).
SQ SEQUENCE 852 AA; 93949 MW; 8255FE625F259A CRC64;

Query Match 38.1%; Score 1805.5; DB 1; Length 852;
Best Local Similarity 47.8%; Pred. No. 3e-97;
Matches 418; Conservative 100; Mismatches 209; Indels 147; Gaps: 23;

QY 21 GAAAGGAGGGLGSGMKYVSGRGVLAARAGDGLLGTGATLGGGGGGLRESRR 80
Db 9 GYVPGTSGEKKLVGFVLDPCA-----PSTRDGAALLIAGSEAPK---RGSVLSPRT 59
QY 81 GKQGRASLIGKPLPYSTSSQCRVRVRYVNYLVNERGMAFYTHAFVLLVFGC 140
Db 60 GGACA-----GKP-----PKRNATYKRLQNLNLYLNERPRGMATYHAYVLLVFC 106

```

QY 141 LITVSTIEPHKCLASSCLLLEFVMIYVGLFETIRMSAGCCCRGMGRRLRFARK 200
 DB 107 LVLVSSTIEKREKSSGALYILEITVTVFVGFVPRIMAGCCCRGRMRGRKLFARK 166
 QY 201 PFCVIDITVLIASIAVAVSAKTOGNIFATSLRSLFLOILMVRMDRGRGTWKLGSVYV 260
 DB 167 PFCVIDIMVLASIAVLAAGSGVAFATSLRSLRFLQILMIRMDRGRGTWKLGSVYV 226
 QY 261 AHSKELITAVYIGFLVLIESFLVYLVKDKANKESTYADALMWTITLTITIGYDQPL 320
 DB 227 AHSKELITAVYIGFLVLIESFLVYLVKDKANKESTYADALMWTITLTITIGYDQPL 286
 QY 321 TWIGRLISAGFALIGTIFPAGLIGSFALIKVOEORHOFKERRRPAANLIGCVMS 380
 DB 287 TWIGRLISAGFALIGTIFPAGLIGSFALIKVOEORHOFKERRRPAANLIGCVMS 346
 QY 381 YAADEKSVSI-ATWK-----PHLKALHTC----- 403
 DB 347 YATNLSTDLHSTWQYERTVTPMISQOTOTYGASRLIPPLNQLMRLNLSKSGLTPR 406
 QY 404 -----SPTNOLISFEKERVMASSPGOSIKSRQASVD--RRSPTDITAGSPTKYOK 454
 DB 407 KEPQPEPSP-SOKVSLKDRV-FSSPRGVAAKGSPPQATVRRSPSADQSLDSSPSKYPK 464
 QY 455 SMSFNDTRFRPSLRKSSQKPYIDADTALGTDDVDEKGGCCVVEDLTPPLKTVIR 514
 DB 465 SMSFNDTRFRPSLRKSSQKPYIDADTALGTDDVDEKGGCCVVEDLTPPLKTVIR 524
 QY 515 AIRMKFHVAKRKKEKTLRPYDVADVIEOYSGHLMCLRLKSLQTRVQDILGKQITSD 574
 DB 525 AVCMRRLVSKRKRESLRPYDVADVIEOYSGHLMCLRLKSLQTRVQDILGKQITSD 584
 QY 575 KKSREKTTAEHTTDDLSMLGRVYKVEKOVOSIESKLDCLDIYQVLRKGSASALALAS 634
 DB 585 -KDKTKGPATELEPEDESMGRKLVKVEKOVLSMEKKLDELVSITYQ--RMG----- 632
 QY 635 FOJPFPC-----EQTSQSPYDVKDLSGSAONSQ--LSRSTANISRLQPT 682
 DB 633 --IPPAETAEYFGAKKEPPAPPIHSPEDSRD--HADHGCLIKIKYRSTSS----- 678
 QY 683 LTPNEFSAQTFFALSPTHSQATOVPISSQSGSAVAATNTJANOINTAPKPAAPTLQIP 742
 DB 679 -----TGQRKYAAPVW--PPAECPPSTSS-----WQOSHQRHGTSPVGHGSLVIR 723
 QY 743 PRLPAIKHLPRPELHPRPALQESISDVTCIVASKENVOYQASNLTR--DRSMKSPD 800
 DB 724 PP-----PAH-ERSLAVSGGNRASTEFRLRLEGTTPACRPSEALRDS-- 764
 QY 801 MGETLLSVCPMPKDLGKSLSVONLIRSTEELN 834
 DB 765 ---DTSISIPSVDHLELRSFSGFISQSKENLN 795

RT "Identification and cloning of neuroblastoma-specific and nerve
 RT tissue-specific genes through compiled expression profiles.";
 RL DNA Res. 3:311-320(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT'S BPNC1 C-284 AND T-306.
 RC TISSUE-Brain, fetal brain, and Temporal cortex;
 RX MEDLINE=98085864; PubMed=9425895;
 RA Singh N.A., Charlier C., Stauffer D., Dupont B.R., Leach R.J.,
 RA Melis R., Ronen G.M., Bjerre I., Quattrebaum T., Murphy J.V.,
 RA McHarg M.L., Gagnon D., Rosales T.O., Peiffer A., Anderson V.E.,
 RA Leppert M.;
 RT "A novel potassium channel gene, KCNQ2, is mutated in an inherited
 RT epilepsy of newborns.";
 RL Nat. Genet. 18:25-29(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE-Fetal brain;
 RX MEDLINE=98092527; PubMed=9430594;
 RA Bjerre C., Schroeder B.C., Kubisch C., Berkovic S.F., Propping P.,
 RA Jentsch T.J., Steinlein O.K.;
 RT "A potassium channel mutation in neonatal human epilepsy.";
 RL Science 279:403-406(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC MEDLINE=99053398; PubMed=9836339;
 RX Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
 RA Dixon J.E., McKinnon D.;
 RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
 RT the M-channel.";
 RL Science 282:1890-1893(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 5).
 RX MEDLINE=99043242; PubMed=9827540;
 RA Tinel N., Jauritzen I., Chouabe C., Lazdunski M., Borsotto M.;
 RT "The KCNQ2 potassium channel: splice variants, functional and
 RT developmental expression. Brain localization and comparison with
 RT KCNQ3.";
 RL FEBS Lett. 438:171-176(1998).
 RN [6]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC TISSUE-Brain, and fetal brain;
 RX MEDLINE=98344027; PubMed=9677360;
 RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
 RA Neubauer M.G., Blamir M.A.;
 RT "Functional expression of two KvLOT1-related potassium channels
 RT responsible for an inherited idiopathic epilepsy.";
 RL J. Biol. Chem. 273:19419-19423(1998).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Brain;
 RX MEDLINE=21114072; PubMed=11160379;
 RA Smith J.S., Iannotti C.A., Dargis P.G., Christian E.P., Aiyar J.;
 RT "Differential expression of KCNQ2 splice variants: implications to M
 RT current function during neuronal development.";
 RL J. Neurosci. 21:1096-1103(2001).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE-Eye;
 RA Strausberg R.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP MUTAGENESIS OF SER-52; GLY-279 AND TYR-284.
 RX MEDLINE=99087323; PubMed=9872318;
 RA Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
 RT "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
 RT channels causes epilepsy.";
 RL Nature 396:687-690(1998).
 RN [10]
 RP INVOLVEMENT IN M-LIKE CURRENT.
 RX MEDLINE=99410758; PubMed=10479678;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
 RA Buckley N.J., London B., Brown D.A.;
 RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to

RT the M-like current in a mammalian neuronal cell.";
 RL J. Neurosci. 19:7742-7756(1999).
 RN [11]
 RP ASSOCIATION WITH KCNE2.
 RX MEDLINE=20487128; PubMed=11034315;
 RA Tinel N., Dicochot S., Lauritzen I., Barhanin J., Lazdunski M.,
 RT Borsotto M.;
 RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
 subunit.";
 RL FEBS Lett. 480:137-141(2000).
 RN [12]
 RP SURFACE EXPRESSION OF HETEROMERS.
 RX MEDLINE=20250883; PubMed=10788442;
 RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
 RT "Surface expression and single channel properties of KCNQ2/KCNQ3,
 RT M-type K⁺ channels involved in epilepsy.";
 RL J. Biol. Chem. 275:13343-13348(2000).
 RN [13]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20150152; PubMed=10684873;
 RA Shapiro M.S., Roche J.P., Kafan E.J., Cruzblanca H., Mackie K.,
 RT Hill B.;
 RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+) channels that underlie the neuronal M current.";
 RL J. Neurosci. 20:1710-1721(2000).
 RN [14]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20178300; PubMed=10713961;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
 RT Brown D.A.;
 RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells via M muscarinic acetylcholine receptors.";
 RL J. Physiol. (Lond) 522:349-355(2000).
 RN [15]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20368587; PubMed=10908292;
 RA Main M.J., Cayan J.E., Dupre J.R., Cox B., Clare J.J., Burbridge S.A.;
 RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant retigabine.";
 RL Mol. Pharmacol. 58:253-262(2000).
 RN [16]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20411474; PubMed=10953053;
 RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
 RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3 potassium channels.";
 RL Mol. Pharmacol. 58:591-600(2000).
 RN [17]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20180045; PubMed=10713399;
 RA Rundfeldt C., Netzer R.;
 RT "The novel anticonvulsant retigabine activates M-currents in Chinese hamster ovary-cells transfected with human KCNQ2/3 subunits.";
 RL Neurosci. Lett. 282:73-76(2000).
 RN [18]
 RP TISSUE DISTRIBUTION AND BIOCHEMICAL CHARACTERIZATION.
 RX MEDLINE=20243795; PubMed=10781098;
 RA Cooper E.C., Aldape K.D., Abosch A., Barbaro N.M., Berger M.S.,
 RT Peacock W.S., Jan Y.N., Jan L.Y.;
 RT "Colocalization and coassembly of two human brain M-type potassium channel subunits that are mutated in epilepsy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4914-4919(2000).
 RN [19]
 RP VARIANT THR-780.
 RX MEDLINE=99254826; PubMed=10323247;
 RA Bievart C., Steinlein O.K.;
 RT "Structural and mutational analysis of KCNQ2, the major gene locus for benign familial neonatal convulsions.";
 RL Hum. Genet. 104:234-240(1999).
 RN [20]
 RP VARIANT BFNC1 TRP-214.
 RX MEDLINE=21037661; PubMed=11175290;
 RA Miraglia del Giudice E., Coppola G., Scuccimarra G., Cirillo G.,

RA Bellini G., Pascotto A.;
 RT "Benign familial neonatal convulsions (BFNC) resulting from mutation of the KCNQ2 voltage sensor.";
 RL Eur. J. Hum. Genet. 8:994-997(2000).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE RESPONSIVENESS TO SYNAPTIC INPUTS. KCNQ2/KCNQ3 CURRENT IS BLOCKED BY LINOPIRINE AND XE991, AND ACTIVATED BY THE ANTICONVULSANT RETIGABINE. MUSCARINIC AGONIST OXOTREMORINE-M STRONGLY SUPPRESSES KCNQ2/KCNQ3 CURRENT IN CELLS IN WHICH CLONED KCNQ2/KCNQ3 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINIC RECEPTORS.
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ3. MAY ASSOCIATE WITH KCNE2.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS: 1 (SHOWN HERE), 2, 3, 4, 5 AND 6/HNSPC; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN ADULT AND FETAL BRAIN. HIGHLY EXPRESSED IN AREAS CONTAINING NEURONAL CELL BODIES, LOW IN SPINAL CHORD AND CORPUS CALLOSUM. ISOFORM 2 IS PREFERENTIALLY EXPRESSED IN DIFFERENTIATED NEURONS, WHEREAS ISOFORM 6 IS PROMINENT IN FETAL BRAIN, UNDIFFERENTIATED NEUROBLASTOMA CELLS, AND BRAIN TUMORS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- PTM: IN XENOPUS OOCYTES KCNQ2/KCNQ3 HETEROMERIC CURRENT CAN BE INCREASED BY INTRACELLULAR CYCLIC AMP, AN EFFECT THAT DEPENDS ON PHOSPHORYLATION OF SER-52 IN THE AMINO TERMINUS REGION.
 CC -1- DISEASE: DEFECTS IN KCNQ2 ARE THE CAUSE OF BENIGN FAMILIAL NEONATAL CONVULSIONS TYPE 1 (BFNC1); ALSO KNOWN AS EPILEPSY. BENIGN NEONATAL TYPE 1 (BN1); BEN1 IS AN AUTOSOMAL DOMINANT FORM OF EPILEPSY IN THE NEWBORN THAT CLEARS SPONTANEOUSLY AFTER A FEW WEEKS AND IS FOLLOWED BY NORMAL PSYCHOMOTOR DEVELOPMENT.
 CC -1- MISCELLANEOUS: INCLUSION OF ISOFORM 6 IN HETEROMULTIMERS RESULTS IN ATTENUATION OF POTASSIUM CURRENT. PROMINENT EXPRESSION OF

Query Match 37.7%; Score 1784; DB 1; Length 872;
 Best local similarity 46.8%; Pred. No. 5.4e-96;
 Matches 411; Conservative 92; Mismatches 196; Indels 180; Gaps 25;

21 GAAAAAGGGRGSGMKVDSGGRVLLNSAARGDGLLTGTRATLTGGGGGLRESRR 80
 9 GYYPSPSGKKLVGVGVDPGA-----PDSIRDGLLLAGSAPK---RGSILSKPRA 59
 81 GKQGRMSLKGPLSTSSQSCRNVKRRVONYLVNTERPRGMAFYHAFFLVFGC 140
 60 GGAGA-----GKP-----PKRNAFYKRLQNFVNLVTERPRGMAFYHAFFLVFSC 106
 141 LILSVSTIPRHTKLASSCLLLEFPMIVFEGLEFIIRMSACCCGRRMGGTLRPRK 200
 107 LVLVSFTIKKEKSEKALYLLLEVTIVFGEYEVYRMAACCCGRRMGGTLRPRK 166
 201 PCVVDITVLINAVSAKTGDNIFATSLRSLRFQLILRMVMDRGGTWMKLGSVVY 260
 167 PECVIDIWLINAVSIIVLAAGSGNVFATSLRSLRFQLILRMVMDRGGTWMKLGSVVY 226
 261 AHSKELTAWYIGFLVLFSSFLVYVVERDKANKESTYADALMWGTTTLTIGYDKTPL 320
 227 AHSKELVTAWYIGFLVLFSSFLVYVVERDKANKESTYADALMWGTTTLTIGYDKTPL 286
 321 TWLGRILSAGFALDISFPALPAGILGSGFALKVQSOHQKHREKRNPAANLTQCVWS 380
 287 TWNGRLLAATTLTIGVSPFALPAGILGSGFALKVQSOHQKHREKRNPAAGLQASMRP 346
 381 YAAD-----EKSVSIATWK-----PHTKALHT----- 402
 347 YATNLSRTDLSTWQYERTVIVPMVSSQOTQYTGASRLPLPLQDELRLNLKSKSGIAFR 406
 403 -----CSP--TNOKLSFEKENVRAASPGQSTKSKQASVGD--RR 437
 407 KDPPPEPSKSGSPCRGLCCGCPGRSSQKVSILKRV-FSSPRGVAAKGSGPOAQTVRR 465


```

FT VARSPLIC 562 597 MISSING (IN ISOFORM 4).
FT VARSPLIC 562 570 IDMIIVGPP -> SCDMKGVLA (IN ISOFORM 5).
FT VARSPLIC 571 759 MISSING (IN ISOFORM 5).
FT VARSPLIC 562 623 IDMIIVGPPSTPRDKKPTKPGTAPASRESPQSPYSPRVHIV
GPGPTTDRKRTKGAPEELP -> QELPAPQSGHEQPG
QONAMHGHOGGLGRCAQOCQYQIMRSLPTLLASCCFLICF
HYVCF (IN ISOFORM 6).
FT VARSPLIC 624 759 MISSING (IN ISOFORM 6).
FT CONFLICT 125 125 A -> P (IN REF. 1; BAA37161).
FT CONFLICT 326 326 P -> Q (IN REF. 1; BAA37160/BAA37165).
SQ SEQUENCE 759 AA: 84450 MW: C1D12DBFF3979D5F CXC64.

Query Match 37.18; Score 1756; DB 1; Length 759;
Best Local Similarity 50.58; Pred. No. 1.9e-94;
Matches 392; Conservative 77; Mismatches 165; Indels 142; Gaps 19;

21 GAAAAAGGGRIGSGKKDVGSGRGVLLNAAAAGDLLLLLGTAAATGCGGGGGLRESRR 80
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
9 GYVPGTSGKKLVGVGLDPGA-----PDSTRDALLAAGSAPK--RGSVLSKPR 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
81 GKGAARMSLGKPLSTYSOSCRNNKYRRVONLYLVLEPRGMATYHAFFVLLVPGC 140
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
60 GGAGA-----GKP-----PKRNAFYRKLQNFVLYVERPRGMATYHAFFVLLVSC 106
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 LILSVSTYPTHTKASCLLIEFVIVFGLFETIRINSAGCCCRYGQGLRFARK 200
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 LVLVSTIKEYEKSESGALYIEIVTVYVGEYFVIMAAAGCCCRYGMRGRKLFARK 166
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201 PFCVDTVLINAVSAKTGNIATSLRSRFLQILRMVMDRGGKWLGLSVY 260
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 PFCVDTVLINAVSAKTGNIATSLRSRFLQILRMVMDRGGKWLGLSVY 226
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261 AHSKELTAMVIGFVLIFSSFLVLEKPAKNEFSTYADALMMGTTLTIGYGDKPL 320
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227 AHSKELTAMVIGFVLIFSSFLVLEKPAKNEFSTYADALMMGTTLTIGYGDKPL 286
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
321 TWLGLSLSGFLLGIFSPALPAGILGSGFALKVQEOHROKHEKRRNPAANLIQCVRS 380
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
287 TWNGRLAATFVLIGVSPFALPAGILGSGFALKVQEOHROKHEKRRNPAANLIQCVRS 346
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
381 YAAD-----EKSVSIATWK--PHLKALHNC-----SPT 406
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
347 YATNLSRDLDHSTWYERTVYPMTRLLPPLQLELRLMKSKSGLTFRKEPEPEPSP- 405
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 NOKLSFERVMAVSPGOSIKSROASVGD--RRSPSTITAEQSPYKQSMSPNDRTRF 464
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
406 SOKVSLKORV--ESSPRGMAAKGKSPQAOQTVRRSPALDQSLDPSKVPKMSFGDRRT 464
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
465 RPSLRLKSSQKPVLDADTALGTDVYDEKGCOCQDVSEDLTPPLKTVIRAIRMKFHA 524
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
465 ROAFRIKGAASRQNSEASLPEDIEDNKSCNCEFTEDLTPLKYSIRAVCYMRFLYS 524
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
525 KRKFETLRPVYKVIIEOYSAGHMLRLCRISLOT----- 560
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
525 KRKFETLRPVYKVIIEOYSAGHMLRLCRISLOT----- 560
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
525 KRKFETLRPVYKVIIEOYSAGHMLRLCRISLOT----- 560
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
585 TAPSRSPQSPRVHIVGRPTITD-KDRTKGAPEELPEDSPSMGRKLVGEVQVLSME 643
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
609 SKLDCLDIYQVVLKGSASALASFOJPPPEC-----EQSDYSPVDSKDLISG 659
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
644 KKLPLFVSIYQ--RWG-----IPPAETEAFFGAKKEPEPAPYPHSPEDSRD-- 687
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
660 SAONSGC---LSRSTANISRLGLOFLITPNESAOFFVALSPMHSAQATVPISOS 712
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
688 HADHNGCIITKIVRSTSS-----TGQNNYAAPPAI--PPAOCPPST 726
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-1like 3.
GN KCNQ3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606.
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-310 AND GLY-318.
RC TISSUE=Brain.
RX MEDLINE=99087323; PubMed=9872318;
RA Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
RT "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
channels causes epilepsy."
RL Nature 396:687-690(1998).
RN [2]
RP SEQUENCE OF 48-872 FROM N.A., AND VARIANT EBN2 VAL-310.
RC TISSUE=Brain.
RX MEDLINE=9805869; PubMed=9425900;
RA Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J.,
RT Leppert M.;
RT "A pore mutation in a novel KQT-1like potassium channel gene in an
idiopathic epilepsy family."
RL Nat. Genet. 18:53-55(1998).
RN [3]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Brain, and Fetal brain.
RX MEDLINE=98344027; PubMed=9677360;
RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
RA Neubauer M.G., Blamhar M.A.;
RT "Functional expression of two KvLOT1-related potassium channels
responsible for an inherited idiopathic epilepsy."
RL J. Biol. Chem. 273:19419-19423(1998).
RN [4]
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
RA Buckley N.J., London B., Brown D.A.;
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
the M-like current in a mammalian neuronal cell."
RL J. Neurosci. 19:7742-7756(1999).
RN [5]
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315;
RA Tinel N., Diocot S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
subunit."
RL FEBS Lett. 480:137-141(2000).
RN [6]
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10784442;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
RT "Surface expression and single channel properties of KCNQ2/KCNQ3,
M-type K+ channels involved in epilepsy."
RL J. Biol. Chem. 275:13343-13348(2000).
RN [7]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10684873;
RA Shapiro M.S., Roche J.P., Kattan E.J., Cruzblanca H., Mackie K.,
RA Hille B.;
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+)
channels that underlie the neuronal M current."
RL J. Neurosci. 20:1710-1721(2000).
RN [8]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA Brown D.A.;
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
via M1 muscarinic acetylcholine receptors."

```

RL J. Physiol. (Lond) 522:349-355(2000).
 RN [9]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20368587; PubMed-10908292;
 RA Main M.J., Cryan J.E., Dupere J.R., Cox B., Clare J.J., Burbridge S.A.;
 RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
 retigabine.";
 RL Mol. Pharmacol. 58:253-262(2000).
 RN [10]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20411474; PubMed-10953053;
 RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
 RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
 potassium channels.";
 RL Mol. Pharmacol. 58:591-600(2000).
 RN [11]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20180045; PubMed-10713399;
 RA Rundfeldt C., Netzer R.;
 RT "The novel anticonvulsant retigabine activates M-currents in Chinese
 hamster ovary-cells transfected with human KCNQ2/3 subunits.";
 RL Neurosci. Lett. 282:73-76(2000).
 RN [12]
 RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
 RX MEDLINE-21095345; PubMed-1159685;
 RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
 RT "Characterization of KCNQ5/Q3 potassium channels expressed in
 mammalian cells.";
 RL Br. J. Pharmacol. 132:381-384(2001).
 RN [13]
 RP VARIANT BFNC2 ARG-309.
 RX MEDLINE-20309392; PubMed-10852552;
 RA Hirose S., Zentgraf A., Akiyoshi H., Fukuma G., Iwata H., Inoue T.,
 RA Kaneo S., Mitsudomi M., Muranaka H., Kurokawa T., Hanai T., Wada K.,
 RA Yonekura M., Tsubota M.;
 RT "A novel mutation of KCNQ3 (C.925T->C) in a Japanese family with
 benign familial neonatal convulsions.";
 RL Ann. Neurol. 47:822-826(2000).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 EXCITABILITY. ASSOCIATES WITH KCNQ2 OR KCNQ5 TO FORM A POTASSIUM
 CHANNEL WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL
 UNDERLYING THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND
 DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
 DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS
 WELL AS THE RESPONSIVENESS TO SYNAPTIC INPUTS.
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ2 OR KCNQ5. MAY ASSOCIATE WITH
 KCNQ2.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ3 ARE THE CAUSE OF BENIGN FAMILIAL
 CC NEONATAL CONVULSIONS TYPE 2 (BFNC2); ALSO KNOWN AS EPILEPSY,
 CC BENIGN NEONATAL TYPE 2 (BENT2); BFNC2 IS AN AUTOSOMAL DOMINANT FORM
 CC OF EPILEPSY IN THE NEWBORN THAT CLEARS SPONTANEOUSLY AFTER A FEW
 CC WEEKS AND IS FOLLOWED BY NORMAL PSYCHOMOTOR DEVELOPMENT.
 CC -1- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT IN XENOPUS
 CC OOCYTES BY CO-EXPRESSION OF EITHER KCNQ3(MOT) AND KCNQ2 AT THE
 CC RATIO OF 1:1, OR OF KCNQ3(MOT), KCNQ3(WT) AND KCNQ2 AT THE RATIO
 CC OF 1:1:2, TO MIMIC THE SITUATION IN A HETEROZYGOUS PATIENT WITH
 CC BFNC2 DISEASE.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KOT
 CC SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----

DR EMBL: AF071491; AAC96101.1; -;
 DR EMBL: AF071478; AAC96101.1; JOINED.
 DR EMBL: AF071479; AAC96101.1; JOINED.
 DR EMBL: AF071480; AAC96101.1; JOINED.
 DR EMBL: AF071481; AAC96101.1; JOINED.
 DR EMBL: AF071482; AAC96101.1; JOINED.
 DR EMBL: AF071483; AAC96101.1; JOINED.
 DR EMBL: AF071484; AAC96101.1; JOINED.
 DR EMBL: AF071485; AAC96101.1; JOINED.
 DR EMBL: AF071486; AAC96101.1; JOINED.
 DR EMBL: AF071487; AAC96101.1; JOINED.
 DR EMBL: AF071488; AAC96101.1; JOINED.
 DR EMBL: AF071489; AAC96101.1; JOINED.
 DR EMBL: AF071490; AAC96101.1; JOINED.
 DR EMBL: AF033347; AAB97314.1; -;
 DR HSPF: Q54397; 1BL8.
 DR Genew: HGNC:6297; KCNQ3.
 DR MIM: 602232; -;
 DR MIM: 121201; -;
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR006536; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF03520; KCNQ1_channel; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Multigene family; Disease mutation.
 KM SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 122 142
 FT TRANSMEM 153 173
 FT TRANSMEM 197 217
 FT TRANSMEM 226 247
 FT TRANSMEM 262 282
 FT DOMAIN 304 324
 FT TRANSMEM 331 351
 FT DOMAIN 13 24
 FT VARIANT 309 309
 FT VARIANT 310 310
 FT VARIANT 310 310
 FT MUTAGEN 310 310
 FT MUTAGEN 318 318
 FT MUTAGEN 318 318
 FT SEQUENCE 872 AA; 96742 MW; BB79C69EBE851A84 CRC64;
 Query Match 34.2%; Score 1620.5; DB 1; Length 872;
 Best Local Similarity 42.2%; Pred. No. 1.6e-86;
 Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;
 7 GGEDEGAAGLVWVSGAAAAAGGGRGSGMKVDVSGR-----VILNSAARGDGLL 60
 14 GGGDGGGGG-----GGANPDAGGDAAGDEKRVGLAPGVDTALGAGADKDTLL 68
 61 LGRRATLGGGGGGLRSGKQAGARMSLQK-PLSTSSOSCRNNVYRRVONTLYNVL 119
 69 L-----EGGRDEQRTPQS--IGLAKTPLSRPK--RNNAKYRIQLTIYVAL 115
 120 ERPRGMAFYHAFVLLVEGCLLSVSTPHTKYLASSCLLLEFWIVVGFETIRI 179
 116 ERPRGMAFYHAFVLLVEGCLLSVSTPHTKYLASSCLLLEFWIVVGFETIRI 175
 180 WSAAGCCCRGKRGKGRIFARKEPVIDITVILASIVASAKTQGNIFATSLRSRFLQI 239
 176 WAAAGCCCRGKRGKGRIFARKEPVIDITVILASIVASAKTQGNIFATSLRSRFLQI 234
 240 LRWVRMDRGRGKTKLGSVYVAHSKELITAMVIGLVLFSSFLVYVEKDA----- 291
 235 LRWVRMDRGRGKTKLGSVYVAHSKELITAMVIGLVLFSSFLVYVEKDA----- 294
 292 --NKESTYADALMWGITITLTIGYGKTPLTWLGRLISAGFALLGISFFALPAGILSG 349


```

Db 233 LQILRLRMRRGCTWLLGSAICAHSEKLTANTYIGLTLTLSSFLVYLVKDVPEMDA 292
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 292 -NKEFSTYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGIL 346
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 QGEEMKEEFETAYADALMGLITLATIGYDXTPLTWLGRLLSAGFALLGISFPALPAGIL 352
Qy 347 GSGFALKVQDQHRKHFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PIL 397
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 GSGGALVQDQHRKHFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PIL 412
Qy 398 KALHTCSPTNOKLSFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PIL 457
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 RKQGLMAAAGKGLLDVRLSNRGSNTK-----GLFTPLNDALIESPSKEKPVGSND 466
Qy 458 FNDTRRPRSLRLK-----SSQRPVLDADLTGTDVYDEKGCOCVSVDDLPLPKT 511
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 467 LNNKRRRTAFRMKAYAFWQSS-----DAGTG---DPMTEDRGYNDFLIEDMPTLKA 518
Qy 512 VTRAIRLMKFFHAKRKFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PIL 571
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 519 AIRAVRLDQHRKHFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PIL 578
Qy 572 TSDKRSREK-----ITAEHTTDLTSLMGRVYKVKOVQSLIESKLD 612
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 579 STRKHKKSQKSAFTYPSQSPRNEPYVARATSETEQSGMKFVKVROYHDMGKLD 638
Qy 613 CLDITVQVLRKGSASALALASFOIRPECEOTSDYQSV-----SKDLSGSAONSCLSR 669
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 639 FLVYMHMHQMER-----LQVHVEYPTKGCASSPBEKEDNYSDLKTIICNV 688
Qy 670 STSNINSGLOFILTP-NEFSAQTFYALSPTHMSQATQVPISSQSGSAVAATNTINQIN 728
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 689 SESGPPDPPIYFHOVIDRQVGYGFANDP-----VKLRGGSSSTKAQANLS----- 737
Qy 729 TAPKPAATTLQIPPLPAIKHLPRETLHPNAGLQESISDVTTCLVASKENVOYAQSN 788
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 738 -SGSTVABRPVLPLTLTLDSCSVYH-----SQFLQGPYSD 773
Qy 789 LTRKRSMAKSFDMGEGTILSCVPMVKDLGKSLVONLIRSEBELNIQSLGSSSSGRGS 848
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 774 HISPR-QHRSITRSDTPLST-----MSVNH-----EELERSPSGFSISODRDD 816
Qy 849 QDFYR-----KWRSEKLTIDEVGEPEDETDF 877
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 817 YVFGPSSGSSSMKREKRYIAE-----GETDIDTDF 846

```

```

CC -1 SUBUNIT: HETEROMULTIMER WITH KCNQ2 (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
CC -1 DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE325548; AKL1221.1; -
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR000636; M_channel_nlg.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF03520; KCNQ1_channel; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Multigene family.
FT TRANSEM 122 142 SEGMENT S1 (POTENTIAL).
FT TRANSEM 153 173 SEGMENT S2 (POTENTIAL).
FT TRANSEM 197 217 SEGMENT S3 (POTENTIAL).
FT TRANSEM 226 247 SEGMENT S4 (POTENTIAL).
FT TRANSEM 262 282 SEGMENT S5 (POTENTIAL).
FT DOMAIN 304 324 SEGMENT H5 (POTENTIAL).
FT TRANSEM 331 351 SEGMENT S6 (POTENTIAL).
FT DOMAIN 13 24 POLY-GLY.
SQ SEQUENCE 866 AA; 95644 MW; 4399616107A0424 CRC64;

Query Match 33.6%; Score 1589.5; DB 1; Length 866;
Best Local Similarity 41.1%; Pred. No. 9.9e-85;
Matches 394; Conservative 104; Mismatches 272; Indels 189; Gaps 30;

7 GGEBCGAAGLVKSGAAGGAGGRLGSGMDVEGRGR-----VLNSAARGGLL 60
14 GGGGGGGGG-----GGAANPAGGDAAGDEERKVLGAPDVEQYTLALGAGADKDTLL 68
Qy 61 LGTRATITGGGGGGLRESRGKQGRMSLTK-PLSYTSSGCRNRVRYRYONYLYNL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 L-----EGGDEGQRRTPOG--IGLAKTPLSRPK---RNNAKTRRIQTLIYDAL 115
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 ERPRGMAFIYHAFVLVFGCLLSVSTIPBHTKLASSCLLLEFVMIVFGLFIIRI 179
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 ERPRGMALYHALVFLVGLLILAVLTFRREYVSGDWLLETFALFIFGAEFALRI 175
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 180 WSAGCCCRKRWKQGLRTRARKFVYIDTIVLAASTAVSARKQGNFAISALRSLEIQI 239
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 WAAGCCCRKRWKQGLRTRARKFVYIDTIVLAASTAVSARKQGNFAISALRSLEIQI 234
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 LRMVMDRRGGTWLGLSVAVSHKELTANTYIGLTLTLSSFLVYLVKDVPEMDA----- 291
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 LRLMLMDRRGGTWLGLSVAVSHKELTANTYIGLTLTLSSFLVYLVKDVPEMDA 294
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 292 -NKEFSTYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGILSG 349
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 EMKEEFETAYADALMGLITLATIGYDXTPLTWLGRLLSAGFALLGISFPALPAGILSG 354
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 350 FALKVQDQHRKHFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PILKAL 400
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 355 LALKVQDQHRKHFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PILKAL 414
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 401 HTCSPTNOKLSFEKRRNPANLIQCWRSYAADKSVS-TATMK-----PILKAL 460
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 QLDPAASOKLGLLDVRLSNRGSNTK-----GLFTPLNDALIESPSKEKPVGSNN 468

```

RESULT 9
C103_BOVIN
ID C103_BOVIN STANDARD: PRT: 866 AA.
AC P58126;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 3.
GN KCNQ3
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Raae J.L.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNQ2 TO FORM A POTASSIUM CHANNEL
CC WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING
CC THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
CC POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
CC THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE
CC RESPONSIVENESS TO SYNAPTIC INPUTS (BY SIMILARITY).

QY 461 RTFRPSRLK-----SSQPKVVDADALGTDVYDEKGGCCDVSVEDLTPPLKTVIR 514
 Db 469 KERFTAFMKAYAFWQSSSE-----DAGTG---DPTAEDRGYDGLIEDMIPILKAIR 520
 QY 515 AIRIKMFHAKRKREKTELPYDVKYDEQYASAGHLDLCRKISQTRVDOLGKQITSD 574
 Db 521 AVRILOFLYKKKFKETLRYDKVDYETQYASAGHLDLMSRKLYQTRIDMTFTPPSPSTP 580
 QY 575 KKS-----EKITAHEHT---TDDLSMLGRVYKVKOVQOSTESKLDLL 615
 Db 581 KHKKSQGAFTYPSQSPRNEEYVARPTSETEDOSMKGKFEVVEQVHMGKKLDLY 640
 QY 616 DIYOQVLR-----KGSASLALASFOIPEPECQTSYQSPVDSKDLSGSAQN 663
 Db 641 DMHLOHMERLOVHVAGFSPSKGASS-----PAEAQOKED-RRDADLKTIIICNYS 689
 QY 664 SGCLSRSTANISRGLOFLTFNEFSAQTFYALSPTHSQAQVPIQOSDSAAVAATNTI 723
 Db 690 TG-----APDAPYSFHQVPVK-----VGPYGEF 713
 QY 724 ANQINTAPKPAAPTLLQIPPLPAIKHLRPRETLHPNPAGLQESISDVTCIVA-SKENV 782
 Db 714 AHD-----PVNL-----PLGG-----PSSGKHATPYAERPTVPLILTLIDSGSYRS 756
 QY 783 QVQASNLTKDR---SMRKSFDMDGETLLSVCPMPVKDLGSLSYQNLIRSTEELNITLQSG 839
 Db 757 QVELHGPCSDRKSPQRNRKSTRDSDPLSL-----MSVNH-----EELERSPSG 800
 QY 840 SESSGSRGSGODEFP---KWRESKLEFTEDEVEGPEETETDTPDAAPAREAAFAASDL 894
 Db 801 FSIQODRDYAFGPGSGSSWMREKRLAE-----GETDIDTEFTPSGSLPLSGTGC 854

RESULT 10
 ID CIOI_HUMAN STANDARD: PRT: 676 AA.
 AC P51787; Q92960; O00347; Q06007; Q90UMN8; Q90UMN9; Q94787;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 1 (KVLQT1) (Kv1.9).
 GN KCNQ1 OR KCNA9 OR KVLQT1 OR KCNA8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Kidney;
 RX MEDLINE=97459933; PubMed=9312006;
 RA Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,
 Barhanin J.;
 RT "Properties of KVLQT1 K+ channel mutations in Romano-Ward and Jervell
 and Lange-Nielsen inherited cardiac arrhythmias.";
 RL EMBO J. 16:5472-5479(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS LQT1, AND VARIANT
 RP SRR-643
 RX MEDLINE=99013427; PubMed=9799083;
 RA Itoh T., Tanaka T., Nagai R., Kikuchi K., Ogawa S., Okada S.,
 Yamagata S., Yano K., Yazaki Y., Nakamura Y.;
 RT "Genomic organization and mutational analysis of KVLQT1, a gene
 responsible for familial long QT syndrome.";
 RL Hum. Genet. 103:290-294(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LQT1 MET-587 AND
 RP HIS-591.
 RX MEDLINE=99147971; PubMed=10024302;
 RA Neyroud N., Richard P., Vignier N., Donger C., Denjoy I., Demay L.,
 Shkolnikova M., Pece K., Chevallier P., Hainque B., Coumel P.,
 Schwartz K., Guicheney P.;
 RT "Genomic organization of the KCNQ1 K+ channel gene and identification
 of C-terminal mutations in the long-QT syndrome.";

RL Circ. Res. 84:290-297(1999).
 [4]
 RP SEQUENCE OF 96-156 FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=97055938; PubMed=8900283;
 RA Sanginetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,
 Atkinson D.L., Keating M.T.;
 RT "Coassembly of K(V)LQT1 and mink (Isk) proteins to form cardiac I(Ks)
 potassium channel.";
 RL Nature 384:80-83(1996).
 RN [5]
 RP SEQUENCE OF 1-129 FROM N.A.
 RX MEDLINE=97268689; PubMed=9108097;
 RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Shalaby F.Y.,
 Blamir M.A.;
 RT "KVLQT1, a voltage-gated potassium channel responsible for human
 cardiac arrhythmias.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4017-4021(1997).
 RN [6]
 RP SEQUENCE OF 130-676 FROM N.A., AND VARIANTS LQT1.
 RX MEDLINE=96120034; PubMed=8528244;
 RA Wang Q., Curran M.E., Splawski I., Burn T.C., Millholland J.M.,
 Varrault T.J., Shen J., Timothy K.W., Vincent G.M., de Jager T.,
 Schwartz P.J., Towbin J.A., Moss A.J., Atkinson D.L., Landes G.M.,
 Connors T.D., Keating M.T.;
 RT "Positional cloning of a novel potassium channel gene: KVLQT1
 mutations cause cardiac arrhythmias.";
 RL Nat. Genet. 12:17-23(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Heart;
 RX MEDLINE=97450920; PubMed=9305853;
 RA Jiang M., Tseng-Crank J., Tseng G.-N.;
 RT "Suppression of slow delayed rectifier current by a truncated isoform
 of KVLQT1 cloned from normal human heart.";
 RL J. Biol. Chem. 272:24109-24112(1997).
 RN [8]
 RP MUTAGENESIS OF ALA-178; LEU-273 AND THR-312.
 RX MEDLINE=97462827; PubMed=9323054;
 RA Shalaby F.Y., Levesque P.C., Yang W.-P., Little W.A., Conder M.L.,
 Jentsch T.J., Blamir M.A.;
 RT "Dominant-negative KVLQT1 mutations underlie the LQT1 form of long QT
 syndrome.";
 RL Circulation 96:1733-1736(1997).
 RN [9]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20178300; PubMed=10713961;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
 Brown D.A.;
 RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
 via M1 muscarinic acetylcholine receptors.";
 RL J. Physiol. (Lond) 522:349-355(2000).
 RN [10]
 RP IDENTIFICATION OF A SUBUNIT ASSEMBLY DOMAIN.
 RX MEDLINE=20120797; PubMed=10654932;
 RA Schmitt N., Schwarz M., Peretz A., Abitbol I., Attali B., Pongs O.;
 RT "A recessive C-terminal Jervell and Lange-Nielsen mutation of the
 KCNQ1 channel impairs subunit assembly.";
 RL EMBO J. 19:332-340(2000).
 RN [11]
 RP POSSIBLE INTERACTION WITH KCNE3.
 RX MEDLINE=20110524; PubMed=10646604;
 RA Schroeder B.C., Waldegger S., Fehr S., Bleich M., Warth R.,
 Greger R., Jentsch T.J.;
 RT "A constitutively open potassium channel formed by KCNQ1 and KCNE3.";
 RL Nature 403:196-199(2000).
 RN [12]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=20169042; PubMed=10704188;
 RA Tranebjærg L., Bathen J., Tyson J., Bitner-Glindzicz M.;
 RT "Jervell and Lange-Nielsen syndrome: a Norwegian perspective.";
 RL Am. J. Med. Genet. 89:137-146(1999).
 RN [13]

CC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Colon;
 RX MEDLINE=21114838; PubMed=11220365;
 RA Kunzlemaun K., Hubner M., Schreiber R., Levy-Holzman R., Garty H.,
 Bleich M., Marth R., Slavik M., von Hahn T., Greger R.,
 RT "Cloning and function of the rat colonic epithelial K⁺ channel
 KVLQT1.";
 RL J. Membr. Biol. 179:155-164(2001).
 RN [2]
 RP SEQUENCE OF 134-352 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97460452; PubMed=9314834;
 RA Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Levitan E.S.,
 RT "Decreased expression of Kv4.2 and novel Kv4.3 K⁺ channel subunit
 mRNAs in ventricles of renovascular hypertensive rats.";
 RL Circ. Res. 81:533-539(1997).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
 WITH KCNE1 (MINK) TO FORM THE I(Ks) CARDIAC POTASSIUM CURRENT.
 CC ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT.
 CC -1- SUBUNIT: HEPEROMULTIMER WITH KCNE1 (MINK).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 SUBFAMILY.
 CC -1- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 FRAMESHIFT AT POSITION 321.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ133685; CAB38863.1; -
 DR EMBL: U92655; AAB51395.1; ALT_FRAME.
 DR HSSP: Q54397.1BL8.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF03520; Ion_trans.1.
 DR PRINTS: PR00169; KCHANNEL.
 KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 122 142 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 148 168 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 197 217 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 226 248 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 262 282 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 300 320 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 332 352 SEGMENT S6 (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 170 170 E -> K (IN REF. 2).
 FT CONFLICT 182 182 S -> T (IN REF. 2).
 FT CONFLICT 185 185 V -> L (IN REF. 2).
 FT CONFLICT 255 255 V -> F (IN REF. 2).
 SQ SEQUENCE 669 AA: 74579 MW: 2374CA1290020939 CRC64;

Query Match 23.3%; Score 1101; DB 1; Length 669;
 Best Local Similarity 38.6%; Pred. No. 1.4e-56;
 Matches 275; Conservative 106; Mismatches 190; Indels 142; Gaps 22;

OY 3 RHAG-----GEEGAGLWVKSAAAGGRLGSMKDVESGRVLLSAAARGDG 57
 DB 12 RRAGGRLGARRGSGAGLAKKCPFSLAEGCPTG-----GYYVAVIATPGARG 61

OY 58 LLL-----LGTAAATLGGGGGLRESRGKOGARMILLKPLSTYSQSCR 103
 DB 62 LAPPMPSPVSPVAPADLGP-----PRVSDPDR-----VSIYSR 97
 OY 104 RNKYR-RVONYLYNVLNTERPGW-AFIYHAEVFLVPGCLLSVSTPEHKLSSCLL 161
 DB 98 RPLLRKHIDGRVYNFLERPRGKCFYHFFVFLVLCFLFSVSTEQVALAAGTLF 157
 OY 162 ILEFVIVLVEGLEFIIRIMVSGCCCRVKGWGRFARKPFCVIDIYLIASIAVSAKT 221
 DB 158 IMEIVLVFEGTEVYVRLMSAGSKSKYGVINGRLFAFKPISIDLIYVAVMVLGVGS 217
 OY 222 OGNIPTSALRSRLFOQLLRVNRDRGCTKKLLGSVYVANSKEITANYTGFVLVSS 281
 DB 218 KGOVFNTSARGLRELOILRLHVDROGGWRLLGSVFIHRQELITLYIGFLIFSS 277
 OY 282 FLVYLVEKDA-----NKEFSTYADALWGTITLTITIGYGDPTPLTWGLRLSAGFALLGI 336
 DB 278 YEVYLAEKDAVNSGRIFESGYADALWGVYVTTTIGYGDVPTQWVGKTIASCSVFAT 337
 OY 337 SFPAALAGILGSGFALKVQEOHROKHFEKRRNPAANLIQCVWRSTADEKSVIATWPH 396
 DB 338 SFPAALAGILGSGFALKVQOKOROKHFNROIIPAAASLIQTAMRCYAAENPDSS--TWKLY 395
 OY 397 LK---ALHTC-----SPTNKLSPKREVRNMASSPGOSIKSRQASV-----GDRRSS 440
 DB 396 VRKPARSHLLSPKPKKSVWKKKFKLDKDKNGLSGKEIFVNPHTTCDDPERDRDH 455
 OY 441 TDTTASGSPKVKQMSFNDRTFRPSLRKLSQPKPYIDATLGTDDVYDEKGCQCDV 500
 DB 456 FSI--DGYDSSVRS-----PTL-LevstPH-----FLRTSFMED-----DDL 491
 OY 501.SWEDTLPLP-----KTVIRATILMFVAKKFKETLRPYDKVDVIOQSAGILD 550
 DB 492 EETLLPTPTTHVSQLDHNRATIKVIRMOYFAKKRFOQARKYDADVADVIOXSQHILN 551
 OY 551 MLCRIKSLQTRVQILGKGQ--ITSDKRSREKITAHEHTTDDLMLGVVAVKEVOYSIE 608
 DB 552 LAMRIKELQRRDQSGIKPSLFIPISEKSDR-----GSNTIGARLNVEKDVTDLD 603
 OY 609 SKLDCLLDIYQOVL-----RKGSAS-ALALASFOIPPE 641
 DB 604 QRLVITITDMLHQLSLQGGPTCNRSQVAVASDERGSINPLFLPNSLPIYE 656

RESULT 12
 CIO1_MOUSE STANDARD: PRT; 604 AA.
 AC P97414; 088702;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 1 (KVLQT1) (Kv1.9).
 GN KCNQ1 OR KCNA9 OR KVLQT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RC TISSUE=Heart;
 RX MEDLINE=97055937; PubMed=8900282;
 RA Barhanin J., Lesage F., Guillemane E., Fink M., Lazdunski M.,
 RT "Kv1.9 and Isk (mink) proteins associate to form the I(Ks) cardiac
 potassium current.";
 RL Nature 384:78-80(1996).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM II), AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6;
 RX MEDLINE=98282243; PubMed=9618174;
 RA Paulsen M., Davies K.R., Bowden L.M., Villar A.J., Franck O.,


```

CC      OUTER HAIR CELLS (OHCs) OF THE COCHLEA. RECIPROCAL LONGITUDINAL
CC      GRADIENTS OF EXPRESSION IS PRESENT IN IHCS AND OHCs. THE STRONGEST
CC      EXPRESSION IN IHCS IS IN THE BASE OF THE COCHLEA AND IN THE APEX
CC      FOR OHCs. A BASAL TO APICAL GRADIENT OF EXPRESSION IS ALSO PRESENT
CC      IN BOTH TYPE I AND TYPE II SPIRAL GANGLION CELLS.
CC      -1- DEVELOPMENTAL STAGE: AT P0 EXPRESSION IS PRIMARILY IN THE BASAL
CC      HOOK TO LOWER MIDDLE TURN OF THE COCHLEA AND PROGRESSIVELY EXPANDS
CC      TOWARD THE APEX OVER TIME. BY P8, THE EXPRESSION IS EVIDENT IN
CC      BOTH IHCS AND OHCs ALONG THE ENTIRE LENGTH OF THE COCHLEA. THEN
CC      THE ADULT PATTERN BEGINS TO EMERGE, AS EXPRESSION IN BASAL OHCs
CC      AND IN APICAL IHCS DECREASES.
CC      -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC      CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC      EVERY THIRD POSITION (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC      SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      CC
CC      EMBL; AF249748; AAF6433.1; -
CC      DR InterPro: IPR003946; KCON1_channel.
CC      DR Pfam: PF03520; KCON1_channel; 1.
CC      CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC      KM Multigene family.
CC      FT NON_TER 1 1
CC      FT NON_TER 168 168
CC      SQ SEQUENCE 168 AA; 18844 MW; F442BCD8EC25512E CRC64;
CC
CC      Query Match 9.4%; Score 446.5; DB 1; Length 168;
CC      Best Local Similarity 56.6%; Pred. No. 1.9e-19;
CC      Matches 98; Conservative 30; Mismatches 28; Indels 17; Gaps 5;
CC
QY      414 ERYMASPRGSGSIKSRQ--ASVGDRRSPSTDTLAE-GSPITYOKSWSTNDRFRFRSLRL 470
DB      1 DIRIRISQKRTGSPSKOHLPPIPTSPSSDEQVGSASPSKOKSWSTNDRFRFRASLRL 60
QY      471 K---SSQKRPVINDATFALGTDDVDYDEKCCDQSVEDTLPLPKTYAIRIKMFVARRK 527
DB      61 KPRCSAEGCP-----SEVVAEKSQYCELTYYDDVMPAVKTYIRSVRIKLFLVARRK 111
QY      528 FKETLRPYDVXDVIEOYASGHIDMLCRISLQFRVDQILGKGQITSDDKKSREK 580
DB      112 FKETLRPYDVXDVIEOYASGHIDMLGRIKSLQARVDQIVGRG--PGDRKTRRK 162
CC
RESULT 20
C101_PIG STANDARD: PRT; 123 AA.
AC 09RTU7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 1 (KVLQTL) (Kv1.9)
DE (Fragment).
GN KCON1 OR KVLQTL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Coronary artery;
RA Imaizumi Y., Ohya S.;
RT "Effects of Ms-551 on delayed rectifier K current in coronary artery
RT smooth muscle cells";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES

```

```

CC WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT.
CC ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETEROMULTIMER WITH KCNE1 (MINK) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KOT
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB033207; BAA88580.1; -.
CC HSSP: Q54397; 1BL8.
CC InterPro: IPR001622; K+channel_pore.
CC InterPro: IPR003091; K_channel.
CC InterPro: IPR000636; M+channel_nlg.
CC Pfam: PF00520; Ion_trans; 1.
CC PRINTS: PR00169; KCHANNEL.
CC K+ ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family.
CC NON_TER 1
CC TRANSMEM 1
CC TRANSMEM 27 18 SEGMENT S3 (POTENTIAL).
CC TRANSMEM 27 49 SEGMENT S4 (POTENTIAL).
CC TRANSMEM 63 83 SEGMENT S5 (POTENTIAL).
CC DOMAIN 101 121 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
CC CARBOHD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
CC NON_TER 123 123
CC SEQUENCE 123 AA; 13602 MW; A6CEC4201C6836CA CRC64;

Query Match 8.7%; Score 409.5; DB 1; Length 123;
Best Local Similarity 62.6%; Pred. No. 1.8e-17;
Matches 77; Conservative 20; Mismatches 21; Indels 5; Gaps 1;

QY 204 VIDTIVLAVASAKTOGNIFATSLRSLRPLQILIRVMDRGRGTWKLGSVVAHS 263
DB 1 IIDIVVAVASMVLCVSGKGVFAISIGIRLQILRMHVDROGRTWKLGSVVFTHR 60
QY 264 KELLTAWYIGLVLFSSFLVYLVEKDA-----NKEFSYADALMWTITLTITGYDKT 318
DB 61 QELTTTIGLGLIFSSYFYLAERKDAVNESGVFEFSYADALMGTVTITGYGDKV 120
QY 319 PLT 321
DB 121 PQT 123

RESULT 21
CIRK_HUMAN STANDARD: PRT: 854 AA.
AC 014721:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv2.1 (DHK1).
GN KCNB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

```

```

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L02840; AAA36156.1; -.
CC HSSP: Q54397; 1BL8.
CC Genew: HGNC:6231; KCNB1.
CC MIM: 600397; -.
CC InterPro: IPR000210; BMR_POZ.
CC InterPro: IPR001622; K+channel_pore.
CC InterPro: IPR003091; K_channel.
CC InterPro: IPR003131; K_tetra.
CC InterPro: IPR004350; Kv2channel.
CC InterPro: IPR004351; Kv22channel.
CC InterPro: IPR003968; Kv_channel.
CC InterPro: IPR000636; M+channel_nlg.
CC InterPro: IPR003973; Shab_channel.
CC Pfam: PF00520; Ion_trans; 1.
CC Pfam: PF02214; K_tetra; 1.
CC Pfam: PF03521; Kv2channel; 1.
CC PRINTS: PR00169; KCHANNEL.
CC PRINTS: PR01514; KV2CHANNEL.
CC PRINTS: PR01495; SHABCHANNEL.
CC SMART: SM00225; ETV; 1.
CC K+ ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC NON_TER 1
CC TRANSMEM 183 182 SEGMENT S1 (POTENTIAL).
CC TRANSMEM 205 224 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 225 246 SEGMENT S2 (POTENTIAL).
CC TRANSMEM 247 256 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 257 278 SEGMENT S3 (POTENTIAL).
CC TRANSMEM 279 290 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 291 312 SEGMENT S4 (POTENTIAL).
CC TRANSMEM 313 326 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 327 348 SEGMENT S5 (POTENTIAL).
CC TRANSMEM 349 388 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 389 410 SEGMENT S6 (POTENTIAL).
CC DOMAIN 411 854 CYTOPLASMIC (POTENTIAL).
CC MOD_RES 440 440 CYTOPLASMIC (POTENTIAL).
CC MOD_RES 442 492 PHOSPHORYLATION (BY PKA) (POTENTIAL).
CC CARBOHD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 854 AA; 95521 MW; 360DEB3E45731EDA CRC64;

Query Match 6.2%; Score 291.5; DB 1; Length 854;
Best Local Similarity 20.2%; Pred. No. 1.5e-09;
Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33;

QY 115 LYNVLEPRGMA--FIYHAFVFLVFGCLISVFSTIPRFTK-----ASSCLTLE 164
DB 171 LMDLEKPNSSVAAKIALIISIMFYLTALSL-NTLPRLQSLDEFGQSDNQLAHYE 229
QY 165 FVMIVFGLFETIRIWSACCCRYRGQGRLEFRARPFVVIDTIVLAVASAKTOGN 224

```

```

Db 230 AVCIAMFTMYELLRLSSP-----KKW-----KFKGPLNAIDLAILPYV-----T 272
OY 225 IFATSLRL-----RFLQILRMVMDRGGMWKLGSVVAHAKEL-ITAN 270
Db 273 IFLTESNKSVALOFQVNRVVOIFRLIKLILKLAHSHGLSLGTLRLRSYELGILL 332
OY 271 YIGFLVLIFSSFLVYLVERDA-NKESTYADALIMWGTITLTTGYGDKPLPLWIGRLLSA 329
Db 333 FLANGIMIFSS-LVFAEKDEDDTKFKSLPASPWMTITMTYGYDIDYKTLGKIVG 391
OY 330 GPALIGIFFPALPACILSGFALKVOEOHROKHFEKRRNPANLIOCWRSYADEKSVS 389
Db 392 LCCIAGVLVAILPIIYVNFSEFEYKEOKROEKAIRR-----EALBRANKGS 440
OY 390 IATWPHKALHTCPTNOKLSFKERVNM-----ASPRGOSIKRQASVGRBSPSTITA 445
Db 441 IVS-----MNMKDAFANSIEMMDIYERNGEMWKKDKVQDNHLSPNKWKWT 487
OY 446 EGSPTKVOKSMFNDRTFRPRLRLKLSQPKPIYIDATLGTDDYDEKGCQCDVSIEDL 505
Db 488 KRTLSSETSSKSFETKEGQSPKARSSSPQHL-----NQQLEDMTNKA----- 533
OY 506 TPLKTVIRAIRIMKFWAKRRFKETLRPYDKVIEQYSAGHLDMLCRISLQTRVDQI 565
Db 534 ----KQSQPIINTKESAAQSKPELEMEISPS-----PVALPLPTREGV 575
OY 566 LCKGQITSKSKREKITAHEHTTDLMLGRVYKVEKOVSTISKDLIDLYQVLRK 625
Db 576 I-----DMRS-----MSIDSIFISCARD-PPEATRFS 601
OY 626 SASALALASFOIPECEQTSQSDYQSPVDSKDLGSAONSGLSRSTSANTSRGLQITLTP 685
Db 602 HSPPLSLPS-----KTGGSTAP-EVGMRGALGASG--GRFYANPS-----P 640
OY 666 NEFSAQTFYALSP-----TMHSQATQVPISSQSD-----GSAVAA 719
Db 641 DASQHSFPIESPSSKSMKTNPNLKLRLALKVFMGEPSPPLPYLGMYHDLRNHGSAAA 700
OY 720 T-----NTIANQINTAPKRAAPTTLQIPPLPAIKHLPRETLHPN-----PAGLOSIS 769
Db 701 VAGLCATLIDRAVLSPSSSYTTASAKTP-----PRSPKHTAIAFNEAGVHOYT- 752
OY 770 DVTTLVASKENVQVVAQSNILTKDRSMRKSFPDMGEGTLLSYCPMPKDLGKSLSYQNLIRS 829
Db 753 DADT-----DDEGQLIYSVSSPKKLPLPSTSPK----- 781
OY 830 TEELNIQISGSSGSGSODPYPKWRBSKLFITDEVEGPELETDTFDPAAPAREAAAF 889
Db 782 -----FSTGRSEKNHF-----ESSPLPTSPKFLRONCI 810
OY 890 ASDSLRTGSRSSQICKAGE--STDALSLP 918
Db 811 YSTALTGKPGSQGQCKLELNHSPVRLP 841

```

```

RT "A novel potassium channel with delayed rectifier properties isolated
RT from rat brain by expression cloning.";
RT Nature 340:642-645(1989).
RN [2]
RP REVISIONS.
RA Frech G.C.;
OY Submitted (Feb-1990) to the EMBL/Genbank/DBJ databases.
CC -I FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I SUBCELLULAR LOCATION: Integral membrane protein.
CC -I TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMPUS, CEREBELLUM, AND
CC OLFACTORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
CC RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF THE
CC ATRIUM AND VENTRICLE AND IN SKELETAL MUSCLE.
CC -I DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -I SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X16476; CAA34497.1; -.
DR PIR: S05448; CHRBD1.
DR HSSP: S054397; 1BL8.
DR InterPro: IPR000210; BTR_PQZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K+channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR004350; Kv21channel.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1514; KV21CHANNEL.
DR PRINTS: PRO1491; KVCHANNEL.
DR PRINTS: PRO1495; SHABCHANNEL.
DR SMART: SM00225; BTR; 1.
KW Ionic channel; Transmembrane; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
KW DOMAIN 1
FT DOMAIN 182
FT TRANSMEM 183
FT TRANSMEM 204
FT TRANSMEM 205
FT TRANSMEM 224
FT TRANSMEM 225
FT TRANSMEM 246
FT TRANSMEM 247
FT TRANSMEM 256
FT TRANSMEM 257
FT TRANSMEM 278
FT TRANSMEM 279
FT TRANSMEM 291
FT TRANSMEM 312
FT TRANSMEM 313
FT TRANSMEM 326
FT TRANSMEM 327
FT TRANSMEM 333
FT TRANSMEM 348
FT TRANSMEM 349
FT TRANSMEM 388
FT TRANSMEM 389
FT TRANSMEM 410
FT TRANSMEM 411
FT TRANSMEM 412
FT TRANSMEM 413
FT TRANSMEM 414
FT TRANSMEM 415
FT TRANSMEM 416
FT TRANSMEM 417
FT TRANSMEM 418
FT TRANSMEM 419
FT TRANSMEM 420
FT TRANSMEM 421
FT TRANSMEM 422
FT TRANSMEM 423
FT TRANSMEM 424
FT TRANSMEM 425
FT TRANSMEM 426
FT TRANSMEM 427
FT TRANSMEM 428
FT TRANSMEM 429
FT TRANSMEM 430
FT TRANSMEM 431
FT TRANSMEM 432
FT TRANSMEM 433
FT TRANSMEM 434
FT TRANSMEM 435
FT TRANSMEM 436
FT TRANSMEM 437
FT TRANSMEM 438
FT TRANSMEM 439
FT TRANSMEM 440
FT TRANSMEM 441
FT TRANSMEM 442
FT TRANSMEM 443
FT TRANSMEM 444
FT TRANSMEM 445
FT TRANSMEM 446
FT TRANSMEM 447
FT TRANSMEM 448
FT TRANSMEM 449
FT TRANSMEM 450
FT TRANSMEM 451
FT TRANSMEM 452
FT TRANSMEM 453
FT TRANSMEM 454
FT TRANSMEM 455
FT TRANSMEM 456
FT TRANSMEM 457
FT TRANSMEM 458
FT TRANSMEM 459
FT TRANSMEM 460
FT TRANSMEM 461
FT TRANSMEM 462
FT TRANSMEM 463
FT TRANSMEM 464
FT TRANSMEM 465
FT TRANSMEM 466
FT TRANSMEM 467
FT TRANSMEM 468
FT TRANSMEM 469
FT TRANSMEM 470
FT TRANSMEM 471
FT TRANSMEM 472
FT TRANSMEM 473
FT TRANSMEM 474
FT TRANSMEM 475
FT TRANSMEM 476
FT TRANSMEM 477
FT TRANSMEM 478
FT TRANSMEM 479
FT TRANSMEM 480
FT TRANSMEM 481
FT TRANSMEM 482
FT TRANSMEM 483
FT TRANSMEM 484
FT TRANSMEM 485
FT TRANSMEM 486
FT TRANSMEM 487
FT TRANSMEM 488
FT TRANSMEM 489
FT TRANSMEM 490
FT TRANSMEM 491
FT TRANSMEM 492
FT TRANSMEM 493
FT TRANSMEM 494
FT TRANSMEM 495
FT TRANSMEM 496
FT TRANSMEM 497
FT TRANSMEM 498
FT TRANSMEM 499
FT TRANSMEM 500
FT TRANSMEM 501
FT TRANSMEM 502
FT TRANSMEM 503
FT TRANSMEM 504
FT TRANSMEM 505
FT TRANSMEM 506
FT TRANSMEM 507
FT TRANSMEM 508
FT TRANSMEM 509
FT TRANSMEM 510
FT TRANSMEM 511
FT TRANSMEM 512
FT TRANSMEM 513
FT TRANSMEM 514
FT TRANSMEM 515
FT TRANSMEM 516
FT TRANSMEM 517
FT TRANSMEM 518
FT TRANSMEM 519
FT TRANSMEM 520
FT TRANSMEM 521
FT TRANSMEM 522
FT TRANSMEM 523
FT TRANSMEM 524
FT TRANSMEM 525
FT TRANSMEM 526
FT TRANSMEM 527
FT TRANSMEM 528
FT TRANSMEM 529
FT TRANSMEM 530
FT TRANSMEM 531
FT TRANSMEM 532
FT TRANSMEM 533
FT TRANSMEM 534
FT TRANSMEM 535
FT TRANSMEM 536
FT TRANSMEM 537
FT TRANSMEM 538
FT TRANSMEM 539
FT TRANSMEM 540
FT TRANSMEM 541
FT TRANSMEM 542
FT TRANSMEM 543
FT TRANSMEM 544
FT TRANSMEM 545
FT TRANSMEM 546
FT TRANSMEM 547
FT TRANSMEM 548
FT TRANSMEM 549
FT TRANSMEM 550
FT TRANSMEM 551
FT TRANSMEM 552
FT TRANSMEM 553
FT TRANSMEM 554
FT TRANSMEM 555
FT TRANSMEM 556
FT TRANSMEM 557
FT TRANSMEM 558
FT TRANSMEM 559
FT TRANSMEM 560
FT TRANSMEM 561
FT TRANSMEM 562
FT TRANSMEM 563
FT TRANSMEM 564
FT TRANSMEM 565
FT TRANSMEM 566
FT TRANSMEM 567
FT TRANSMEM 568
FT TRANSMEM 569
FT TRANSMEM 570
FT TRANSMEM 571
FT TRANSMEM 572
FT TRANSMEM 573
FT TRANSMEM 574
FT TRANSMEM 575
FT TRANSMEM 576
FT TRANSMEM 577
FT TRANSMEM 578
FT TRANSMEM 579
FT TRANSMEM 580
FT TRANSMEM 581
FT TRANSMEM 582
FT TRANSMEM 583
FT TRANSMEM 584
FT TRANSMEM 585
FT TRANSMEM 586
FT TRANSMEM 587
FT TRANSMEM 588
FT TRANSMEM 589
FT TRANSMEM 590
FT TRANSMEM 591
FT TRANSMEM 592
FT TRANSMEM 593
FT TRANSMEM 594
FT TRANSMEM 595
FT TRANSMEM 596
FT TRANSMEM 597
FT TRANSMEM 598
FT TRANSMEM 599
FT TRANSMEM 600
FT TRANSMEM 601
FT TRANSMEM 602
FT TRANSMEM 603
FT TRANSMEM 604
FT TRANSMEM 605
FT TRANSMEM 606
FT TRANSMEM 607
FT TRANSMEM 608
FT TRANSMEM 609
FT TRANSMEM 610
FT TRANSMEM 611
FT TRANSMEM 612
FT TRANSMEM 613
FT TRANSMEM 614
FT TRANSMEM 615
FT TRANSMEM 616
FT TRANSMEM 617
FT TRANSMEM 618
FT TRANSMEM 619
FT TRANSMEM 620
FT TRANSMEM 621
FT TRANSMEM 622
FT TRANSMEM 623
FT TRANSMEM 624
FT TRANSMEM 625
FT TRANSMEM 626
FT TRANSMEM 627
FT TRANSMEM 628
FT TRANSMEM 629
FT TRANSMEM 630
FT TRANSMEM 631
FT TRANSMEM 632
FT TRANSMEM 633
FT TRANSMEM 634
FT TRANSMEM 635
FT TRANSMEM 636
FT TRANSMEM 637
FT TRANSMEM 638
FT TRANSMEM 639
FT TRANSMEM 640
FT TRANSMEM 641
FT TRANSMEM 642
FT TRANSMEM 643
FT TRANSMEM 644
FT TRANSMEM 645
FT TRANSMEM 646
FT TRANSMEM 647
FT TRANSMEM 648
FT TRANSMEM 649
FT TRANSMEM 650
FT TRANSMEM 651
FT TRANSMEM 652
FT TRANSMEM 653
FT TRANSMEM 654
FT TRANSMEM 655
FT TRANSMEM 656
FT TRANSMEM 657
FT TRANSMEM 658
FT TRANSMEM 659
FT TRANSMEM 660
FT TRANSMEM 661
FT TRANSMEM 662
FT TRANSMEM 663
FT TRANSMEM 664
FT TRANSMEM 665
FT TRANSMEM 666
FT TRANSMEM 667
FT TRANSMEM 668
FT TRANSMEM 669
FT TRANSMEM 670
FT TRANSMEM 671
FT TRANSMEM 672
FT TRANSMEM 673
FT TRANSMEM 674
FT TRANSMEM 675
FT TRANSMEM 676
FT TRANSMEM 677
FT TRANSMEM 678
FT TRANSMEM 679
FT TRANSMEM 680
FT TRANSMEM 681
FT TRANSMEM 682
FT TRANSMEM 683
FT TRANSMEM 684
FT TRANSMEM 685
FT TRANSMEM 686
FT TRANSMEM 687
FT TRANSMEM 688
FT TRANSMEM 689
FT TRANSMEM 690
FT TRANSMEM 691
FT TRANSMEM 692
FT TRANSMEM 693
FT TRANSMEM 694
FT TRANSMEM 695
FT TRANSMEM 696
FT TRANSMEM 697
FT TRANSMEM 698
FT TRANSMEM 699
FT TRANSMEM 700
FT TRANSMEM 701
FT TRANSMEM 702
FT TRANSMEM 703
FT TRANSMEM 704
FT TRANSMEM 705
FT TRANSMEM 706
FT TRANSMEM 707
FT TRANSMEM 708
FT TRANSMEM 709
FT TRANSMEM 710
FT TRANSMEM 711
FT TRANSMEM 712
FT TRANSMEM 713
FT TRANSMEM 714
FT TRANSMEM 715
FT TRANSMEM 716
FT TRANSMEM 717
FT TRANSMEM 718
FT TRANSMEM 719
FT TRANSMEM 720
FT TRANSMEM 721
FT TRANSMEM 722
FT TRANSMEM 723
FT TRANSMEM 724
FT TRANSMEM 725
FT TRANSMEM 726
FT TRANSMEM 727
FT TRANSMEM 728
FT TRANSMEM 729
FT TRANSMEM 730
FT TRANSMEM 731
FT TRANSMEM 732
FT TRANSMEM 733
FT TRANSMEM 734
FT TRANSMEM 735
FT TRANSMEM 736
FT TRANSMEM 737
FT TRANSMEM 738
FT TRANSMEM 739
FT TRANSMEM 740
FT TRANSMEM 741
FT TRANSMEM 742
FT TRANSMEM 743
FT TRANSMEM 744
FT TRANSMEM 745
FT TRANSMEM 746
FT TRANSMEM 747
FT TRANSMEM 748
FT TRANSMEM 749
FT TRANSMEM 750
FT TRANSMEM 751
FT TRANSMEM 752
FT TRANSMEM 753
FT TRANSMEM 754
FT TRANSMEM 755
FT TRANSMEM 756
FT TRANSMEM 757
FT TRANSMEM 758
FT TRANSMEM 759
FT TRANSMEM 760
FT TRANSMEM 761
FT TRANSMEM 762
FT TRANSMEM 763
FT TRANSMEM 764
FT TRANSMEM 765
FT TRANSMEM 766
FT TRANSMEM 767
FT TRANSMEM 768
FT TRANSMEM 769
FT TRANSMEM 770
FT TRANSMEM 771
FT TRANSMEM 772
FT TRANSMEM 773
FT TRANSMEM 774
FT TRANSMEM 775
FT TRANSMEM 776
FT TRANSMEM 777
FT TRANSMEM 778
FT TRANSMEM 779
FT TRANSMEM 780
FT TRANSMEM 781
FT TRANSMEM 782
FT TRANSMEM 783
FT TRANSMEM 784
FT TRANSMEM 785
FT TRANSMEM 786
FT TRANSMEM 787
FT TRANSMEM 788
FT TRANSMEM 789
FT TRANSMEM 790
FT TRANSMEM 791
FT TRANSMEM 792
FT TRANSMEM 793
FT TRANSMEM 794
FT TRANSMEM 795
FT TRANSMEM 796
FT TRANSMEM 797
FT TRANSMEM 798
FT TRANSMEM 799
FT TRANSMEM 800
FT TRANSMEM 801
FT TRANSMEM 802
FT TRANSMEM 803
FT TRANSMEM 804
FT TRANSMEM 805
FT TRANSMEM 806
FT TRANSMEM 807
FT TRANSMEM 808
FT TRANSMEM 809
FT TRANSMEM 810
FT TRANSMEM 811
FT TRANSMEM 812
FT TRANSMEM 813
FT TRANSMEM 814
FT TRANSMEM 815
FT TRANSMEM 816
FT TRANSMEM 817
FT TRANSMEM 818
FT TRANSMEM 819
FT TRANSMEM 820
FT TRANSMEM 821
FT TRANSMEM 822
FT TRANSMEM 823
FT TRANSMEM 824
FT TRANSMEM 825
FT TRANSMEM 826
FT TRANSMEM 827
FT TRANSMEM 828
FT TRANSMEM 829
FT TRANSMEM 830
FT TRANSMEM 831
FT TRANSMEM 832
FT TRANSMEM 833
FT TRANSMEM 834
FT TRANSMEM 835
FT TRANSMEM 836
FT TRANSMEM 837
FT TRANSMEM 838
FT TRANSMEM 839
FT TRANSMEM 840
FT TRANSMEM 841
FT TRANSMEM 842
FT TRANSMEM 843
FT TRANSMEM 844
FT TRANSMEM 845
FT TRANSMEM 846
FT TRANSMEM 847
FT TRANSMEM 848
FT TRANSMEM 849
FT TRANSMEM 850
FT TRANSMEM 851
FT TRANSMEM 852
FT TRANSMEM 853
FT TRANSMEM 854
FT TRANSMEM 855
FT TRANSMEM 856
FT TRANSMEM 857
FT TRANSMEM 858
FT TRANSMEM 859
FT TRANSMEM 860
FT TRANSMEM 861
FT TRANSMEM 862
FT TRANSMEM 863
FT TRANSMEM 864
FT TRANSMEM 865
FT TRANSMEM 866
FT TRANSMEM 867
FT TRANSMEM 868
FT TRANSMEM 869
FT TRANSMEM 870
FT TRANSMEM 871
FT TRANSMEM 872
FT TRANSMEM 873
FT TRANSMEM 874
FT TRANSMEM 875
FT TRANSMEM 876
FT TRANSMEM 877
FT TRANSMEM 878
FT TRANSMEM 879
FT TRANSMEM 880
FT TRANSMEM 881
FT TRANSMEM 882
FT TRANSMEM 883
FT TRANSMEM 884
FT TRANSMEM 885
FT TRANSMEM 886
FT TRANSMEM 887
FT TRANSMEM 888
FT TRANSMEM 889
FT TRANSMEM 890
FT TRANSMEM 891
FT TRANSMEM 892
FT TRANSMEM 893
FT TRANSMEM 894
FT TRANSMEM 895
FT TRANSMEM 896
FT TRANSMEM 897
FT TRANSMEM 898
FT TRANSMEM 899
FT TRANSMEM 900
FT TRANSMEM 901
FT TRANSMEM 902
FT TRANSMEM 903
FT TRANSMEM 904
FT TRANSMEM 905
FT TRANSMEM 906
FT TRANSMEM 907
FT TRANSMEM 908
FT TRANSMEM 909
FT TRANSMEM 910
FT TRANSMEM 911
FT TRANSMEM 912
FT TRANSMEM 913
FT TRANSMEM 914
FT TRANSMEM 915
FT TRANSMEM 916
FT TRANSMEM 917
FT TRANSMEM 918
FT TRANSMEM 919
FT TRANSMEM 920
FT TRANSMEM 921
FT TRANSMEM 922
FT TRANSMEM 923
FT TRANSMEM 924
FT TRANSMEM 925
FT TRANSMEM 926
FT TRANSMEM 927
FT TRANSMEM 928
FT TRANSMEM 929
FT TRANSMEM 930
FT TRANSMEM 931
FT TRANSMEM 932
FT TRANSMEM 933
FT TRANSMEM 934
FT TRANSMEM 935
FT TRANSMEM 936
FT TRANSMEM 937
FT TRANSMEM 938
FT TRANSMEM 939
FT TRANSMEM 940
FT TRANSMEM 941
FT TRANSMEM 942
FT TRANSMEM 943
FT TRANSMEM 944
FT TRANSMEM 945
FT TRANSMEM 946
FT TRANSMEM 947
FT TRANSMEM 948
FT TRANSMEM 949
FT TRANSMEM 950
FT TRANSMEM 951
FT TRANSMEM 952
FT TRANSMEM 953
FT TRANSMEM 954
FT TRANSMEM 955
FT TRANSMEM 956
FT TRANSMEM 957
FT TRANSMEM 958
FT TRANSMEM 959
FT TRANSMEM 960
FT TRANSMEM 961
FT TRANSMEM 962
FT TRANSMEM 963
FT TRANSMEM 964
FT TRANSMEM 965
FT TRANSMEM 966
FT TRANSMEM 967
FT TRANSMEM 968
FT TRANSMEM 969
FT TRANSMEM 970
FT TRANSMEM 971
FT TRANSMEM 972
FT TRANSMEM 973
FT TRANSMEM 974
FT TRANSMEM 975
FT TRANSMEM 976
FT TRANSMEM 977
FT TRANSMEM 978
FT TRANSMEM 979
FT TRANSMEM 980
FT TRANSMEM 981
FT TRANSMEM 982
FT TRANSMEM 983
FT TRANSMEM 984
FT TRANSMEM 985
FT TRANSMEM 986
FT TRANSMEM 987
FT TRANSMEM 988
FT TRANSMEM 989
FT TRANSMEM 990
FT TRANSMEM 991
FT TRANSMEM 992
FT TRANSMEM 993
FT TRANSMEM 994
FT TRANSMEM 995
FT TRANSMEM 996
FT TRANSMEM 997
FT TRANSMEM 998
FT TRANSMEM 999
FT TRANSMEM 1000

```

FT MOD_RES 492 492 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 853 AA: 95280 MW: 7A08998839716165 CRC64;
 Query Match 6.1%; Score 289; DB 1; Length 853;
 Best Local Similarity 19.7%; Pred. No. 2.1e-09;
 Matches 176; Conservative 134; Mismatches 269; Indels 316; Gaps 37;
 QY 115 LYNVLEPRGMA---FYHAFVFLVAGCLLSVFSTPEHTKL-----ASSCLLIE 164
 DB 171 LMDLLEKPNSSVAAKLAIISIMFIVLSTALSL-NLPELOSDEFGSDNPOLAHVE 229
 QY 165 FMYIVVGFLEFTRIRISAGCCCRKQWGRLEAPKPCFVIDTVLAVASAKTOGN 224
 DB 230 AVCIAMFTEYELRFLSSP-----KKW-----KEFGPLNADLALIEYV-----T 272
 QY 225 IFATSLARSL-----RFQILMVRDRRGCTKKLGSVYANSKEL-ITAW 270
 DB 273 IFLESNKSVLOPQVRRVQVIRIMKILKILARHSTGLQSLGFTLRSTYNELGLIL 332
 QY 271 YIGFVLVLFSSFLVLYVEKDA-NKESTVADALMGTITLTIGYGDKPTPLWGLRLSA 329
 DB 333 FLAMGIMIPSS-LVFEAKDEDDTKFKSIPASFWMATITMTVTGDIYPTLGLKIYG 391
 QY 330 GFALLGISFALPAGLGSFALKVQDQKHQKHEKRRNPANLIGCVMSYADEKSVS 389
 DB 392 LCCINGVLVIALPIPIIVNNSEFEYKQKQKAKIKRR----- 429
 QY 390 IATWRPHLKALHTCSPTNOKLSFERVMASSPRGQSIKSRQASVGDRRSPSTDITAEESP 449
 DB 430 -----EALERAKRNGSIY----- 442
 QY 450 TKVQKSWSEFNDTRFRPRLSLKSSQPKPVADTALCTDDVYDKGCCQDVSVEDLPPL 509
 DB 443 -----SWNMKDAFARSIEM-----MDIYVENKNG----- 465
 QY 510 KTVIRAIRIMKRVHAKRKKEKTRIPVDKDYIEQYSGHIDMLCRISLQTRVDOILKG 569
 DB 466 ESIARKDKVQDNHLSKNKWKWT-----KRALSETSSS-----KSFEK----- 503
 QY 570 QITSKRSKEKITAEHETDDLSMLGRVYVKEVQVIESKLDCLLIYQOVLKRGASA 629
 DB 504 EOGSEPKARSSSPQH-----LNVOOLE-----DMYSMAKTQSPPI 540
 QY 630 L---ALASFOIPPECEQTSYQSPVDSKDLSSAONSGLSRSTANISNGLOFILPN 686
 DB 541 LNTKEMAPQSKPPELEMS--MSPVAPL---PARTEGVIDMSMSID---SFISAT 592
 QY 687 EESAGTFYALSP--TMHSQATQVPIQO-----SDGSAVATNTTIANQINT-----AP 731
 DB 593 DPEATREFSHSLASLSKAGSSTADEVGMRGALGASGRITETNP IPTSRSGFEVESP 652
 QY 732 KPAAPTTLQIP-----PLPAIKHLPPRETLHPNP-----AGLOESIS 769
 DB 653 RSSMKTNNPLKIRALKVNFVEDPTLLPSL-----GLYHPLNRKGAANAVAL-ECAS 707
 QY 770 DVTYGLVASKENVQAQSNLTKDRSMRK-----SEDMG-----GETILSYCP 811
 DB 708 LLDKPVLPSESSITYTASARTPPRSPEKHTAIAFNFEAGVHHYIDTJDEGQLLYSDS 767
 QY 812 MVRPDIGKSLSVQNLIRSTEELINQLSGSESSSRSSQDYPFKMKRESKLPITDEEVGPEE 871
 DB 768 SPFASLHGISTSK-----FSTGAR----- 786
 QY 872 TETDTPDAPOPAPAR-----EAFASDSLRTGSRSSQICKAGEST--DALSLP 918
 DB 787 TEKNHFESEPLPTSKFLRPNCVYSSEGL-TGKGPQAGQCKLENHTPPVHMLP 840
 RESULT 23
 CIRC_HUMAN
 ID CIRC_HUMAN STANDARD: PRT: 806 AA.
 AC 092953;
 DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv2.2.
 GN KCNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98275219; PubMed=9612272;
 RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
 RA Flynn E.R., Kenyon J.L., Horowitz B.;
 RT "Molecular identification of a component of delayed rectifier current
 in gastrointestinal smooth muscles."
 RL Am. J. Physiol. 274:G901-G911(1998).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U69962; AAB08433.1; -.
 DR HSSP: Q54397; IBL8.
 DR GeneW: HGNC:6232; KCNB2.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR004351; Kv22channel.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.
 DR Pfam: PF03521; Kv2channel_1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01515; KV22CHANNEL.
 DR PRINTS: PR01491; KYCHANNEL.
 DR PRINTS: PR01495; SHABCHANNEL.
 DR SMART: SM00225; BTB; 1.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT DOMAIN 1 190
 FT TRANSMEM 191 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 254
 FT DOMAIN 255 264
 FT TRANSMEM 265 286
 FT DOMAIN 287 298
 FT TRANSMEM 299 320
 FT DOMAIN 321 334
 FT TRANSMEM 335 356
 FT DOMAIN 357 396
 FT TRANSMEM 397 418
 FT SEGMENT S1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SEGMENT S2 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SEGMENT S3 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT SEGMENT S4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SEGMENT S5 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SEGMENT S6 (POTENTIAL).

FT DOMAIN 419 806 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 806 AA: 90990 MW: 2ABEBCE05A90E6 CRC64:
 Query Match 6.0%; Score 282; DB 1; Length 806;
 Best Local Similarity 22.2%; Pred. No. 5e-09;
 Matches 150; Conservative 105; Mismatches 238; Indels 182; Gaps 28;
 115 LYNNLEPRGMA---FYHAFVFLVFGCLLSVSTPE-----HTKLASSC 159
 DB 179 LMDLEKPNSSVAAKILAIIVSLFTLSTALST-NLPELQEDFEGQLNDNRQLAH-- 235
 QY 160 LLLEFVIVVGFLEFIRISAGCCCRVGRGRLRFARKPCVVDITVLASIAVSA 219
 DB 236 ---VEANCIAFMETMEYLRLFLSS-----PNMKKFFKGLVNDLAILPYVY---- 279
 QY 220 KTGONIFATSAIRSL-----RFLQILNRVMDRGGVTKLLGSVYVAHAKEL 266
 DB 280 ---TIFLESNKSVLQFQNVRRVQVIFRIMRLILKLARHSTGLQSLGFLRLRSYNEL 335
 QY 267 -ITAMVIGFLVLISSEFLVYLVKEDAN--KESTYADALMWGTTTLTIGYDKPTLTWIG 324
 DB 336 GLILFLFAMGIMISS-LVFEAKEDDATKFTSIPASEFWATITMTVGIDYPTLLG 394
 QY 325 RLISAGFALLGISFEALPAGILSGFALKVQDHRQKHFEKRRNP-----AANL 373
 DB 395 KIVGGLGCIAGVIALPIPIIVNPFSEYKQKQKQKAKIKREALERAKRNGSIYMN 454
 QY 374 IQCVWRST-----AADEKSVSTATMKPKHLKALHTCSPTNOKLSFER 415
 DB 455 KDAFARSMELIDVAVERKAGESANTKDSADNHLSPSRMKARKAL---SETSSNKSFEENK 511
 QY 416 VRMASPRQSIKRSQASVGDNRSPSTDTIAGESP--TKYOK--SWSPNDRFRFSPRLKS 472
 DB 512 YQESQOKS-----HEQILNFTSSPOHLSQOKLEMLYNEITKTQP-----H 553
 QY 473 SQPKVIDADTALGTDVYDEKGCOCOVSEDLTPPLKTVIRA-----IRIMKF 521
 DB 554 SHPN--DCQEKPERPAAVEE-----EIMEEYVQCEQLAVAQTEVYDMKSTSSIDSF 606
 QY 532 HVAKKEKETLPRPYKVDIYEOYSAGHLMCLRIKSLQTRVQDILKGQITSPKSKSEKI 581
 DB 607 TSCATDFETER-----SPLPPPSASHLOM-----KEPTDLPG--- 639
 QY 582 TAEHETTDLSMLGIVNKEKQVQVQSTESKLD--CLLDIYQVLRKGSASALALASFOIPE 640
 DB 640 TEEHORANGPPPL--TLSEKGPAPARDGTLLEAPVITVNLASGSGCL----- 687
 QY 641 ECEQTSIDYQSPYDSKDLSSAONSGLSRSTSANISRGLOFILTPEFSAQTEFVALSPM 700
 DB 688 -----HSPLOSDNATDPSKSS--LKGSNPLKRSRLKVNKENNGSA-----PQTP 730
 QY 701 HSOATQVPISSODGS 715
 DB 731 PSTARLPVPTADFS 745
 RESULT 24
 CTRB_CANFA STANDARD; PRT; 806 AA.
 AC Q95167;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Voltage-gated potassium channel protein Kv2.2.
 GN KCNB2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98275219; PubMed=9612272;

RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
 RA Flynn E.R., Kenyon J.L., Horowitz B.:
 RT "Molecular identification of a component of delayed rectifier current
 RT in gastrointestinal smooth muscles";
 RL Am. J. Physiol. 274:G901-G911(1998).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U69963; AB08432.1; -.
 DR HSSP; Q54397; 1BL8.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K.tetra.
 DR InterPro: IPR004351; Kv2channel.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR006366; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam; PF00520; Ion_trans_1.
 DR Pfam; PF02214; K.tetra_1.
 DR Pfam; PF03521; Kv2channel_1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01491; KCHANNEL.
 DR PRINTS; PR01495; SHABCHANNEL.
 DR SMART; SM00225; BTB.1.
 DR K+ ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT DOMAIN 1 190
 FT TRANSMEM 191 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 254
 FT TRANSMEM 255 264
 FT TRANSMEM 265 286
 FT TRANSMEM 287 298
 FT TRANSMEM 299 320
 FT DOMAIN 321 334
 FT TRANSMEM 335 356
 FT TRANSMEM 357 396
 FT DOMAIN 397 418
 FT TRANSMEM 419 806
 FT CARBOHYD 287 287
 SQ SEQUENCE 806 AA: 90283 MW: D962EC256760B743 CRC64;
 Query Match 5.8%; Score 276.5; DB 1; Length 806;
 Best Local Similarity 22.2%; Pred. No. 1e-08;
 Matches 162; Conservative 99; Mismatches 248; Indels 221; Gaps 31;
 117 NLYERPRG-----NAFYHAFVFLVFGCLLSVSTPEHTKL-----ASSCLLIL 163
 DB 181 DLEKPNSSVAAKILAIIVSNLFI---VLSIALST-NLPELQEDFEGQPNNDPQLAHV 236

```

QY 164 EFMVIVFLEFIRIWSAGCCCRNMGRLRFAPKPCVITIVLIASIAVSAKTQG 223
DB 237 PAVCNAMFMEYLRLFLSS-----PKMKFKFGPLNVIDLAILPYV----- 279
QY 224 NIFATSAKSL-----RFOIRAMVMDRGCTWKLIGSVAVHAKEL-ITA 269
DB 280 TLEFESNNSVLOFONVRVVOIFRIMRILRIKLIAHSTGLQSIGFLIRRSYNELGLLI 339
QY 270 WIGFVLVLFSSFLVYLVKEDAN-KEPSTYADALMGMGTTITTYGDKFTLWGLLS 328
DB 340 LFLANGIMIFSS-LVFEFAEKDADATFTSTIPASWTMTITWTIVGIDYKFTLIGKSVG 398
QY 339 AGFALLGISFEPALPACILGSGFALKVQEOHRQKHFERRND-----AANLIQCV 377
DB 399 GLCCAGVGLVIALPIIPIVPEFSEFYKEQKREKAIKREALEKAKNGSLVSNMLKNAF 458
QY 378 WRSY-----AADEKSVIATWPKPLKALHTCSPTNOKISFEKERVMA 419
DB 459 ARSMELIDVAVERKAGSSSTKDSADNHLSPSRKMKARAKL--SETSSNKSYEKKYQEV 515
QY 420 SPRGOSIKSRQASVGDRRSPSTDTAEGSP--TKVOK-SWSENDRTPRPRLRLKSSQPK 476
DB 516 SOKDS-----HEQUNTSISSSPQHLISAKLEMLYNETITQP-----HPA 555
QY 477 PYIADPTALGTDVYDEKGCQCCDVSDLTPLKTVIRA-----TRINKFHVAK 525
DB 556 PNPDQEOEPDRPSAYEE-----EIMEEYVCPQQLAVAGVIVDKSTSIDSTSCA 610
QY 526 RKFKETLRPYDKVIEYQSAHGLMLCRKSLQTRVDQLLGQITSDKKSREKITAEN 585
DB 611 TDFETTER-----SPPLPSASHLQW-----RPPDLAG-----TDEH 643
QY 586 ETT--DLSMLGRVYKVEKOVOSIESKLDLDIYQOVLRKGSASALASFOIPPECE 643
DB 644 QRARCPPLMLAR-----CKGAPGRAILLEY----- 669
QY 644 QTSYQASVVD--SKDLSGSAONS-----GCLSRSTSANI-----SRGLQILTPNE 687
DB 670 -----AAVDITVSLDASGSKGSHQPLQPDNSASESPKSLKSNPLKSLRNFKEKR 723
QY 688 FSAQTFVYALPTMHQATQVPISSQSGSAVAANTNTANQNTAPKPAAPITLOPPPLPA 747
DB 724 GSA-----POTPESTARPLVPTTADFSL-----TAPQLISTILLEETPSOGDRPCWAPR 772
QY 748 IKH---LPR 753
DB 773 ARHTVRDLPR 782

```

```

CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE OLFACTORY BULB, FOLLOWED BY THE CEREBRAL CORTEX, HIPPOCAMPUS,
CC AND CEREBELLUM. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
CC WHOLE TONGUE EPITHELIUM AND CIRCUMVALLATE PAPILLAE.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M77482; AAA40905.1; -.
CC HSSP: Q54397; 1BL8.
CC InterPro: IPR000210; BTB_POZ.
CC InterPro: IPR001622; K+channel_pore.
CC InterPro: IPR003091; K_channel.
CC InterPro: IPR004351; K_tetra.
CC InterPro: IPR004351; Kv2channel.
CC InterPro: IPR003968; Kv_channel.
CC InterPro: IPR000636; M+channel_nlg.
CC InterPro: IPR003973; Shab_channel.
CC Pfam: PF00520; Ion_trans; 1.
CC Pfam: PF02214; K_tetra; 1.
CC PRINTS: PR00169; KCHANNEL.
CC PRINTS: PR01515; KV22CHANNEL.
CC PRINTS: PR01491; KVCHANNEL.
CC PRINTS: PR01495; SHABCHANNEL.
CC SMART: SM00225; BTB; 1.
CC DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC KW Glycoprotein; Multigene family; Phosphorylation.
CC FT DOMAIN 1 190
CC FT TRANSMEM 191 190
CC FT TRANSMEM 191 190
CC FT TRANSMEM 191 190
CC FT TRANSMEM 213 232
CC FT TRANSMEM 213 232
CC FT TRANSMEM 233 254
CC FT TRANSMEM 233 254
CC FT TRANSMEM 255 264
CC FT TRANSMEM 255 264
CC FT TRANSMEM 265 286
CC FT TRANSMEM 265 286
CC FT TRANSMEM 287 298
CC FT TRANSMEM 287 298
CC FT TRANSMEM 299 320
CC FT TRANSMEM 299 320
CC FT TRANSMEM 321 334
CC FT TRANSMEM 321 334
CC FT TRANSMEM 335 356
CC FT TRANSMEM 335 356
CC FT TRANSMEM 357 396
CC FT TRANSMEM 357 396
CC FT TRANSMEM 397 418
CC FT TRANSMEM 397 418
CC FT DOMAIN 419 802
CC FT DOMAIN 419 802
CC FT DOMAIN 528 531
CC FT CARBOHYD 287 287
CC FT SEQUENCE 802 AA; 90702 MW; 792CC09A5BD8D7F CRC64;

```

Query Match 5.7%; Score 272; DB 1; Length 802;
Best Local Similarity 24.4%; Pred. No. 1.9e-08;
Matches 121; Conservative 82; Mismatches 191; Indels 102; Gaps 21;

```

QY 115 LYNVLEPRGMA--FIYHAFVFLVFGCLISVFSTIPE-----HTKLASSC 159
DB 179 LMDLLEKPNSSVAAKIALIVSLIFVISTIALSL-NTLPELGENDERGQPSDNKKLAH-- 235
QY 160 LILIEFVAVVGLFIRIWSAGCCCRNMGRLRFAPKPCVITIVLIASIAVSA 219
DB 236 --VEAVCIAMFTMEYLRLFLSS-----PKMKFKFGPLNVIDLAILPYV----- 279

```


Seq	SEQUENCE	769 AA;	82116 MW;	BCACD5AB2D6D9EC	CRC64;
QY	Query Match	5.38;	Score 251;	DB 1;	Length 769;
Db	Best Local Similarity	23.28;	Pred. No. 3e-07;		
	Matches	96;	Conservative	65;	Mismatches 162; Indels 90; Gaps 13;
QY	3 RHHAEGEGGAAGLMTVKSAAAAAAGGGRUGSGKMDVESGRVYLNSAARGDGLLLG 62				
Db	191 RQHMDAEALDSEFAPDPSSANANNAGAHGAGLDD-EAGAG-----GGGLDQAG 239				
QY	63 TRAAITL-----GGGGGLRESRRKQGRMSLGLPLSTYSQSCRNVKTRRQNYLYN 117				
Db	240 GELKRLCFODAGGAGGLPGAGAGAG-----TMMRRQRPVWA 278				
QY	118 VLERP-----RGMAFYHAFVFLVLCGLILSY-----FSTIPEHTKLASS----- 158				
Db	279 LFEQDPYSSRAARYAFASLPIILISTITTFCELEHGFHISNKVYQASPIFGAPENIT 338				
QY	159 -----CLILIEFVMIIVFGEFLTIRIMSAGCCCRYRGMGRLRPAKRFECVIDITVL 210				
Db	339 NVEVETPEPLTVYEGVCVVMPTFEFLMKV-----PDRVEFLKSLNIIDCVAI 389				
QY	211 I-----ASINVYSKTKQGNIFATALSIRELOILRMVRMDRGGTKMLGSVYANSKE 265				
Db	390 LPFYLEVGLSGLSSKAAKVDY--GFLRVRFRVRLIRLTKLRFHVGLEVLSTHTLPASTNE 447				
QY	266 -LITAWYIGFVLLLFSSFLVLYVEKDANKE-----FSTYADALMWTITLTITIGY 315				
Db	448 FLILITFLALGLVFATWYIYAERIGADPPDILGSNHTYFNKINPIGFWAVVMTTLGYG 507				
QY	316 DKTYLTWLGRLSLGAFALLGISFPALPAGILIGSGFALKVQDQHOKHEKRRN 368				
Db	508 DMVPRKTSGLMVLGICALAGVLTAMPVIVNFGMYISLAMAQKILPKRKN 560				
RESULT 27					
CIRG_HUMAN					
ID_CIRG_HUMAN	STANDARD:	PRT;	582 AA.		
AC	003721;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Voltage-gated potassium channel protein Kv3.4 (KSH11C).				
GN	KCNK4				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=92396711; Pubmed=1381835;				
RA	Vega-Ssenz de Miera E., Moreno H., Fuenling D., Kentros C., Rudy B.;				
RT	"Cloning of Shila (Shaw-like) cDNAs encoding a novel high-voltage-				
RT	activating, TEA-sensitive, type-A K ⁺ channel.";				
RL	Proc. R. Soc. Lond., B, Biol. Sci. 248:9-18(1992).				
CC	-!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM				
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED				
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE				
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH				
CC	WHICH K ⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL				
CC	GRADIENT.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- DOMAIN: THE SEGMENT SA IS PROBABLY THE VOLTAGE-SENSOR AND IS				
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT				
CC	EVERY THIRD POSITION.				
CC	-!- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL				
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR				
CC	COMPARTMENTS.				
CC	-!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER				
CC	CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				

```
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC at the European Bioinformatics Institute. There are no restrictions on  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; M64676; AAA57263.1; .  
DR HSSP; 063734; 1ZTN.  
DR Genew; HGNC:6236; KCNCA4.  
DR MIM; 176285;  
DR InterPro; IPR000210; BRP_PoZ.  
DR InterPro; IPR001622; K+-channel_pore.  
DR InterPro; IPR003191; K_channel.  
DR InterPro; IPR003131; K_tetra.  
DR InterPro; IPR003968; Kv_channel.  
DR InterPro; IPR000636; M-channel_nlg.  
DR InterPro; IPR003974; Shaw_channel.  
DR Pfam; PF00520; Ion_trans; 1.  
DR Pfam; PF02214; K_tetra; 1.  
DR PRINTS; PR00169; KCHANNEL.  
DR PRINTS; PR01491; KVCHANNEL.  
DR PRINTS; PR01498; SHAWCHANNEL.  
DR SMART; SMO0225; btb; 1.  
DR Tonic channel; Transmembrane; Ion transport; Voltage-gated channel;  
KM Glycoprotein; Multigene family; Phosphorylation.  
FT DOMAIN 1 226 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 227 247 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 248 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 298 SEGMENT S2 (POTENTIAL).  
FT TRANSMEM 299 312 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 313 333 SEGMENT S3 (POTENTIAL).  
FT DOMAIN 334 380 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 381 401 SEGMENT S4 (POTENTIAL).  
FT TRANSMEM 402 422 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 423 443 SEGMENT S5 (POTENTIAL).  
FT TRANSMEM 444 451 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 452 472 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 473 582 CYTOPLASMIC (POTENTIAL).  
FT CAROARD 236 256 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CAROARD 255 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 582 AA; 64527 MW; 8EBE55AACA33A9F CRC64;  
  
Query Match 5.3%; Score 250.5; DB 1; Length 582;  
Best Local Similarity 23.7%; Pred. No. 2, 2e-07;  
Matches 103; Conservative 65; Mismatches 181; Indels 85; Gaps 15  
  
QY 29 GRLGSGMKDYESGRGVLLNSAAARGDGLLGTRAAITGGGGGLRESRRKOGARMS 88  
DB 166 GGGSAGCSDEAGDDERELALQLGPHEG-----GAChGAGSGGC---RGMDPRMWA 214  
QY 89 LLGRKLSTSSQSCRNRVVRVONLVLEBRPMGATIFAAYFLVEFGCL----- 141  
DB 215 LFEDPYSSRA-----RVAFASLEFLIVSITTF-CLETHEARN 252  
QY 142 -----ILVSFTPEHTKL--ASSCLLILEFWIIVEGLEFIIRIMSAGCCRYRGM 191  
DB 253 IDRNVTETLRVCNTISVHFRREVENEPILTLYEGVCVFLETFLEIVRI----VCC----- 303  
QY 192 QGRLPAPRKPCFVIDTIVL-----ASIAVVASAKTDGNIFANSAALSRLFLOTLBRVRMD 246  
DB 304 PDLTDFVKNLNIIDIVALLPYLELEVLEGSLSKARADVL--GEFLRVAVIRILRFKFL 361  
QY 247 RRGGWTKMLGVSVVYASHKE-LITAWYIGFLVIFESSFLVIYK-----DANKER 295  
DB 362 RFFVGVLRYVGHILRASTNEFLILLIIFLAGVLIFAI-MIYYARIGARSDPRGNHTDE 420  
QY 296 STYADALMWGITTTTIGYGXDTPTLTWIGRLLSAGFALLGISFFALPAGLIGSGFLAKVO 355  
DB 421 KNIPIGFWAAVYTMTTIGYGDWMFKTWSGMIWGALCALAGVLIITAPRVPIVNNFGMYXS 480  
QY 356 -EQHQHKERRKRNPANLIIQCVMRSYADEXSVSIATMKPHKALHTOSPNOKLSPEK 414
```


DB 481 LAMAKOKLPRKKHVRPAQLESMPYCKSEET-----SPRSTYCSPTSPAREGMIE 534
 OY 415 RVRASPRGOSIKS 428
 DB 535 RKRAGEIRGWEKGS 548

RESULT 28
 CIRC_DROME STANDARD: PRT: 985 AA.
 ID CIRC_DROME 076805; 091779; 091700;
 AC 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Shab.
 CN SHAB OR CG1066.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-Oregon-R;
 RX MEDLINE=9146139; PubMed=2493160;
 RA Butler A., Wei A.G., Baker K., Salkoff L.;
 RT "A family of putative potassium channel genes in Drosophila."; Science 243:943-947(1989).
 RL [2]
 RN SEQUENCE FROM N.A. (LONG ISOFORM).
 RX MEDLINE=9023553; PubMed=2333511;
 RA Wei A.G., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family conserved in Drosophila and mouse."; Science 248:599-603(1990).
 RL [3]
 RN SEQUENCE FROM N.A. (LONG ISOFORM).
 RX MEDLINE=90245668; PubMed=2336395;
 RA Butler A., Wei A.G., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila."; Nucleic Acids Res. 18:2173-2174(1990).
 RL [4]
 RN SEQUENCE FROM N.A. (SHORT ISOFORM), AND MUTAGENESIS.
 RC STRAIN-Canton-S;
 RX MEDLINE=99348357; PubMed=10419540;
 RA Hegde P., Gu G.G., Chen D., Free S.J., Singh S.;
 RT "Mutational analysis of the Shab-encoded delayed rectifier K(+) channels in Drosophila."; J. Biol. Chem. 274:22109-22113(1999).
 RL [5]
 RN SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borovoy D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Slier E., Spradling A.C., Stepleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
 CC -1- DEVELOPMENTAL STAGE: Expressed in late embryos and pupae.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE DELAYED RECTIFIER CLASS. SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -1- CAUTION: Ref.5 sequence differs from that shown due to erroneous gene model prediction.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M32659; AAA28896.1; -;
 DR EMBL: AF084525; AAC33365.1; -;
 DR EMBL: AE003476; AAG22237.1; ALT-SEQ.
 DR EMBL: AE003476; AAG22233.1; ALT-INIT.
 DR PIR: S15058; S15058.
 DR HSSP: Q54397; 1BL8.
 DR Flybase: FBgn003383; Shab.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003969; kv6_channel.
 DR InterPro: IPR003970; kv8_channel.
 DR InterPro: IPR003971; kv9_channel.
 DR InterPro: IPR003968; kv_channel.
 DR InterPro: IPR000636; KvChannel_n19.
 DR InterPro: IPR003973; Shab_channel.
 DR InterPro: IPR003975; Shal_channel.
 DR Pfam: PF00520; Ion_trans_3.
 DR Pfam: PF02214; Ion_trans_2.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01492; KV6CHANNEL.
 DR PRINTS: PR01493; KV8CHANNEL.

[illegible]

ID	CIKE_HUMAN	STANDARD:	PRT:	757 AA.
AC	Q14003;			
AD	15-JUL-1998 (Rel. 36, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Voltage-gated potassium channel protein Kv3.3 (KSHIID).			
GN	KCNK3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RA	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Lens epithelium;			
RX	MEDLINE=20179629; PubMed=10712820;			
RA	Rae J.L., Shepard A.R.;			
RT	"Kv3.3 potassium channels in lens epithelium and corneal			
RT	endothelium.";			
RL	Exp. Eye Res. 70:339-348(2000).			
RN	[2]			
RP	SEQUENCE OF 291-651 FROM N.A.			
RA	Lee J.E., Garbutt J.H., Phillips K.L., Roses A.D.;			
RT	"A human chromosome 19 Shaw type potassium channel gene.";			
RL	Submitted (JAN-1992) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	-1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A			
CC	HEPTAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- DOMAIN: THE SEGMENT 54 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL			
CC	ACTIVITY AND/OR TARGETING TO THE CHANNEL TO SPECIFIC SUBCELLULAR			
CC	COMPARTMENTS.			
CC	-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF055989; AAC24118.1; -			
DR	EMBL; Z11585; CAA77671.1; -			
DR	HSSP; Q54397; 1BL8.			
DR	Genew; HGNC:6235; KCNC3.			
DR	MIM: 176264; -			
DR	InterPro: IPR000210; BTF_POZ			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR003091; K_channel			
DR	InterPro: IPR003131; K_tetra.			
DR	InterPro: IPR003968; Kv_channel			
DR	InterPro: IPR000636; M+channel_nlg			
DR	InterPro: IPR003974; Shaw_channel			
DR	Pfam; PF00520; Ion_trans; 1.			
DR	Pfam; PF02214; K_tetra; 1.			
DR	PRINTS; PR00169; KCHANNEL			
DR	PRINTS; PR01491; KVCHANNEL			
DR	PRINTS; PR01498; SHAWCHANNEL			
DR	SMART; SM00225; BTF; 1.			
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KW	Glycoprotein; Multigene family; Phosphorylation.			
FT	DOMAIN 1 290 CYTOPLASMIC (POTENTIAL).			

```

FT TRANSMEM 291 309 SEGMENT S1 (POTENTIAL).
FT DOMAIN 310 350 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 351 370 SEGMENT S2 (POTENTIAL).
FT DOMAIN 371 379 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 398 SEGMENT S3 (POTENTIAL).
FT DOMAIN 399 411 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 434 SEGMENT S4 (POTENTIAL).
FT DOMAIN 435 447 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 448 469 SEGMENT S5 (POTENTIAL).
FT DOMAIN 470 517 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 518 539 SEGMENT S6 (POTENTIAL).
FT DOMAIN 540 757 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 38 POLY-PRO.
FT DOMAIN 39 42 POLY-GLN.
FT DOMAIN 81 85 POLY-GLY.
FT DOMAIN 229 234 POLY-GLY.
FT DOMAIN 577 587 POLY-PRO.
FT DOMAIN 596 599 POLY-PRO.
FT DOMAIN 668 673 POLY-ALA.
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 757 AA; 80520 MW; 266F6B2B82AC5A52 CRC64;

Query Match 5.2%; Score 247; DB 1; Length 757;
Best Local Similarity 23.5%; Pred. No. 4,9e-07;
Matches 93; Conservative 63; Mismatches 150; Indels 90; Gaps 13;

QY 20 SGAAGAAAGGRLGSGMKDVGSRGRVILNSAARGDGLLLGTRATL-----GGGGGG 74
DB 208 AGAANNAAGAHGDLDD-EGAG-----GGGIDGAGGELKRLCFODAGGAGG 256
QY 75 LRESRRGOGARMSLLGRLPLSTSSOSCRNRYRYVQNYLVNLERP---RQMATIYHA 131
DB 257 PPGAGGAGG-----TWRRWQRPVALFEDPYSSRARARVAF 295
QY 132 FVFLVFLFCILISV-----FSTIPERTKLASS-----CLLILEFVM 167
DB 296 SLFLISITTFECLETHGEFHISNKTYQASPIGAPENITNVEVEPEFLTYEGVC 355
QY 168 IVFGELETTIRWSAGCCCRNRGWRGLRFRAPKPCVIDTYI-----ASIAVVSAKTQ 222
DB 356 VVWFEEFLMR-----TFC-----PDKVEFLKSLNIIDCVALLPYLEVGSLGSKAA 406
QY 223 GNIFATSLRSRLFIQILRMVMDRGRGTWKLGSVVAHSKE-LITAWYIGFLVIJESS 281
DB 407 KDVL--GFLRVAREVILITFKLTHFVGLRVGHTLRASSTNEFLILLITFLAGVLIFAT 464
QY 282 FLVYLVEKDANKE-----FSTYADALMWGITLTIGYGDKTPLTWLGRILSNGFA 332
DB 465 MIYVAERIGADDDLLGSNHTYFKNIPIGFWMAVYMTLTIGYDMYPTKMSGLVGLALCA 524
QY 333 LLGISFPLPAGILGSGALKVQEOHROKHFEKRN 368
DB 525 LAGVLTIAMPVIVNFGMYSLAMAKOKLPKKN 560

RESULT 30
CIRK_RAT STANDARD; PRT; 889 AA.
AC Q01956;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv3.3 (KSHIID).
GN KCNC3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS KSHIID.1 AND KSHIID.2).
RC TISSUE=Brain;

```

```

RX MEDLINE=92396711; PubMed=1381835;
RA de Miera E.V.-S., Moreno H., Fruhling D., Kentros C., Rudy B.;
RT "Cloning of Shil1 (Shaw Like) cDNAs encoding a novel high-voltage-
RT activating, TEA-sensitive, type-A K+ channel."
RL Proc. R. Soc. Lond., B. Biol. Sci. 248:9-16(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
CC HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; KSHIID.1 (shown here) and
CC KSHIID.2; are produced by alternative splicing.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-stb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M84210; AAA73182.1; -
DR EMBL; M84211; AAA41470.1; -
DR HSSP; Q54397; 1BL8.
DR InterPro: IPR0000210; BTB_POZ.
DR InterPro: IPR001622; K+-channel_pore.
DR InterPro: IPR003091; K+channel.
DR InterPro: IPR003131; K+letra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+-channel_nlg.
DR InterPro: IPR003974; Shaw_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K+letra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01491; KVCCHANNEL.
DR SMART; SM00225; BTB; 1.
DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Alternative splicing; Phosphorylation.
FT DOMAIN 1 291 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 292 310 SEGMENT S1 (BY SIMILARITY).
FT DOMAIN 311 351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 352 371 SEGMENT S2 (BY SIMILARITY).
FT DOMAIN 372 380 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 381 399 SEGMENT S3 (BY SIMILARITY).
FT DOMAIN 400 412 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 413 435 SEGMENT S4 (BY SIMILARITY).
FT DOMAIN 436 448 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 449 470 SEGMENT S5 (BY SIMILARITY).
FT DOMAIN 471 518 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 519 540 SEGMENT S6 (BY SIMILARITY).
FT DOMAIN 541 889 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 662 679 NDGLVEEDDPKPNQDPA -> EAGARTGVRGFGWSSG
FT VARSPLIC 680 889 MISSING (IN ISOFORM KSHIID.2).
SQ SEQUENCE 889 AA; 94393 MW; 5142C047B4FC367 CRC64;

Query Match 5.2%; Score 244; DB 1; Length 889;
Best Local Similarity 23.0%; Pred. No. 9.1e-07;
Matches 95; Conservative 65; Mismatches 163; Indels 90; Gaps 13;

```

```

QY 3 RHAGGEEGAGAGLWVKSAAAAAGGRLGSGMKDYSGRGRVLLNSAARGDLILLG 62
D 192 RQHRNAEEALDSFEAPDSSGNANANGADADGLD- EAAG- -----GGGLDAG 240
QY 63 TRAAVL-----GGGGGLRESRRGKOGARMSLLGKPLSYTSOSCRNRVRYVNYLYN 117
D 241 GELKRLCFQDQAGGAGPAGGPGAGG-----TWMRRQPRWMA 279
QY 118 VLERP---RGMAFIHAFVLLVFGCLLSV-----FSTIPERTKLASS----- 158
D 280 LPEDYSSRAKRYVAPASLEFLITISTTCLETHEGTHISNKTWTQASPIGAPPENIT 339
QY 159 -----CLLLEFEMIVVGFLEFIIRIMSACCCRRYGMQGLRPARKFCYIDTIVL 210
D 340 NVEVTEPEFLVVEGVVWFTEFEIMRV-----TFC-----PKVELLSKSLNIIDCVAI 390
QY 211 I-----ASIAVVSANTQGNIFATSALRSIFQILRMVRMDRRGGTWKLLGSVYASKE 265
D 391 LPFLYLEVGLSGLSKRAKAVL--GFLRVYRFVRIHIFKLRHFVGLRVGLHGLTLASTNE 448
QY 266 -LITAMVIGFLVLIIPSPFLVYLVKDNKE-----FSTYADALMGTITITITIGYG 315
D 449 FLILILFALGLVLIATMIYMERIGADDDDLIGSNHTYFKNIPIGFWMAVVTMTTIGYG 508
QY 316 DKTPDLTWLGRLLSAGFALGIFSFALPAGILSGFALKVOEOROKHFEKRRN 368
D 509 DMRYKTMGMLVGCALCALAGVLTAMPVPIVNFPMYSLMAKOKLPKKN 561

```

RESULT 31
CIRK_RAT STANDARD: PRT: 638 AA.

AC P22462; P22461; P22463; 063735;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv3.2 (KSHIIIA).
GN KCNC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RL [1]
RN SEQUENCE FROM N.A. (ISOFORMS KV3.2B AND KV3.2C).
RP TISSUE-Brain;
RC MEDLINE=91348257; PubMed=1879548;
RA Lunau C.J., Wiedmann R., Smith J.S., Williams J.B.,
RT "Shaw"-like rat brain potassium channel cDNAs with divergent 3'
ends.";
RT FEBS Lett. 288:163-167(1991).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM KV3.2B).
RP MEDLINE=92262488; PubMed=1374908;
RA Baker H., Pollock J., Ellisman M., Kentros C., Miera E., Serodio P.,
RT "Region-specific expression of a K+ channel gene in brain.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:4603-4607(1992).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM KSHIIIA.1).
RP TISSUE-Brain;
RC MEDLINE=90311375; PubMed=2367536;
RA McCormack T., de Miera E.C.V.-S., Rudy B.,
RT "Molecular cloning of a member of a third class of Shaker-family K+
channel genes in mammals.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:5227-5231(1990).
RN [4]
RN REVISIONS.
RX MEDLINE=91219512; PubMed=2023956;
RA McCormack T., de Miera E.C.V.-S., Rudy B.,
RT "Molecular cloning of a member of a third class of Shaker-family K+
channel genes in mammals.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:4060-4060(1991).

```

RN [5]
RP SEQUENCE FROM N.A. (ISOFORM GT10).
RX MEDLINE=92331599; PubMed=1378392;
RA Relling J., Wunder F., Stocker M., Lichthagen R., Mastiaux F.,
RA Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,
RA Veh R., Pongs O.;
RT "Characterization of a Shaw-related potassium channel family in rat
RT brain.";
RL EMBL J. 11:2473-2486(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; KV3.2B (shown here), KV3.2C,
CC KSHIIIA.1 and GT10; are produced by alternative splicing.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@slb-slb.ch).
CC -----
DR EMBL; M59211; AAA41819.1; -
DR EMBL; M59313; AAA41820.1; ALT_SEQ.
DR EMBL; M84203; AAA42143.1; -
DR EMBL; M34052; AAA42142.1; -
DR EMBL; X62839; CAA44643.1; -
DR HSSP; G54397; 1BL9.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01498; SHAWCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Alternative splicing; Phosphorylation.
FT DOMAIN 1 229
FT TRANSMEM 230 248
FT DOMAIN 249 283
FT TRANSMEM 284 303
FT DOMAIN 304 314
FT TRANSMEM 315 337
FT DOMAIN 338 345
FT TRANSMEM 346 368
FT DOMAIN 369 381
FT TRANSMEM 382 401
FT DOMAIN 402 450
FT TRANSMEM 451 473
FT DOMAIN 474 638
FT DOMAIN 56 99
FT CARBOHD 259 259
FT CARBOHD 266 266
FT MOD_RES 564 564

```

SEGMENT S1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
GLY/PRO-RICH (INSER).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PHOSPHORYLATION (BY PKA) (POTENTIAL).


```

QY 378 WRSTAADKSVSIATWPKLALHTCSPTNOKLSFKERVMAASPRGOSIKSROASVGD RR 437
DB 505 SPICKSHET-----SPDSTYSDTSPAPREGEVNERKRAOSKON-----GDAN 548
QY 438 SPSDITAE-----SPTXOKSSEFDRFR 465
DB 549 AVLSDEGAGLTOPLASFTPERRALRRSGTDR 583

RESULT 33
CIRK_MOUSE STANDARD: PRT: 654 AA.
AC 061423;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.4.
GN KCNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AKR;
RX MEDLINE=94292198; PubMed=8020965;
RA Wyome R.S., Korenberg J.R., Kinoshita K.D., Aiyar J., Coyne C.,
RA Chen X.N., Hustad C.M., Copeland N.G., Gutman G.A., Jenkins N.A.,
RA Chandy K.G.;
RT "Genomic organization, nucleotide sequence, biophysical properties,
RT and localization of the voltage-gated K+ channel gene KCNA4/Kv1.4 to
RT mouse chromosome 2/human 11p14 and mapping of KCNC1/Kv3.1 to mouse
RT 7/human 11p14.3-p15.2 and KCNA1/Kv1.1 to human 12p13."
RL Genomics 20:191-202(1994).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 003723; AAB60668.1; -
CC DR HSSP: P15385; 1270.
CC DR MGD: MGI:96661; Kcna4.
CC DR InterPro: IPR000210; BTB_POZ.
CC DR InterPro: IPR001622; K+channel_pore.
CC DR InterPro: IPR004051; KV14channel.
CC DR InterPro: IPR003091; K_channel.
CC DR InterPro: IPR003131; K_tetra.
CC DR InterPro: IPR003968; kv_channel.
CC DR InterPro: IPR000636; M+channel_nlg.
CC DR InterPro: IPR003972; Shaker_channel.
CC DR Pfam: PF00520; Ion_trans_1.
CC DR Pfam: PF02214; K_tetra_1.

```

```

DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1511; KV14CHANNEL.
DR PRINTS: PRO1491; KVCHANNEL.
DR PRINTS: PRO1496; SHAKERCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 309 327 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 372 393 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 405 425 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 444 462 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 479 498 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 540 562 SEGMENT S6 (POTENTIAL).
FT DOMAIN 38 50 POLY-ALA.
FT DOMAIN 62 65 POLY-HIS.
FT DOMAIN 83 89 POLY-ARG.
FT DOMAIN 123 137 POLY-GLU.
FT DOMAIN 162 166 POLY-GLN.
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 600 600 PHOSPHORYLATION (BY PKA) (POTENTIAL).
SQ SEQUENCE 654 AA; 73473 MW; 8693651A30BD36D4 CRC64;

Query Match 5.1%; Score 240.5; DB 1; Length 654;
Best Local Similarity 19.7%; Pred. No 9.7e-07;
Matches 105; Conservative 75; Mismatches 163; Indels 191; Gaps 17;

QY 37 KDVESGRGVNLNSAARGDGLLLGTRAAITGGGG-----GLRES 78
DB 133 EEEBEGR---FYSEEDHDGCGSYTDLLPDQDGGGGYSVRYSDCCERVYINSGLEPF 189
QY 79 RRGKQGRM-SLKGRLPTSSQSCRN----- 105
DB 190 TOMKTLAOPPELLGPERKTOYFDPLRNEYFDRNRPSDALIYYQSGRLRPVNP 249
QY 106 -----KYRRVQNY-----LYNVLERP-----RG 124
DB 250 FDIETEEVVFYQGEALAKFREDEGVREEDRALPENEFKKIMLFEPESSPRNG 309
QY 125 WAFIHAFFVFLVPGCLLISVSTPE-----HTKLASSC----- 159
DB 310 IAIV-----SVAILIVISVFCELTPEFRDRLIMALSAGHSRLINDTSAPHLENSGH 365
QY 160 -----LILFEFMYVFGLEFIRILMSAGCCCRYRGMQRLRPARKPCYDITIVIT-- 211
DB 366 TIFNDPEFLVEVCIWFSFEVYRCFAC-----TSQALFFKIMINITIDIVSTILPY 416
QY 212 -ASIAVSAKTQG-----NIFATSALNSLRELOILRMVMDRRGGTWKLLGSVYAHS 263
DB 417 FTTLGTDLAQOOGGNGOQOQAMSFALIRILRVFRIRKLSHSGGLDILGHTLRASM 476
QY 264 KELITAWYIGLVLFSSFLVLYVEND-ANKESTYADALAMWGTITITTTGCGKTPWTW 322
DB 477 RELGLLIFFLFGLVLFSSAVYFAEADPTHTQSLPDATWMAVMTVTVGGMKPKITV 536
QY 323 LGRLLSAGFALLIGIFFALPAIGILSGFALKVQEOHRKHFERRRNPANILQCVWMSYA 382
DB 537 GGIKIVGSLCANGVLTIALPVPYIVSNFN---YFIRETNEEGTOLTQNAVSC----- 587
QY 383 ADEKSVSIATWPKLALHTCSPTNOKLSFKERVMAASPRGOSIKSROASVGD RR 436
DB 588 -----PVL-----PSNLLKKFR-----SSRSSSLGDK 609

RESULT 34
CIRK_MOUSE STANDARD: PRT: 655 AA.
AC 061423;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Voltage-gated potassium channel protein Kv1.4 (RCK4) (RHK1) (RK4).
 GN KCNA4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90059914; PubMed=2555158;
 RA Stuenkel W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Glese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Heart;
 RX MEDLINE=90346174; PubMed=2384173;
 RA Tseng-Crank J., Tseng G.-N., Schwartz A., Tanouye M.A.;
 RT "Molecular cloning and functional expression of a potassium channel
 RT cDNA isolated from a rat cardiac library.";
 RL FEBS Lett. 268:63-68(1990).
 RN [3]
 RP STRUCTURE BY NMR OF 1-37.
 RX MEDLINE=97152495; PubMed=9000078;
 RA Artz C., Geyer M., Fakler B., Schott M.K., Guy H.R., Frank R.,
 RA Ruppersberg J.P., Kalbitzer H.R.;
 RT "NMR structure of inactivation gates from mammalian voltage-dependent
 RT potassium channels.";
 RL Nature 385:272-275(1997).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: HEART AND BRAIN
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X16002; CA34133.1; -;
 DR EMBL; M32867; AAA41469.1; -;
 DR PIR; S06710; S06710.
 DR PDB; 1ZTO; 05-JUN-97.
 DR InterPro: IPR000210; BTF, POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004051; KV14channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; KV_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PR01511; KV14CHANNEL.
 DR PRINTS; PR01491; KCHANNEL.
 DR PRINTS; PR01496; SHAKERCHANNEL.
 DR SMART; SM00225; BTF, 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation; 3D-structure.
 FT TRANSMEM 310 328 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 373 394 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 406 426 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 445 463 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 480 499 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 541 563 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 38 50 POLY-ALA.
 FT DOMAIN 62 65 POLY-HIS.
 FT DOMAIN 92 95 POLY-GLY.
 FT DOMAIN 124 138 POLY-GLU.
 FT DOMAIN 163 167 POLY-GLY.
 FT DOMAIN 435 438 POLY-GLN.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 601 601 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CONFLICT 42 42 A -> L (IN REF. 2).
 FT CONFLICT 84 88 EEEAT -> RRRQ (IN REF. 2).
 FT CONFLICT 95 95 MISSING (IN REF. 2).
 FT CONFLICT 310 310 G -> A (IN REF. 2).
 SQ SEQUENCE 655 AA; 73390 MW; 40AEF2F901A05F43 CRC64;
 Query Match 5.1%; Score 240.5; DB 1; Length 655;
 Best Local Similarity 19.7%; Pred. No. 9.7e-07;
 Matches 105; Conservative 75; Mismatches 163; Indels 191; Gaps 17;
 QY 37 KDVSGRGVYVLTNSAARAGDGLLGLTRATLGGGG-----GLRES 78
 DB 134 EEEEGEGR---FYEEEDHGGCSTYDILLPODDGGGGGSSVRYSDCCERYVYNSGLIRE 190
 QY 79 RRGKGARM--SLGKPLSYTSSQSCRN-----105
 DB 191 TQMTLAFPEPTLLGDPEKPYQFDPLRENYFEDNRPSFDALTYYSQGRGLRPPVNP 250
 QY 106 -----VKRRVQNT-----LYNVIERP-----RG 124
 DB 251 FDIPEEYKFYQLEALIKFREDEGFVREEDRALPENEFKKQIWLFEYESSSPARG 310
 QY 125 WAFIYHAFVFLVGCCLTLYESTIPE-----HTKIASCC-----159
 DB 311 IAIY-----SVLVILISTVFCLFETLPEFRDROLIMALSAGHSRLNDTSAPHLENGH 366
 QY 160 -----LLIEFVMIIVVGELEFIIRIMSGCCCRVYRGQGRLFARFKPCVITDITLI-- 211
 DB 367 TIFNDPFIVETVCIVWFSFEVYRCFAC-----PSQALFFKNIMNIIDIVSILPY 417
 QY 212 -ASIAVVSATKQG-----NIFATSRLSLRFLOILMVRNDRRGGTAKLLGSVYIAR 263
 DB 418 FITLGTDLAQQGGGNGGQOQAMSPAILRIIRLVVFRFLKSRHSKGLQILGHTLRASM 477
 QY 264 KELLTAMVIGFLVIFSSFLVYLYVEKD--ANKEFSYADALMGTTITLTIGYGDPTPLM 322
 DB 478 RELGLLIFELITGVILSSAVYFPADEPTTHFQSIPDAFMVAVYMTITVIGDMPITIV 537
 QY 323 LGRLLSAGFALLGISFFALPAGILSGFALKVQEOHRKHFKRRNPANLITQCVWRSYA 382
 DB 538 GGRITVGLCALAGVLTALPVVIAVSNTN--YFHFRETENEGQOLQONAVSC-----588
 QY 383 ADEKSVSIATVKKPHLKLHHTCSPTNOKLSFKRRVYMASRGSISRQASVDR 436
 DB 589 -----PYL-----PSNLKKFR-----STSSSLDCK 610
 RESULT 35
 CIR3_HUMAN STANDARD; PRT; 523 AA.
 ID CIR3_HUMAN
 AC P22001;

```

DT 01-ANG-1991 (Rel. 19, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.3 (HPCN3) (HGK5) (HUKIII)
DE (HLK3).
GN KCNA3 OR HGK5.
OS Homo sapiens (Human).
OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eularchia; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=91095456; PubMed=1986382;
RA Philpson L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RT Nelson D.J., Steiner D.F.;
RT "Sequence and functional expression in Xenopus oocytes of a human
RT Insulinoma and Islet potassium channel.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=92189730; PubMed=1547020;
RA Cai Y.-C., Osborne P.B., North R.A., Dooley D.C., Douglass J.;
RT "Characterization and functional expression of genomic DNA encoding
RT the human lymphocyte type n potassium channel.";
RT DNA Cell Biol. 11:163-172(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92235098; PubMed=1373731;
RA Attali B., Komey G., Honore E., Schmid-Alliana A., Mattei M.-G.,
RA Lessage F., Ricard P., Barhanin J., Lazdunski M.;
RT "Cloning, functional expression, and regulation of two K+ channels in
RT human T lymphocytes.";
RT J. Biol. Chem. 267:8650-8657(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95130104; PubMed=7829094;
RA Foldner K., Douglass J., Swanson R.;
RT "Confirmation of the assignment of the gene encoding Kv1.3, a
RT Voltage-gated potassium channel (KCNA3) to the proximal short arm of
RT human chromosome 1.";
RT Genomics 23:295-296(1994).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT 54 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M55515; AAA36425.1; -
DR EMBL: M38217; AAB88073.1; -
DR EMBL: M65217; AAA59457.1; -

```

DR	EMBL: U23499; AAC31761.1; .
DR	HSSP; Q54397; 1BL8
DR	Genew; HGNC:6221; KCMA3.
DR	MIM; 176263; .
DR	InterPro; IPR000210; BTP_POZ.
DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR004050; K13channel.
DR	InterPro; IPR003091; K_channel.
DR	InterPro; IPR003131; K_tetra.
DR	InterPro; IPR003968; KV_channel.
DR	InterPro; IPR000636; M+channel_nlg.
DR	InterPro; IPR003972; Shaker_channel.
DR	Pfam; PF00520; ion.trans. 1.
DR	Pfam; PF02214; K_tetra. 1.
DR	PRINTS; PR00169; KCHANNEL.
DR	PRINTS; PR01510; KV13CHANNEL.
DR	PRINTS; PR01491; KVCHANNEL.
DR	PRINTS; PR01496; SHAKERCHANNEL.
DR	SMART; SM00225; BTP. 1.
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel
KW	Glycoprotein; Multigene family; Phosphorylation.
FT	TRANSMEM 183 201 SEGMENT S1.
FT	TRANSMEM 243 264 SEGMENT S2.
FT	TRANSMEM 276 296 SEGMENT S3.
FT	TRANSMEM 311 329 SEGMENT S4.
FT	TRANSMEM 346 365 SEGMENT S5.
FT	TRANSMEM 407 429 SEGMENT S6.
FT	CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES 468 468 PHOSPHORYLATION (BY PAA) (POTENTIAL).
FT	CONFLICT 20 20 A -> G (IN REF. 1).
FT	CONFLICT 37 37 L -> V (IN REF. 1).
FT	CONFLICT 61 61 L -> V (IN REF. 3).
FT	CONFLICT 91 91 L -> V (IN REF. 4).
FT	CONFLICT 257 257 E -> K (IN REF. 1).
FT	CONFLICT 338 338 T -> S (IN REF. 1).
FT	CONFLICT 419 419 S -> T (IN REF. 1).
FT	CONFLICT 488 488 S -> T (IN REF. 1).
QO	SEQUENCE 523 AA; 58303 MW; 8BA2F1C7C802B411 CRC64;

[illegible]

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.3 (RGK5) (RCK3) (KV3).
 GN KCNA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90059914; PubMed=2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stuehmer M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90297965; PubMed=2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Folander K., Luneau C.J., Antanavage J., Oliva C., Bulrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=90278098; PubMed=2351830;
 RA Douglass J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J.,
 RA Adelman J.P.;
 RT "Characterization and functional expression of a rat genomic DNA
 RT clone encoding a lymphocyte potassium channel.";
 RL J. Immunol. 144:4841-4850(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- DOMAINS: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X16001; CAA34132.1; -;
 DR EMBL: M30312; AAA42035.1; -;
 DR EMBL: M31744; AAA41500.1; -;
 DR PIR: S06708; S06708.
 DR PIR: JH0168; JH0168.
 DR HSSP: O54397; 1BL8.
 DR InterPro: IPR000210; BTH_P0Z.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR004050; KV13channel.
 DR InterPro: IPR003091; K_channel.

DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR0510; KV13CHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 185 203 SEGMENT S1.
 FT TRANSMEM 245 266 SEGMENT S2.
 FT TRANSMEM 278 298 SEGMENT S3.
 FT TRANSMEM 313 331 SEGMENT S4.
 FT TRANSMEM 348 367 SEGMENT S5.
 FT TRANSMEM 409 431 SEGMENT S6.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD.RES 470 470 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CONFLICT 106 106 F -> L (IN REF. 1).
 FT CONFLICT 181 181 G -> R (IN REF. 3).
 FT CONFLICT 430 430 V -> L (IN REF. 3).
 SQ SEQUENCE 525 AA; 58424 MW; 6DA8869D5471C401 CRC64;
 Query Match 5.08; Score 237; DB 1; Length 525;
 Best Local Similarity 23.38; Pred. No. 1.2e-06;
 Matches 67; Conservative 63; Mismatches 104; Indels 54; Gaps 8;
 QY 104 RNYKRYVQYVLTNVLRLP-----RGMAFYHAFVLVCGCLLSVSTIPE----- 151
 DB 159 RPLPRDFQKQVWLFEPSSSGPARKAIY----SVLVISIVIFCLFLPFRDCKD 214
 QY 152 -----HTKLAAS-----CLLLEFVAIVGEGFLIRWSAGCCRRY 189
 DB 215 YPASPQDVEAANNSTSGASGSSFSDFVEVETICIIWFSELLVRFAC----- 267
 QY 190 GNGRLFAKPCVIDTYLI---ASLAVSACTQGN---IFATSARSLRFLQILRMV 243
 DB 268 --PSKATFSRNINMLDIDVAIIPEYITLIGELAEKRGQGQAMSLAIRLVKVFIF 325
 QY 244 RMDRGSTWKLSSVYAHKEL-ITAMYIGFLVLISSFLVYKDKANKEFTYADAL 302
 DB 326 KLSRHSKGLDILGTLASMRLEGLLFFELTGIVLSSAVYFAPADPSSGFSNPDAF 385
 QY 303 WMGITLTTTIGYGDKPPLTWGLRLSAGFALLGISFPALPAGILGSGF 350
 DB 386 WMAVVTETVGYGDMHPVTIGKLVGSLCAIAGVLTALPVPVIVSNF 433
 RESULT 37
 CIR4_BOVIN STANDARD; PRT; 660 AA.
 AC 005037;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.4 (BAR4).
 GN KCNA4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=92371645; PubMed=1505668;
 RA Garcia-Guzman M., Calvo S., Cena V., Criado M.;
 RT "Molecular cloning and permanent expression in a neuroblastoma cell

RT line of a fast inactivating potassium channel from bovine adrenal
 RT medulla.
 RL FEBS Lett. 308:283-289(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X57033; CAA40349.1; -
 CC HSSP: P15385; 1270. BMB_POZ.
 CC InterPro: IPR000210; BMB_POZ.
 CC InterPro: IPR001622; K+channel_pore.
 CC InterPro: IPR004051; KV14channel.
 CC InterPro: IPR003091; K_channel.
 CC InterPro: IPR003131; K_tetra.
 CC InterPro: IPR003968; KV_channel.
 CC InterPro: IPR000636; M+channel_nlg.
 CC InterPro: IPR003972; Shaker_channel.
 CC Pfam: PF00520; Ion_trans_1.
 CC Pfam: PF02214; K_tetra_1.
 CC PRINTS: PR00169; KCHANNEL.
 CC PRINTS: PR01511; KV14CHANNEL.
 CC PRINTS: PR01491; KCHANNEL.
 CC PRINTS: PR01496; SHAKERCHANNEL.
 CC SMART: SM00225; BTB_1.
 CC DR SMCRT; SM00225; BTB_1.
 CC DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC KW TRANSMEM 316 334 SEGMENT S1 (POTENTIAL).
 CC FT TRANSMEM 379 400 SEGMENT S2 (POTENTIAL).
 CC FT TRANSMEM 412 432 SEGMENT S3 (POTENTIAL).
 CC FT TRANSMEM 451 469 SEGMENT S4 (POTENTIAL).
 CC FT TRANSMEM 486 505 SEGMENT S5 (POTENTIAL).
 CC FT TRANSMEM 547 569 SEGMENT S6 (POTENTIAL).
 CC FT DOMAIN 38 50 POLY-ALA.
 CC FT DOMAIN 53 59 POLY-GLY.
 CC FT DOMAIN 62 65 POLY-HIS.
 CC FT DOMAIN 83 87 POLY-ARG.
 CC FT DOMAIN 131 137 POLY-GLY.
 CC FT DOMAIN 162 173 POLY-GLY.
 CC FT DOMAIN 441 444 POLY-GLN.
 CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 607 607 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT SEQUENCE 660 AA; 73512 MW; 14FAE859677929D5 CRC64;

Query Match 5.08; Score 235.5; DB 1; Length 660;

Best Local Similarity 23.78; Pred. No. 1.9e-06;

Matches 74; Conservative 57; Mismatches 116; Indels 65; Gaps 10;

139 GCCTLTSVFSTPE---HTKLASSCLLIEFPMIVFGLFETIRMSAGGCCCYRGMQGL 195
 356 GGLINDTSAPHPENSGHT-IFNDPFIVETVCIWSEFVRCFAC-----PSQA 405

QY 196 REARKPECVIDRTVL---ASIAVSAKTOG-----NIFATSALRSLEQLIRMYM 245
 DB 406 LFFKNTMINIIDIVSILPYFTLTGLDLAQOQGGGQOQOAMSFAILRIILRVFRIRKL 465
 QY 246 DRGGTAKLLGSVYVAHSHKELITAWYIGFVLFFSFLVLYEVD-ANKESTYADALWM 304
 DB 466 SHRSKGLQTLGHTLRASMRLEGLLIFPLFGVILFSSAVYFAEADPTTHQSPDAPMW 525
 QY 305 GTITLTITGYDKTPLTWAGRLSAGFALLGISFALPAGLIGSGFALKVOEHRQKPE 364
 DB 526 AVYMTTAVYGDMKPTVGGKIVGSLCAIGVLTALPVIVSNFN---YFHYRETFNE 582
 QY 365 KRRNPANLIQCVWRSYVADEKSVSTATWPHKALHTCSPTNOKLSPKEVRASPRQ 424
 DB 583 EPTQLQNAVSC-----PYL-----PSNLKKFR----- 606
 QY 425 SIKRSQAVGDR 436
 DB 607 --STSSSLGDK 616
 RESULT 38
 ID CIK4_MUSPF STANDARD; PRT; 654 AA.
 AC Q28527;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.4 (FK1).
 GN KCNA4.
 OS Muscota putorius furo (Ferret).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 CC Mustela.
 CC NCBI_TaxID=9669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart ventricle;
 RX MEDLINE=95029958; PubMed=7943383;
 RA Comer M.B., Campbell D.L., Rasmussen R.L., Lamson D.R.,
 RA Morales M.J., Zhang Y., Strauss H.C.;
 RT "Cloning and characterization of an Ito-like potassium channel from
 RT ferret ventricle."
 RL Am. J. Physiol. 267:H1383-H1395(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. LEFT AND RIGHT
 CC VENTRICLE, AND KIDNEY BUT NOT IN SKELETAL MUSCLE, ENDOTHELIAL
 CC CELLS, AORTA, AND LIVER.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).


```

DR InterPro: IPR004051; KV14channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003972; Shaker_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0151; KV14CHANNEL.
DR PRINTS: PRO1491; KVCHANNEL.
DR PRINTS: PRO1496; SHAKERCHANNEL.
DR SMART: SM00223; BTB; 1.
DR K10ic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMM 308 326 SEGMENT S1 (POTENTIAL).
FT TRANSMM 371 392 SEGMENT S2 (POTENTIAL).
FT TRANSMM 404 424 SEGMENT S3 (POTENTIAL).
FT TRANSMM 443 461 SEGMENT S4 (POTENTIAL).
FT TRANSMM 478 497 SEGMENT S5 (POTENTIAL).
FT TRANSMM 539 561 SEGMENT S6 (POTENTIAL).
FT DOMAIN 62 65 POLY-HIS.
FT DOMAIN 123 137 POLY-GLU.
FT DOMAIN 162 165 POLY-GLY.
FT DOMAIN 433 436 POLY-GLY.
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 90 90 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT MOD_RES 599 599 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT CONFLICT 38 38 R -> A (IN REF. 3 AND 4).
FT CONFLICT 42 42 EEEAT -> RRRRO (IN REF. 3 AND 4).
FT CONFLICT 84 84 V -> S (IN REF. 3 AND 4).
FT CONFLICT 304 304 D -> S (IN REF. 3 AND 4).
FT CONFLICT 542 542 A -> G (IN REF. 3 AND 4).
FT CONFLICT 631 631
SQ SEQUENCE 653 AA: 73288 MW: 7466781PF827D6F27 CRC04;

Query Match 4.9%; Score 233; DB 1; Length 653;
Best Local Similarity 23.6%; Pred. No. 2.6e-06;
Matches 70; Conservative 54; Mismatches 110; Indels 62; Gaps 9;

QY 152 HTKSLASCLLIEFWIYVGFLEFIRIRMSAGCCCRKRGQRLRRKRPCCVIDTYLI 211
Db HT-IPNDFEFLVETVCIVFSEFVRCFAC-----PSQALFFKNIMNIIDIVSIL 413
QY 212 ---ASIAVSAKTQS-----NIFATSLRSLRFLQILMVMMDRGGTWKILGSVYA 261
Db PFTITLGTDLAQGGGNGQQQAMSFALIRILRIVRFRIFKLSRSGLOLIGHTLRA 473
QY 414 PYFTITLGTDLAQGGGNGQQQAMSFALIRILRIVRFRIFKLSRSGLOLIGHTLRA 473
Db 262 HSKELITAWYIGFLVLISSFLVLYVEKD-ANKREFSTYADALMWGTTTLTIGYDRTPL 320
QY 474 SMRELGLIFLFLFGLVLISSAVYFAEADPTTFHQSIPDAFMWAVYMTTIGYDGMKPI 533
Db 321 TWLGRLLSAGFALLGISFALPAGILGSGFALKVQOHQKHEKRRNPANLIQCVWRS 380
QY 534 TVGKRIYGVLCALAGVLTALPVPVIVSNF--YFHRTENEEOQLTQNAVSC--- 586
Db 381 YAADESVSIATWPKFLKALHTCSPTNOKLSFEKVRVMAVSPRQGSJKRSQASVGR 436
QY 587 -----PYL-----PSNLAKRR-----STSSSSLDK 608
Db -----PYL-----PSNLAKRR-----STSSSSLDK 608

RESULT 40
CDS_DROME STANDARD: PRT: 656 AA.
AC C1KS_DROME P08511: Q24521: P08512: P08513: Q24277: Q9VWZ9:
DT 01-AUG-1988 (Rel. 08, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Shaker.
DE SH OR CG12348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

```

```

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=87292096; PubMed=2441471;
RA Tempel B.L., Papazian D.M., Schwarz T.L., Jan Y.N., Jan L.Y.;
RT "Sequence of a probable potassium channel component encoded at Shaker
RL locus of Drosophila."
RL Science 237:770-775(1987).
RN [2]
RP SEQUENCE OF 1-257 FROM N.A. (BETA ISOFORM).
RX MEDLINE=87273502; PubMed=2440582;
RA Kamb A., Iverson L.E., Tanouye M.A.;
RT "Molecular characterization of Shaker, a Drosophila gene that encodes
RL a potassium channel."
RL Cell 50:405-413(1987).
RN [3]
RP SEQUENCE FROM N.A. (DELTA ISOFORM).
RC STRAIN=Canton-S, and Oregon-R.
RA Baumann A., Krah-Jentgens I., Mueller R., Mueller-Holtkamp F.,
RA Seidel R., Keskemethy N., Casal J., Ferrus A., Pongs O.;
RT "Molecular organization of the maternal effect region of the Shaker
RL complex of Drosophila: characterization of an I(A) channel transcript
RL with homology to vertebrate Na(+) channel."
RL EMBO J. 6:3419-3429(1987).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; GAMMA AND EPSILON).
RC STRAIN=Canton-S;
RX MEDLINE=88296413; PubMed=2456921;
RA Pongs O., Keskemethy N., Mueller R., Krah-Jentgens I.,
RA Baumann A., Kiltz H.H., Canal I., Llamazares S., Ferrus A.;
RT "Shaker encodes a family of putative potassium channel proteins in
RL the nervous system of Drosophila."
RL EMBO J. 7:1087-1096(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; GAMMA AND B).
RX MEDLINE=88122563; PubMed=2448635;
RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
RT "Multiple potassium channel components are produced by alternative
RL splicing at the Shaker locus in Drosophila."
RL Nature 331:137-142(1988).
RN [6]
RP ERRATUM.
RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
RL Nature 332:740-740(1988).
RN [7]
RP SEQUENCE OF 450-534 FROM N.A.
RC STRAIN=H4;
RX MEDLINE=90166523; PubMed=3272175;
RA Kamb A., Tseng-Crank J., Tanouye M.A.;
RT "Multiple products of the Drosophila Shaker gene may contribute to
RL potassium channel diversity."
RL Neuron 1:421-430(1988).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mayas A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

```


ID	CIRK MOUSE	STANDARD:	PRT:	528 AA.
AC	P16390:			
DT	01-AUG-1990 (rel. 15, Created)			
DT	01-FEB-1996 (rel. 33, Last sequence update)			
DT	15-JUN-2002 (rel. 41, Last annotation update)			
DE	Voltage-gated potassium channel protein Kv1.3 (MK3).			
GN	KCNA3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90161996; PubMed=2305265;			
RA	Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,			
RA	Shanushani S., Tempel B.L., Gutman G.A.;			
RT	"A family of three mouse potassium channel genes with intronless			
RT	coding regions.";			
RL	Science 247:973-975(1990).			
CC	-I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	-I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE			
CC	RATE OF INACTIVATION OF THE CHANNEL, WHILE THE TAIL MAY PLAY A ROLE			
CC	IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL			
CC	TO SPECIFIC SUBCELLULAR COMPARTMENTS.			
CC	-I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	-I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@lsb-sib.ch).			
CC	-----			
CC	EMBL: M30441; AAA39716.1; -.			
DR	HSSP: O54397; 1BL8.			
DR	MGD: MGI:96660; Kcn3.			
DR	InterPro: IPR000210; RTB_POZ.			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR004050; KV13channel.			
DR	InterPro: IPR003091; K_channel.			
DR	InterPro: IPR003131; K_tetra.			
DR	InterPro: IPR003968; kv_channel.			
DR	InterPro: IPR000636; M+channel_nig.			
DR	InterPro: IPR003972; Shaker_channel.			
DR	Pfam: PF00520; Ion_trans; 1.			
DR	Pfam: PF02214; K_tetra; 1.			
DR	PRINTS: PRO0169; KCHANNEL.			
DR	PRINTS: PRO1510; KV13CHANNEL.			
DR	PRINTS: PRO1491; KYCHANNEL.			
DR	PRINTS: PRO1496; SHAKERCHANNEL.			
DR	SMART: SM00225; RTB; 1.			
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KW	Glycoprotein; Multigene family; Phosphorylation.			
FT	TRANSMEM 188 206	SEGMENT S1.		
FT	TRANSMEM 248 269	SEGMENT S2.		
FT	TRANSMEM 281 301	SEGMENT S3.		
FT	TRANSMEM 316 334	SEGMENT S4.		
FT	TRANSMEM 351 370	SEGMENT S5.		
FT	TRANSMEM 412 434	SEGMENT S6.		
FT	CARBOHYD 62 62	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 231 231	N-LINKED (GLCNAC. . .) (POTENTIAL).		

[illegible]

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: X12589; CAA31102.1; -
 DR EMBL: M26161; AAA41982.1; -
 DR PIR: A41353; A41353.
 DR PIR: S01161; S01161.
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004048; K+channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1508; KYLCHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 168 186 SEGMENT S1.
 FT TRANSMEM 221 242 SEGMENT S2.
 FT TRANSMEM 254 274 SEGMENT S3.
 FT TRANSMEM 290 309 SEGMENT S4.
 FT TRANSMEM 326 345 SEGMENT S5.
 FT TRANSMEM 387 408 SEGMENT S6.
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT MOD_RES 322 322 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RES 445 445 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64;

Query Match 4.9%; Score 230; DB 1; Length 495;
 Best Local Similarity 19.6%; Pred. No. 2.7e-06;
 Matches 75; Conservative 80; Mismatches 142; Indels 86; Gaps 10;

OY 104 RNYYRRQNYLYNLEBRP--GNAFYHAFYFLVFGCLLSVFSTIE----- 151
 DB 142 RPLPEKEYQROVWLLFEYPSSGPARVAIVSVWVLLSVIFCETLELDKDDKDTGT 201
 OY 152 -----HTKLASSCLLLEFVMIVFEGLEFIIRISAGCCCRYGMOGRLEFPARK 200
 DB 202 IHRIDNTVITYTSNFTDPFIVERLCTIWFSEFLVRFAC-----PSKTFPKN 252
 OY 201 PCVVIDTVLT--ASIAVVSATOGN-----IFATSLRSLRFLOILRMVRMDRGGTW 252
 DB 253 IMNFDIAIIPYFTLTLEIEOGNOGEOATSLAIRVIRLIVAVRFIKLSRSGKL 312
 OY 253 KLLGSVVAHAKEL-ITAMVIGFLVLFSSFLVYLVKXANKEFSTYADALMMGTITLT 311
 DB 313 QILGTLASMEIGELLFFLTIGVLTSSAVYFAEAEASHFSSIPAFEMVAVSMGT 372
 OY 312 IGYGDKPLTWLGRLLSAGFALLGISFPAIIGSSGALKVQEOHROKHFEKRRNPAA 371
 DB 373 VGYGMYVTITGKIVGSLCAIAGVLTIALPVPVIVSNN--YFHRREGSEQ----- 424
 OY 372 NLIQCWMSYADEKSVSIATWPKPHIKALHTCSP-----TNOKLSFEKRYMAS 420
 DB 425 -----AQLHVSPPNLASDSDLRRSSSTISKSEYMEIEE 459
 OY 421 PRGOSIKS-ROASVGDRRSPSTD 442
 DB 460 DMNNSIAHYROANIRGTCTAYD 482

RESULT 43

CIRD_HUMAN
 ID CIRD_HUMAN STANDARD; PRT; 511 AA.
 AC P48347;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein Kv3.1 (Kv4) (NGK2).
 GN KCNC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93194190; PubMed=8449507;
 RA Ried T., Rudy B., de Miera E., Lau D., Ward D.C., Sen K.;
 RT "Localization of a highly conserved human potassium channel gene
 (NGK2-KV4; KCNC1) to chromosome 11p15.";
 RL Genomics 15:405-411(1993).
 RN [2]
 RP SEQUENCE OF 244-475 FROM N.A.
 RX MEDLINE=93016011; PubMed=1400413;
 RA Griesmer S., Ghanshani S., Dehlefs B., McPherson J.D.,
 RA Wasmuth J.J., Gutman G.A., Cahalan M.D., Chandry K.G.;
 RT "The Shaw-related potassium channel gene, Kv3.1, on human chromosome
 11, encodes the type 1 K+ channel in T cells.";
 RL J. Biol. Chem. 267:20971-20979(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: S56770; AAB25764.1; -
 DR EMBL: M96747; AAA59458.1; -
 DR HSSP: Q54397; 1BL8.
 DR Genew: HGNC:6233; KCNC1.
 DR MIM: 176258; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003974; Shaw_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1498; SHAWCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family.
 FT DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).
 FT

```

FT TRANSMEM 191 209 SEGMENT S1 (POTENTIAL).
FT DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 267 SEGMENT S2 (POTENTIAL).
FT DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 295 SEGMENT S3 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 309 331 SEGMENT S4 (POTENTIAL).
FT DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 345 366 SEGMENT S5 (POTENTIAL).
FT DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 415 436 SEGMENT S6 (POTENTIAL).
FT DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57942 MW: 10A93478F7120AB CRC64;

Query Match 4.9%; Score 230; DB 1; Length 511;
Best Local Similarity 21.8%; Pred. No. 2.8e-06;
Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

QY 3 RHAGGEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVLLNSAARGDGLLLG 62
DB 110 RQHRDAE-----ALDSFGAPLDSAD-----ADADGEG----- 140
QY 63 TRAAATLGGGGGLRSRKGQARMSLGKPLSTYSQSCRNVKRRVQNYLYNVLERP 122
DB 141 -----DSGDEDELEMT-----KRLALSDSPDRGPGGFWRRWQPRIVALFEDP 183
QY 123 RGMAFI-YHAFVELLVFGLLSV-----FSTIPRHTKL----- 155
DB 184 YSSRRARVYAFSLP-----ILVSITTFCTETHERFNITVKTLENYRNGTOVRYREAE 240
QY 156 ASSCLLLEFVNIIVFGLFETIRMSAGCCCRYGNOGRFLPAKPCVIDTYILI----- 211
DB 241 TEAFLEYIEGVVVFTEFLMRV-----IFC-----PNKVEFLKNSLIIDFVALLPXYL 291
QY 212 -ASIAVNAKQGNIFATSAALSRLQLRLVWRMDRGGTWMKLLGSVYVAHSE-LITA 269
DB 292 EVGSGISLSSAKADVL--GFLRVYREVRLIRFKLTHFVGLVGLHTLNASTNEFLILI 349
QY 270 WYIGFLVLFSSFLVYVEK-----DANKETSTADALMWGITLTITIGYDKTP 319
DB 350 IFLLAGVILFNF-MIYIERIGAQPRDPASETHKNIPIGWMAVYMTLTIGYDWP 408
QY 320 LTMGLRLISAGFALIGISFFALPAGILSGFALKVO--EORORHFEKRRNPANLLOCW 378
DB 409 QTWGSMVLGALCALAGVLTIAMPVYIVNFMGYSLAAMAKOKLPKKKKHPRPQLGS 468
QY 379 RSYADEKSVSIATWKPILKALHTCSPTNOKLSFKERVNRASRGOSI 426
DB 469 PNICK-----SVVNSPHHSTOSDTCPLADEILLEINRAGRKPLRGMSI 511

RESULT 44
CIRK_MOUSE ID STANDARD; PRT: 511 AA.
AC P15388;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein KV3.1 (KV4) (NGK2).
GN KCNC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90092535; PubMed=2599109;
RA Tokoyama S., Imoto K., Kawamura T., Higashida H., Iwabe N., Miyata T.,
RT "Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells.
RT Primary structure and functional expression from cDNAs.";
```

```

RL FEBS Lett. 259:37-42(1989).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; KV3.1 (shown here) and KV4;
CC are produced by alternative splicing.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sib-sdb.ch).
CC -----
DB EMBL: Y07521; CAA68814.1;
DB PIR: S07095; S07095.
DB HSSP: Q54397; IBL8.
DB MGD: MGI:96667; Kcnc1.
DB InterPro: IPR000210; BTB_POZ.
DB InterPro: IPR001622; K+channel_pore.
DB InterPro: IPR003091; K+channel.
DB InterPro: IPR003131; K_tetra.
DB InterPro: IPR003968; Kv_channel.
DB InterPro: IPR000636; M+channel_nlg.
DB InterPro: IPR003974; Shaw_channel.
DB Pfam: PF00520; Ion_trans.1.
DB Pfam: PF02214; K_tetra.1.
DB PRINTS: PR00169; KCHANNEL.
DB PRINTS: PR01491; KVCCHANNEL.
DB PRINTS: PR01498; SHAWCHANNEL.
DB SMART: SM00225; BTB; 1.
DB K+ Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
DB Glycoprotein; Multigene family; Alternative splicing;
DB DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).
DB TRANSMEM 191 209 SEGMENT S1 (POTENTIAL).
DB DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
DB TRANSMEM 248 267 SEGMENT S2 (POTENTIAL).
DB DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
DB TRANSMEM 277 295 SEGMENT S3 (POTENTIAL).
DB DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
DB TRANSMEM 309 331 SEGMENT S4 (POTENTIAL).
DB DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
DB TRANSMEM 345 366 SEGMENT S5 (POTENTIAL).
DB DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
DB TRANSMEM 415 436 SEGMENT S6 (POTENTIAL).
DB DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
DB CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
DB CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57928 MW: 50A939E8F7120F37 CRC64;

Query Match 4.9%; Score 230; DB 1; Length 511;
Best Local Similarity 21.8%; Pred. No. 2.8e-06;
Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

QY 3 RHAGGEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVLLNSAARGDGLLLG 62
DB 110 RQHRDAE-----ALDSFGAPLDSAD-----ADADGEG----- 140
QY 63 TRAAATLGGGGGLRSRKGQARMSLGKPLSTYSQSCRNVKRRVQNYLYNVLERP 122
```



```

Db 142 RPLEKEKOROVMLFEYPRESSGPARVIAVSMVLLISIVIFCETLEPELKDOKDFGT 201
QY 152 -----HTKASSCLLIEVMIVVEGLEFIIRIWSAGCCCRIRYWGCRLEFARK 200
Db 202 VHRIDMTVIYNSNETDPPEFVLELCIIMEFSELVREFAC-----PSKTDFEKN 252
QY 201 PFCVIDFTVL---ASIAVSAKTOGN-----IPATSALRSLEFLOILMVNRDRRGTW 252
Db 253 IMNRTIDYAIIPFLLTGTETAEOEGNOKGEOATSALIRVRLVAVFRIKFSRSGKL 312
QY 253 KLGSSVYVAHSEL-ITAMYIGELVLIFESSFLVYLEKDNKEFSYDAIMMGITLTT 253
Db 313 QILGOTLKASHRELGLLIFLEFICVILTFSSANYFAEAEASHFSSIPRAFMAVYSMT 372
QY 312 IGYEDKTPPLWLGRLLSAGFALLGISFPALPAGILGSGFALVQEOHROKHEKRRNPA 371
Db 373 VGYEDMPEVITIGCKRIVGSLCAIAGVLTALPVPVIVSNEN---YFHRTEGEGE---A 4255
QY 372 NLIOCVARSYAAD-----EKSVSIATWKPRLKALHITCSPTNOKL 410
Db 426 QLHVSSPPLNASDSDLSRRSSSTMSKYEMETLEEDMNNSIARYOVNIPTANTACTNOUC 4855
QY 411 SFKERV 416
Db 486 VNKSKL 491

```

RESULT 46			
CIRD_RAT	ID	STANDARD:	PRT: 585 AA.
AC	CIRD_RAT		
DT	P25122;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-MAY-1992 (Rel. 22, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	Voltage-gated potassium channel protein Kv3.1 (kv4) (NGK2) (RAM2).		
GN	KCNK1.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91219486; PubMed=2023941;		
RA	Luneau C.J., Williams J.B., Marshall J., Levitan E.S., Ojiva C.,		
RA	Smith J.S., Antanavage J., Folander K., Stein R.B., Swanson R.,		
RA	Kaczmarek L.K., Buhrow S.A.;		
RT	"Alternative splicing contributes to K+ channel diversity in the		
RT	mammalian central nervous system.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 88:3932-3936(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92331599; PubMed=1378392;		
RA	Redlitz J., Wunder F., Stocker M., Lichtinghagen R., Mastiani F.,		
RA	Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,		
RA	Veh R., Pongs O.;		
RT	"Characterization of a Shaw-related potassium channel family in rat		
RT	brain.";		
RL	EMBO J. 11:2473-2486(1992).		
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM		
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED		
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE		
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH		
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL		
CC	GRADIENT.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE		
CC	SPlicing.		
CC	-1- TISSUE SPECIFICITY: BRAIN.		
CC	-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS		
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT		
CC	EVERY THIRD POSITION.		
CC	-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL		
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR		

```

CC COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: M68880; AAA41501.1; -.
DR EMBL: X62840; CA44644.1; -.
DR PIR: A39395; A39395.
DR PIR: S22704; S22704.
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+-channel_pore.
DR InterPro: IPR003091; K_channel..
DR InterPro: IPR003131; K_tetra..
DR InterPro: IPR003968; Kv_channel..
DR InterPro: IPR000636; M+-channel_n1g.
DR InterPro: IPR003974; Shaw_channel..
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL..
DR PRINTS: PR01491; KVCHANNEL..
DR PRINTS: PR01498; SHAWCHANNEL..
DR SMART: SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Alternative splicing.
FT DOMAIN 1 190
FT TRANSMEM 191 209
FT TRANSMEM 210 247
FT TRANSMEM 248 267
FT TRANSMEM 268 276
FT TRANSMEM 277 295
FT TRANSMEM 296 308
FT DOMAIN 309 331
FT TRANSMEM 332 344
FT TRANSMEM 345 366
FT TRANSMEM 367 414
FT DOMAIN 415 436
FT DOMAIN 437 585
FT CARBOHYD 220 220
FT CARBOHYD 229 229
FT VARSPIC 512 511
FT VARSPIC 512 585 MISSING (IN SHORT ISOFORM).
FT SEQUENCE 585 AA; 65857 MW; DD4E2D32848E2DCF CRC64;
SQ
Query Match 4.8%; Score 227; DB 1; Length 585;
Best Local Similarity 22.2%; Pred. No. 5, 1e-06;
Matches 92; Conservative 72; Mismatches 138; Indels 112; Gaps 17;
QY 3 RHHAGGEGGAAGILWVSGAAAAAGGGRGSGMKDYVSGRGVLLNSAARGDGLLLG 62
DB 110 ROHRDAEE-----ALDSFGGAPLDNSADD-----ADADGPG----- 140
QY 63 TRATATLGGGGGGLRESRRKGQAGMSLLGKPLSTSSQSCRNNKYRVRQVLYLNLWER 122
DB 141 -----DSGDGDEDELEMT-----KRLALSDSPDGGPGGFWRMOPRIWALEDP 183
QY 123 RGNAFI-YHAFVFLIVGCLILSV-----FSTIPEHTKL----- 155
DB 184 YSSQIYATYVAFASLFF---ILVSTTTCLETHEFNFIYNTKTELENNVNGTQVARYREAE 240
QY 156 ASSGILLLEFVMTVVEGLFETIRITWSAGCCCRKRGWGRLRFARKPCVIDITVLI---- 211
DB 241 TEAFILTYIEGVGVYWFEEFLMRV---VPC-----PNKYEFIKNSLNIIDFVALLPEYL 291
QY 212 -ASIAVVSATQGNIRATSLRSLRFLQIILRMVRMDRGRGTWMLGSSVVAHSKE-LITA 269

```

```

Db      292 EVGLSGLSSAKAKOVL--GFLRAYVRFAVRLILFIILTRFVBLRVGLHTRLRSTNEFLLLI 349
Oy      270 WYGFLLVLSSEFLVYVER-----DANKEFSTYADALMMGGITLTITTYGDKTP 319
Db      350 IFLLAGVLIENFT-MIYAEIRIGAOBPNDPSESEHFNKPIGFWMAVYVMTTLTGWDYRP 408
Oy      320 LTWIGRLLSNAGFALLGISFFALPGIL----GSGFALKVQDQ-----HOKRFEK 365
Db      409 QTWGSGMLVGCALAGVLTITAMPVPIVNMFGMYSLAMAKOKLPKRRKKRHPR 462

RESULT 47
CIRL_MOUSE
ID      CIRL_MOUSE      STANDARD:      PRT;      495 AA.
AC      P16388;
DT      01-AUG-1990 (Rel. 15, Created)
DT      01-AUG-1990 (Rel. 15, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Voltage-gated potassium channel protein Kv1.1 (MK1) (MBK1).
OS      KCMAL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=9016196; PubMed=2305265;
RA      Chandy K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA      Ghanshani S., Tempel B.L., Guitman G.A.;
RT      "A family of three mouse potassium channel genes with intronless
RT      coding regions.";
RT      Science 247:973-975(1990).
[2]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Brain;
RC      MEDLINE=88189348; PubMed=2451788;
RX      Tempel B.L., Jan Y.N., Jan L.Y.;
RA      "Cloning of a probable potassium channel gene from mouse brain.";
RL      Nature 332:837-839(1988).
CC      -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC      ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC      CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC      MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC      WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC      GRADIENT.
CC      -1- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC      RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC      IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC      TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC      -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC      CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC      EVERY THIRD POSITION.
CC      -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC      CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
-----
DR      EMBL; M30439; AAA39711.1; -
DR      EMBL; Y00305; CA668408.1; -
DR      PIR; S06378; S06378.
DR      PIR; A40090; A40090.
DR      HSSP; 054397; 1BLR.
DR      MGD; MGI:96654; Kcna1.
DR      InterPro; IPR000210; BTB_POZ.

```

Query Match	Best Local Similarity	4.8%; Score 226; DB 1; Length 495;
Matches	66; Conservative	74; Mismatches 125; Indels 48; Gaps 8;
DR InterPro; IPR001622; K-channel pore.		
DR InterPro; IPR004048; KV1channel.		
DR InterPro; IPR003091; K_channel.		
DR InterPro; IPR003131; K_tetra.		
DR InterPro; IPR003968; Kv_channel.		
DR InterPro; IPR000636; M-channel_n19.		
DR InterPro; IPR003972; Shaker_channel.		
DR Pfam; PF00520; Ion_trans; 1.		
DR Pfam; PF02214; K_tetra; 1.		
DR PRINTS; PR00169; KCHANNEL.		
DR PRINTS; PR01508; KV1CHANNEL.		
DR PRINTS; PR01491; KVCHANNEL.		
DR PRINTS; PR01496; SHAKERCHANNEL.		
DR SMART; SM00225; BTB; 1.		
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW Glycoprotein; Multigene family; Phosphorylation.		
FT TRANSMEM 168 186 SEGMENT S1.		
FT TRANSMEM 221 242 SEGMENT S2.		
FT TRANSMEM 254 274 SEGMENT S3.		
FT TRANSMEM 290 309 SEGMENT S4.		
FT TRANSMEM 326 345 SEGMENT S5.		
FT TRANSMEM 387 408 SEGMENT S6.		
FT CARBOHD 207 207		
FT MOD_RES 322 322		
FT MOD_RES 446 446		
SO SEQUENCE 495 AA; 56409 MW; C9249F130B943D3D CRC64;		
DR InterPro; IPR001622; K-channel pore.		
DR InterPro; IPR004048; KV1channel.		
DR InterPro; IPR003091; K_channel.		
DR InterPro; IPR003131; K_tetra.		
DR InterPro; IPR003968; Kv_channel.		
DR InterPro; IPR000636; M-channel_n19.		
DR InterPro; IPR003972; Shaker_channel.		
DR Pfam; PF00520; Ion_trans; 1.		
DR Pfam; PF02214; K_tetra; 1.		
DR PRINTS; PR00169; KCHANNEL.		
DR PRINTS; PR01508; KV1CHANNEL.		
DR PRINTS; PR01491; KVCHANNEL.		
DR PRINTS; PR01496; SHAKERCHANNEL.		
DR SMART; SM00225; BTB; 1.		
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW Glycoprotein; Multigene family; Phosphorylation.		
FT TRANSMEM 168 186 SEGMENT S1.		
FT TRANSMEM 221 242 SEGMENT S2.		
FT TRANSMEM 254 274 SEGMENT S3.		
FT TRANSMEM 290 309 SEGMENT S4.		
FT TRANSMEM 326 345 SEGMENT S5.		
FT TRANSMEM 387 408 SEGMENT S6.		
FT CARBOHD 207 207		
FT MOD_RES 322 322		
FT MOD_RES 446 446		
SO SEQUENCE 495 AA; 56409 MW; C9249F130B943D3D CRC64;		
DR InterPro; IPR001622; K-channel pore.		
DR InterPro; IPR004048; KV1channel.		
DR InterPro; IPR003091; K_channel.		
DR InterPro; IPR003131; K_tetra.		
DR InterPro; IPR003968; Kv_channel.		
DR InterPro; IPR000636; M-channel_n19.		
DR InterPro; IPR003972; Shaker_channel.		
DR Pfam; PF00520; Ion_trans; 1.		
DR Pfam; PF02214; K_tetra; 1.		
DR PRINTS; PR00169; KCHANNEL.		
DR PRINTS; PR01508; KV1CHANNEL.		
DR PRINTS; PR01491; KVCHANNEL.		
DR PRINTS; PR01496; SHAKERCHANNEL.		
DR SMART; SM00225; BTB; 1.		
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW Glycoprotein; Multigene family; Phosphorylation.		
FT TRANSMEM 168 186 SEGMENT S1.		
FT TRANSMEM 221 242 SEGMENT S2.		
FT TRANSMEM 254 274 SEGMENT S3.		
FT TRANSMEM 290 309 SEGMENT S4.		
FT TRANSMEM 326 345 SEGMENT S5.		
FT TRANSMEM 387 408 SEGMENT S6.		
FT CARBOHD 207 207		
FT MOD_RES 322 322		
FT MOD_RES 446 446		
SO SEQUENCE 495 AA; 56409 MW; C9249F130B943D3D CRC64;		
DR InterPro; IPR001622; K-channel pore.		
DR InterPro; IPR004048; KV1channel.		
DR InterPro; IPR003091; K_channel.		
DR InterPro; IPR003131; K_tetra.		
DR InterPro; IPR003968; Kv_channel.		
DR InterPro; IPR000636; M-channel_n19.		
DR InterPro; IPR003972; Shaker_channel.		
DR Pfam; PF00520; Ion_trans; 1.		
DR Pfam; PF02214; K_tetra; 1.		
DR PRINTS; PR00169; KCHANNEL.		
DR PRINTS; PR01508; KV1CHANNEL.		
DR PRINTS; PR01491; KVCHANNEL.		
DR PRINTS; PR01496; SHAKERCHANNEL.		
DR SMART; SM00225; BTB; 1.		
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW Glycoprotein; Multigene family; Phosphorylation.		
FT TRANSMEM 168 186 SEGMENT S1.		
FT TRANSMEM 221 242 SEGMENT S2.		
FT TRANSMEM 254 274 SEGMENT S3.		
FT TRANSMEM 290 309 SEGMENT S4.		
FT TRANSMEM 326 345 SEGMENT S5.		
FT TRANSMEM 387 408 SEGMENT S6.		
FT CARBOHD 207 207		
FT MOD_RES 322 322		
FT MOD_RES 446 446		
SO SEQUENCE 4		

DR SMART. SM00225; BTB. 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycophorin; Multigene family; Phosphorylation.
 FT TRANSMEM 242 260 SEGMENT S1.
 FT TRANSMEM 316 336 SEGMENT S2.
 FT TRANSMEM 347 368 SEGMENT S3.
 FT TRANSMEM 387 408 SEGMENT S4.
 FT TRANSMEM 423 444 SEGMENT S5.
 FT TRANSMEM 484 505 SEGMENT S6.
 FT DOMAIN 373 376 POLY-GLY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD.RES 81 81 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 FT MOD.RES 535 535 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 546 546 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 569 569 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 602 AA; 66552 MW; 6A784535FE226ED7 CRC64;
 Query Match 4.7%; Score 223.5; DB 1; Length 602;
 Best Local Similarity 24.9%; Pred. No. 8.4e-06;
 Matches 68; Conservative 49; Mismatches 111; Indels 45; Gaps 8;
 QY 162 ILEFWIIVFGLFIRIMSGCCCRYRGWGLRFPKPCVIDTIVL---IASIAVVS 218
 DB 317 IVETTCVMTFFELVAFAC-----PSKAEFSNNINIIDVAFPIYFIIIGEL 367
 QY 219 AKQV-----GNIFATSLRSIRFIQILRMVMDRGKWKLGISVYVHAKSLITAW 270
 DB 368 AEQPGGGGGOAGMSLALRLVRLRVRFIFKLSRKSGLQILGKTLQASMRGLGLI 427
 QY 271 YIGFLVLISSFLVLYVEKDN-KEFSTYADALMWGTTITLTIGYDGTPLTWGRLISA 329
 DB 428 FLEFICVILLESVAVFREADNHNHSHSPSIDAFWMAVYMTTGVGDMRPITVGKIVGS 487
 QY 330 GFALLISFPALDAGILGSGF-----ALKVDBHROKHREKRRNPANLIIQ 375
 DB 488 LCALACVLTALPVLVPSNFNFYHRETDHEEQALK-EEQGNQRRESGLDTGGQRKVS 546
 QY 376 CVMRSYAAD-----EKSVSTATW-----KPIHKA 399
 DB 547 CSKASCKTKGSGLESSDSIRSGSCPLEKHLKA 579
 RESULT 50
 CIKL.DROME
 ID CIKL.DROME STANDARD; PRT: 490 AA.
 AC P17971; Q9VW11.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Shal (Shal12).
 GN SHAL OR SHAL2 OR CG9262.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=902339553; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RL Science 248:599-603(1990).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245668; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila.";

RL Nucleic Acids Res. 18:2173-2174(1990).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
 RA Abail J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beckova D., Botchan M.R., Bouck J., Brockstein P., Brottler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage J.S., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -I- SUBUNIT: HETEROTRIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CURRENT CLASS.
 CC -I- CAUTION: Ref.3 sequence differs from that shown due to erroneous
 gene model prediction.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

CC -----
DR EMBL: M32660; AAA28895.1; .
DR EMBL: AE003516; AAF49144.1; ALT_SEQ.
DR PIR: A35312; A35312.
DR PIR: S12747; S12747.
DR FLYBase: FBgn0005564; Shal.
DR InterPro: IPR000210; BTR_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003975; Shal_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO1491; KCHANNEL.
DR PRINTS: PRO1497; SHALCHANNEL.
DR SMART: SM00225; BTR; 1.
DR SMART: SM00225; BTR; 1.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Alternative splicing.
FT TRANSMEM 186 204 SEGMENT S1.
FT TRANSMEM 229 250 SEGMENT S2.
FT TRANSMEM 261 282 SEGMENT S3.
FT TRANSMEM 290 308 SEGMENT S4.
FT TRANSMEM 324 345 SEGMENT S5.
FT TRANSMEM 385 406 SEGMENT S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 55918 MW; E178E1C9B07DA74 CRC64;

Query Match 4.7%; Score 222.5; DB 1; Length 490;
Best Local Similarity 23.4%; Pred. No. 7.3e-06;
Matches 78; Conservative 65; Mismatches 136; Indels 55; Gaps 13;

QY 89 LIGKPLSTSSOSCRNWKYRQNYLYNLEPRP---GNAFYHAFVFLVFGCLLS 144
DB 148 LMDDKLSENGDONLQQLTNMQ---KMKRAFENPHTSALVYVYTGFIIV--SYMAN 202
QY 145 VFSTIP-----EHTKLASSCLLLEFVMIIVFGLEFIIRISAGCCCRYRG 190
DB 203 VVEVPCGHRPGRAGTLPCGERYKIVFC---LDTACVMIETAEYLLRLFAA----- 251
QY 191 WQGLRFRARPFQYIDTIVLASTAVSAKQGNIFATLSALSRFLQILRMVRMDRGG 250
DB 252 -PDCKFVRSVMSLIDVAIMP--YYIGLITDNDVSGAEVTLRFRVFRIFKFSRHSQ 308
QY 251 TWKLLGSVVYAHSKELITAWYIGFLV-----LISSFLVYLVEKDN--KEFSTYADAL 302
DB 309 GLRLGTILKSCASEL-----GLVYFLAMALIIIFATVMFY-AEKNVNGTNTSIPAAF 361
QY 303 WMGCTIITLTIGYDGKPTLWLGRLISAGPALIGISFPALPAGILGSGFA-LKVOEQRQK 361
DB 362 WYTLVMTTLTIGYDGMVEETIAGKIYGVCSLSGLVIALPVPVIVSNFSRIYHQNRADK 421
QY 362 HFEKRRNPANLIGQVMSYAA--DEKSVSTATW 393
DB 422 RKAQRKARLARIRIAKASSGAAPVSKKRAAEARW 455

Search completed: June 14, 2003, 17:41:11
Job time : 36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:28 ; Search time 96 Seconds
(without alignments)
1981.057 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHHAGGEGGAAGLWVKS.....SICKAGESTDLSPHYKTK 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1810.5	38.3	842	11	Q923N2 mus musculu
2	1801.5	38.1	870	11	Q8R498 mus musculu
3	1795	37.9	723	11	Q923N4 mus musculu
4	1791.5	37.9	840	11	Q923N1 mus musculu
5	1767	37.3	759	11	Q923M5 mus musculu
6	1753	37.0	747	11	Q923M6 mus musculu
7	1614	34.1	623	11	Q923N0 mus musculu
8	1614	34.1	570	11	Q923M3 mus musculu
9	1234	26.1	473	11	Q923M9 mus musculu
10	1226	25.9	692	5	Q967F8 caenorhabd
11	1199	25.3	347	11	Q923M7 mus musculu
12	1199	25.3	349	11	Q923M8 mus musculu
13	1181	25.0	409	4	Q9BX08 homo sapien
14	1064.5	22.5	294	4	Q9BX07 homo sapien
15	1040	22.0	338	11	Q923M6 mus musculu
16	950	20.1	645	5	Q9XWG9 caenorhabd

17	697	14.7	343	5	Q9V5H7 drosophila
18	549.5	11.6	392	4	Q96A19 homo sapien
19	452.5	9.6	363	4	Q9BQ04 homo sapien
20	437	9.2	97	11	Q9CTU2 mus musculu
21	430	9.1	675	5	Q96YX8 caenorhabd
22	424.5	9.0	399	4	Q9BQ05 homo sapien
23	311	6.6	469	5	Q9V5H6 drosophila
24	308.5	6.5	911	4	Q9BXD3 homo sapien
25	297.5	6.3	858	6	Q9M219 oryctolagus
26	291.5	6.2	858	4	Q14193 homo sapien
27	287.5	6.1	858	6	Q18668 sus scrofa
28	285	6.0	611	6	Q8WNQ3 sus scrofa
29	281.5	5.9	876	13	Q91593 xenopus lae
30	280	5.9	898	13	Q91592 xenopus lae
31	279	5.9	857	11	Q03717 mus musculu
32	274.5	5.8	816	13	Q985V4 oryctolagus
33	274.5	5.8	911	6	Q95L11 oryctolagus
34	267	5.6	959	5	Q97045 oryctolagus
35	262.5	5.5	575	11	Q9CQU4 ratius sp.
36	260.5	5.5	478	5	P91784 polyorchis
37	260.5	5.5	582	4	Q9H1V7 homo sapien
38	256.5	5.4	582	4	Q9H1V7 homo sapien
39	256	5.4	908	5	Q18476 liliigo peal
40	254	5.4	606	4	Q9H1V6 homo sapien
41	248.5	5.3	528	5	P91256 caenorhabd
42	246	5.2	609	5	Q95XD1 caenorhabd
43	245.5	5.2	905	5	Q26344 aplysia sp.
44	245	5.2	484	5	Q22012 caenorhabd
45	245	5.2	647	4	Q9NSA2 homo sapien
46	245	5.2	647	4	Q75671 homo sapien
47	243.5	5.1	662	13	Q90W36 columba liv
48	243	5.1	613	4	Q96PR0 homo sapien
49	243	5.1	638	4	Q96PR1 homo sapien
50	242.5	5.1	490	5	Q9XKD1 caenorhabd
51	241.5	5.1	344	16	Q98QES mycoplasma
52	241	5.1	263	16	Q8YND3 anabaena sp
53	240.5	5.1	480	11	Q9QYU3 ratius ratt
54	240.5	5.1	628	11	Q8R1C0 mus musculu
55	240.5	5.1	662	13	Q9VX88 gallus gall
56	239	5.0	510	5	Q26095 polyorchis
57	237.5	5.0	515	5	Q16968 aplysia cal
58	236	5.0	488	5	Q25376 liliigo opal
59	235.5	5.0	661	6	Q9GLF1 bos taurus
60	233.5	4.9	587	13	Q91A29 oncorhynch
61	233.5	4.9	655	6	Q8WN02 mustela put
62	233.5	4.9	655	11	Q08723 ratius norv
63	233	4.9	516	6	Q28656 oryctolagus
64	232.5	4.9	512	5	Q26597 schistosoma
65	232.5	4.9	651	13	Q9DDN7 apteronotus
66	232.5	4.9	655	4	Q9UH85 homo sapien
67	231.5	4.9	655	6	Q9TTM5 oryctolagus
68	230.5	4.9	655	11	Q920V1 mus musculu
69	230.5	4.9	655	11	Q99P42 ratius norv
70	230	4.9	280	16	Q9RM39 delinococcus
71	230	4.9	592	13	Q9PVD1 xenopus lae
72	230	4.9	636	11	P70622 ratius norv
73	230	4.9	658	13	Q9PRD3 oryctolagus
74	229.5	4.8	630	4	Q9NZV8 homo sapien
75	229.5	4.8	635	4	Q9UK17 homo sapien
76	229	4.8	494	13	Q91830 oncorhynch
77	229	4.8	561	5	Q95PC9 panulirus i
78	229	4.8	636	4	Q9UH86 homo sapien
79	228.5	4.8	485	13	Q90YV3 xenopus lae
80	228.5	4.8	630	4	Q9UNH9 homo sapien
81	228	4.8	279	17	Q8TP82 methanosarc
82	228	4.8	585	6	Q9XSJ8 canis famli
83	228	4.8	651	11	Q03719 mus musculu
84	227.5	4.8	630	4	Q9UBV7 homo sapien
85	227.5	4.8	630	11	Q63881 ratius sp.
86	227	4.8	490	11	Q99249 ratius norv
87	227	4.8	611	11	Q63286 ratius norv
88	227	4.8	636	11	Q920V0 mus musculu
89	227	4.8	636	11	Q62897 ratius norv

90	226.5	4.8	518	13	073606	073606 gallus gall
91	226.5	4.8	540	11	09Jf60	09Jf60 mus musculu
92	226.5	4.8	558	5	062350	062350 caenorhabdi
93	226.5	4.8	630	11	0920V2	0920V2 mus musculu
94	226	4.8	556	5	017535	017535 caenorhabdi
95	226	4.8	636	4	09UK16	09UK16 homo sapien
96	225.5	4.8	632	13	08UW33	08UW33 gallus gall
97	225	4.8	477	11	035174	035174 mus musculu
98	225	4.8	477	11	09ER26	09ER26 rattus norv
99	225	4.8	546	5	026040	026040 panulirus i
100	225	4.8	551	5	095PD0	095PD0 panulirus i
101	225	4.8	579	5	095PC5	095PC5 panulirus i
102	225	4.8	585	5	095PC4	095PC4 panulirus i
103	225	4.8	660	5	095PC8	095PC8 panulirus i
104	225	4.8	660	5	095PC7	095PC7 panulirus i
105	225	4.8	680	5	095PC6	095PC6 panulirus i
106	224	4.7	489	4	09ULS6	09ULS6 homo sapien
107	223.5	4.7	522	5	061335	061335 panulirus i
108	223	4.7	466	4	09UJ96	09UJ96 homo sapien
109	223	4.7	500	4	09UJ94	09UJ94 homo sapien
110	223	4.7	500	6	09GKU7	09GKU7 macaca fasc
111	221.5	4.7	295	17	09YDF8	09YDF8 aerypyrum p
112	221.5	4.7	608	5	095PC3	095PC3 panulirus i
113	221	4.7	409	5	091783	091783 polychus
114	220.5	4.7	597	6	09TS07	09TS07 bos taurus
115	220	4.6	519	4	08TDM1	08TDM1 homo sapien
116	219.5	4.6	489	13	098TDM	098TDM xenopus lae
117	219	4.6	725	6	028649	028649 oryctolagus
118	218.5	4.6	357	5	026039	026039 panulirus i
119	218	4.6	602	11	0921R6	0921R6 mus musculu
120	217.5	4.6	655	4	060577	060577 homo sapien
121	217	4.6	504	11	060565	060565 mesocricetu
122	216	4.6	593	6	028248	028248 canis famli
123	215.5	4.6	460	5	009658	009658 caenorhabdi
124	214.5	4.5	485	16	09KMX2	09KMX2 vibrlo chol
125	214.5	4.5	455	16	067715	067715 aquifex aeo
126	214.5	4.5	489	13	091781	091781 xenopus lae
127	214.5	4.5	494	4	09H3M0	09H3M0 homo sapien
128	214.5	4.5	514	5	076457	076457 aplysia cal
129	214	4.5	489	5	026041	026041 panulirus i
130	214	4.5	636	4	060576	060576 homo sapien
131	213.5	4.5	511	4	016322	016322 homo sapien
132	213.5	4.5	677	13	098TW3	098TW3 xenopus lae
133	213	4.5	503	11	097557	097557 rattus norv
134	212.5	4.5	499	6	09MYX3	09MYX3 oryctolagus
135	212.5	4.5	499	6	028293	028293 canis famli
136	212	4.5	577	5	016976	016976 aplysia cal
137	212	4.5	604	5	08SYL2	08SYL2 drosophila
138	211.5	4.5	476	6	008635	008635 bos taurus
139	211	4.5	204	11	099N66	099N66 mus musculu
140	211	4.5	278	16	082P47	082P47 salmonella
141	211	4.5	278	16	0827E6	0827E6 salmonella
142	211	4.5	503	11	09CZRI	09CZRI mus musculu
143	211	4.5	529	11	061923	061923 mus musculu
144	211	4.5	776	5	019464	019464 caenorhabdi
145	210	4.4	483	13	091829	091829 oncorhynch
146	208.5	4.4	659	13	057662	057662 xenopus lae
147	207.5	4.4	491	4	09BOJ1	09BOJ1 homo sapien
148	207.5	4.4	499	13	098TW4	098TW4 xenopus lae
149	207	4.4	521	5	095XV8	095XV8 caenorhabdi
150	207	4.4	583	5	09YXX0	09YXX0 halocynthia

ALIGNMENTS

RESULT 1
 0923N2
 AC 0923N2: PRELIMINARY: PRT: 842 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE	BM40117.3.1 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 1)).
GN	KCNQ2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Wall M.
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL450341; CAC40730.1; -
DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR003946; KCNQ1_channel.
DR	InterPro; IPR000636; M+channel_jlg.
DR	Pfam; PF00520; Ion_trans.1.
DR	Pfam; PF03520; KCNQ1_channel.1.
SQ	SEQUENCE 842 AA: 92928 MW; C62B86CA8988735 CRC64;
Query Match	
Best Local Similarity 48.4%; Pred. No. 2,7e-122; Length 842;	
Matches 414; Conservative 99; Mismatches 210; Indels 133; Gaps 23;	
QY	21 GAAAAAGGRLGSGMKVDSGRGVLLNSAARGDLLLGTAAATLGCGGGLRESRR 80
DB	9 GVPCTSGEKRLKVGFGVLDPGA-----PDSTRDGLALLIGSEAPK---RGSVLSKPT 59
QY	81 GGGAGMSLLGRLSTSSQSCRNVKRYRQNTLYNLEPRGAFVYHAFVLLVGC 140
DB	60 GGAGA-----GKP-----PKNAYFRKLQNLVYLEPRGAFVYHAFVLLVSC 106
QY	141 LILSVSTPEHTKLASSCLLLEFVMIIVGELFIRMSAGCCCRGQGRLEFRAR 200
DB	107 LVLSVSTIKREKSSGALYILETVIVGVEYFPRVMAAGCCCRGMRGLKFAFK 166
QY	201 PCGVDTYVLASIVASATQGNIFATSLRSIFLQILKMRMDRRGGTWKLLGVY 260
DB	167 PCGVDTIMVLASIVASATQGNIFATSLRSIFLQILKMRMDRRGGTWKLLGVY 226
QY	261 ASKELITMYIGFLVIFSSFLYILEVEKANKFEFSTYADALMMGTLLTIGYDKNPL 320
DB	227 ASKELITMYIGFLVIFSSFLYILEVEKANKFEFSTYADALMMGTLLTIGYDKNPL 286
QY	321 TWLGRLLSAGFALLGISFALPAGILSGFALKVQEOHROKHFERRRPAANLLOCVRS 380
DB	287 TWNGRLLAATFTLIGVSEFALPAGILSGFALKVQEOHROKHFERRRPAAGLISAVRF 346
QY	381 YAAD-----EKSVSIATWK--PILKALHLC-----SPT 406
DB	347 YATNLSRTDLHSTWOYERTVTPMYRLIPNLQLELRNLKSGLTFRKEPEPEPSP- 405
QY	407 NOKLSFERRMASPRGOSIKSROASVGD--RRSPSTDIYAEAGSPTKVQKMSFDRPRF 464
DB	406 SOKVSLKDRV-FSSPGMAKKGSPQAQVYRRSPSADQSIDSPSKPKMSFDRPRRT 464
QY	465 RSLRLKSSQPKFVIDADATLGTDDVYDEKGCOCQDVSEDLTPPLKTVYAIRIMKFRVA 524
DB	465 ROAFRIKGAASRQNSSEASLPGEDIVEDNKSCEFEYTEDLPGLKVISIRAVCVARFLVS 524
QY	525 KKKFKETLPRYDKVYIEQYSAGHLDMLCKIKSIQTRVDQLGQITSDKKSREKITA 584
DB	525 KKKFKESLRPYDMVYIEQYSAGHLDMLCKIKSIQTRVDQLGQITSDKKSREKITA 583
QY	585 HETTDLSMIGRYVKEKQVQSIIESKLCLELDIYQVLRKGSASALASALASQIPEPEC- 642
DB	584 TELPEPSSMGRGKVEKQVLSMEKIDFLVSIITO--RAG-----IPAEIEA 630
QY	643 -----EQTSYQSPVDSKDLGSAQNSGC---LSRSTANISRGLOFILLPNEFSQOT 692
DB	631 YFGAKEPEBPAPVHSPEDSRD---HADKHGCIKIVASTS-----TGOR 672
QY	693 FVALSPHMSQATQVYISQSDGSAVAATNTIANDINAPPAFTTQIPLPLA----- 747

Db 673 NYAAPPA-----IPPAOCPPS--TSWOOSHQHGTSYPVGDHSLVRIPPP-PAHERSL 722
 QY 748 -----IKHLPRPTLHPNPAAGLOESIDVTCTCLVASKENQVQAOSNLTKDRSM 795
 Db 723 SAVGGNNRSTEFRLRLEGTPACRPSREALKDSDTSTISPV-DHEELERSFGFSISOS- 780
 QY 796 RKSFDMGETILSVCP 811
 Db 781 KENLDALGSCYAANVP 796

RESULT 2
 OBR498
 ID 08R498 PRELIMINARY; PRT; 870 AA.
 AC 08R498:
 DT 01-JUN-2002 (TREMUREL. 21, Created)
 DT 01-JUN-2002 (TREMUREL. 21, Last sequence update)
 DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
 DE Potassium channel KCNQ2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Men H., Levitan I.B.;
 RT "Calmmodulin is an auxiliary subunit of KCNQ channels."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF490773; AAM09696.1;
 SQ SEQUENCE 870 AA; 95742 MW; 9C6106C27CE70C5F CRC64;

Query Match 38.1%; Score 1801.5; DB 11; Length 870;
 Best Local Similarity 46.8%; Pred. No. 1.3e-121;
 Matches 413; Conservative 100; Mismatches 211; Indels 159; Gaps 22;

QY 21 GAAAAAGGRLSGMKDVESEGRVLLNSAARGDGLLIGTRAATLGGGGGLRESRR 80
 Db 9 GYVPGTSGEKKLWGFGLDPGA-----PDSTRDGLALLINGSEAPK---RGSVLSKPT 59
 QY 81 GKGARMSLLGKPLSTYSSOSCRNNKRYRQNTLYNLEPRGNAFYHAFFVLLVGC 140
 Db 60 GGAGA-----GKP-----PKRNAFYRKLNFLYNLEPRGNAFYHAFFVLLVGC 106
 QY 141 LIIVSFTIPEHRTKLASSCLLIEFVMIYVGLFIIRMSAGCCCRGMGRRLRFARK 200
 Db 107 LVLSVFTIPEHRTKLASSCLLIEFVMIYVGLFIIRMSAGCCCRGMGRRLRFARK 166
 QY 201 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVNRDRRGGTWKLGSVY 260
 Db 167 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVNRDRRGGTWKLGSVY 226
 QY 261 AHSKELITAVYIGFLVLIFFSFLVYLVKDKANKFESTYADALMWGITLTITIGYDCKPL 320
 Db 227 AHSKELITAVYIGFLVLIFFSFLVYLVKDKANKFESTYADALMWGITLTITIGYDCKPL 286
 QY 321 TWIGRLSAGFALGISEFFALPAGILGSGFALKVOEQRORKEFRKRNPAAMLICVMS 380
 Db 287 TWIGRLSAGFALGISEFFALPAGILGSGFALKVOEQRORKEFRKRNPAAMLICVMS 346
 QY 381 YAAD-----EKSYSIATW----- 393
 Db 347 YATMLRSTDLHSTQWYERVTYVPMSSQOTYGASRLIPLNQLLENLKSKSLRPR 406
 QY 394 -----KPHLALHTGSP--TWOKLSFKERYMAMASPRGOSISRSQASVGD--RR 437
 Db 407 KEPQPEPSKGRKRCGLGCGCGHSSQKSLKRV--FSSPRGMAAKGKSPQATVRR 465
 QY 438 SPSTIDITAEQSPYVOKSMFNDRTFRPSRLIKSSQPKPVADATALCTDQVYDEKGCQ 497
 Db 466 SPADQSLDSDPSKVPKSMFSGDSRTROAFRIKGAARONSEKSLPEDIVEDKSKCN 525
 QY 498 CDVSVEDLTPLPLKTVIRAIRIMKRFHVAKRKFETLRPYDVKVDIEQYSAGHLDMLCRIKS 557

Db 526 CEFVTEDLTPGLKVSIRAVCMRFLVSKRKFESLPRYDWDVIEQYSAGHLDMLCRIKS 585
 QY 558 LOTRVDQIIIGKQITSDKSKREKITAHEHTDLSMGRVYKQVQIESKLDCLDI 617
 Db 586 LOSRDQIVGRGTTID-KORTGPAETTELPEDEPSMGRGKQVLSMEKKLDFLVS 644
 QY 618 YQVLEKSGSALALASFOIPEPEC-----EQTSDYQSPVSDKSLSSAQNOSC-- 666
 Db 645 YQV--RMG-----IPPAETELVFGAKPEPAAPYHSPDSND---HADKHCIT 688
 QY 667 -LSRSTSANISRGLOFLIPNEPSAOTFVALSPHMSQAQVPIQSQSGSAVAATNTIAN 725
 Db 689 KIVRSTSS-----TGQRMNYAAPPA-----IPPAOCPPS--TSWOOSHQ 724
 QY 726 QINTAKKPAAPPTLOIPLPLPA-----IKHLPRPTLHPNPAAGLOESI 768
 Db 725 RHGTSVGDHSGSVLRIPPP-PAHERSLSAVGGNNRSTEFRLRLEGTPACRPSREALKDSD 783
 QY 769 SDVITCLVASKENQVQAOSNLTKDRSMRKSFDMGETILSVCP 811
 Db 784 TSISIPSV-DHEELERSFGFSISOS-KENLDALGSCYAANVP 824

RESULT 3
 ID 0923N4 PRELIMINARY; PRT; 723 AA.
 AC 0923N4:
 DT 01-DEC-2001 (TREMUREL. 19, Created)
 DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)
 DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
 DE BM401L17.3.8 (potassium voltage-gated channel, subfamily O, member 2 (isoform 8)).
 GN KCNQ2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Wall M.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL450341; CAC40728.1;
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR000346; KCNQ1_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF03520; KCNQ1_channel.1.
 DR SEQUENCE 723 AA; 80540 MW; 0F8738B23EAD7DC3 CRC64;

Query Match 37.9%; Score 1795; DB 11; Length 723;
 Best Local Similarity 53.2%; Pred. No. 2.9e-121;
 Matches 394; Conservative 77; Mismatches 163; Indels 106; Gaps 18;

QY 21 GAAAAAGGRLSGMKDVESEGRVLLNSAARGDGLLIGTRAATLGGGGGLRESRR 80
 Db 9 GYVPGTSGEKKLWGFGLDPGA-----PDSTRDGLALLINGSEAPK---RGSVLSKPT 59
 QY 81 GKGARMSLLGKPLSTYSSOSCRNNKRYRQNTLYNLEPRGNAFYHAFFVLLVGC 140
 Db 60 GGAGA-----GKP-----PKRNAFYRKLNFLYNLEPRGNAFYHAFFVLLVGC 106
 QY 141 LIIVSFTIPEHRTKLASSCLLIEFVMIYVGLFIIRMSAGCCCRGMGRRLRFARK 200
 Db 107 LVLSVFTIPEHRTKLASSCLLIEFVMIYVGLFIIRMSAGCCCRGMGRRLRFARK 166
 QY 201 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVNRDRRGGTWKLGSVY 260
 Db 167 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVNRDRRGGTWKLGSVY 226
 QY 261 AHSKELITAVYIGFLVLIFFSFLVYLVKDKANKFESTYADALMWGITLTITIGYDCKPL 320
 Db 227 AHSKELITAVYIGFLVLIFFSFLVYLVKDKANKFESTYADALMWGITLTITIGYDCKPL 286

```

QY 321 TWIGLISAGFLLIGSPALPAGILIGSGFALKVOEHOHOKHEKRRBNPAANLIGCWRS 380
D 287 TWNGFLLAATFLLIGVSPFALPAGILIGSGFALKVOEHOKHEKRRBNPAAGLIGSAWR 346
QY 381 YAAD-----EKSVIATWK--PHLKALITTC-----SPT 406
D 347 YATINSTRDLHSTWQYERTVTVPMRLIPNLQLELLNLNKSGLTFKEQPDESP- 405
QY 407 NOKLSFEKRVNRAASRGOSIKRSKASVGD--KRSPETDITAECSPIKVKVOSMFNDRTF 464
D 406 SOKVSLKRV--FSSPRGMAAKGKSPQAOQTVRRSPADSLDSDPSKRVKSWFGRSRP 464
QY 465 RPSLRKSSOPKPYVDADTALGTDDVYDEKGGQCDVSEDLPTPLTVYRAIRIKMFYA 524
D 465 ROAFRIKGAASRONSEASLPEPDIYEDBNKSCNCEVFETDLPLGLKVSIRAVCMFVLS 524
QY 525 KRKRKRETRPDKVYIEQYSAGHLDMLCRIKSLQTRVQDILGKGITSDKRSREKITAE 584
D 525 KRKRKRESTRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVQIYGRGPTTD--KURTKGPAE 583
QY 585 HETDDLSMLRRVYVEKOVOSIESKLDLIDYIOVULKGSASALALASFQIPREC-- 642
D 584 TELEDPEPMGRKGVKEQVOLSMEKKLDPLVSIYQ--RMG-----IIPAEETA 630
QY 643 -----EQTSDYOSPVNDKDLSSGAONSGC--LSRSTANISRGLOPILTPNERSAOT 692
D 631 YFGAKEPPAPAPYHPEDSRD--HADKHGCIITIKIVRSTSS-----TGQR 672
QY 693 FYALSPTHSQATOVPIOS 712
D 673 NYAAPPAI--PPAOCPPSTS 690

```

Query	Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	21	GAATAAAGGGGGLSGMKDVEGRRRVLVLSNAAGDGLLLGTRATVGGGGGGLRESTR	80	37.98; 1791.5; 48.08; Pred. No. 6.5e-121; 227; 217; 127; 22					
DB	9	GVPVTSGEKKLKAVGVLDPGA-----PDSTDGALLINGSEPK--RGSVLSKPRPT	59						
QY	81	GKQAGRSLLGKPLSTYSOSCRNNVYKRYRQNTLYNLEPRGAFYTHAVFLVPGC	140						
DB	60	GGAGA-----GKP-----PKNNAYRKQNFNLVNLLEPRGAFYTHAVFLVPGC	106						
QY	141	LILSVSTIEBHKKLASSCLLIEFVNIIVVGFETIRMSAGCCCRYRGMQGLRFARK	200						

[illegible]

RESULT 5		
0923N5		
ID	0923N5	PRELIMINARY; PRT; 759 AA.
AC	0923N5;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	BM40117.3.11 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 1)).	
DE	KCNQ2.	
CN		
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Wall M.,	
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AL450341; CAC40727.1; -	
DR	InterPro; IPR001622; K+channel_pore.	
DR	InterPro; IPR003946; KCNQ1_channel.	

DR InterPro: IPR000636; M-channel_nlg.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF03520; KCNQ1_channel_1.
 DR SEQUENCE 759 AA; 84494 MW; D828BE47D0DE3C4A CRC64;

Query Match 37.3%; Score 1767; DB 11; Length 759;
 Best Local Similarity 50.8%; Pred. No. 3.3e-119;
 Matches 394; Conservative 77; Mismatches 163; Indels 142; Gaps 19;

OY 21 GAAAAAGGRLSGMKDVGSGRGLVLSAARGDGLLGLTRAATLGGGGGLRESRR 80
 DB 9 GYPTSEKRLKLVFVGLDPGA-----PDSTRDGLALLIAGEAAR---RGSVLSPRT 59
 OY 81 GKGARMSLGRPLSTSSQCRNVKRYRNVNYLVNERPGMAFIYHAEVLLVFGC 140
 DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFVLEPRGMFIYHAEVLLVFGC 106
 OY 141 LILSVFTIPHTKLASSCLLLEFMYVFGLEFIIRIMSAGCCCRYRMOGRLEPARK 200
 DB 107 LVLSEFTIKEYEKSEGLTYLEIYIVFGEYEVRIWMAACCCCRKRWGRGLPARK 166
 OY 201 PFCVIDIYLVASIVASAKTOGNIFATSLNSLRLOILRMVMDRGGTWMKLLGSVY 260
 DB 167 PFCVIDIYLVASIVASAKTOGNIFATSLNSLRLOILRMVMDRGGTWMKLLGSVY 226
 OY 261 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTITIGYGDPTL 286
 OY 321 TWLGRLLSAGFALLIGISFPALPAGILGSGFALKVQEOHROKHREKRNPAANTLQCVWRS 380
 DB 287 TWNGRLAATFTLLIGVSFPALPAGILGSGFALKVQEOHROKHREKRNPAANTLQCVWRS 346
 OY 381 YAAD-----EKVSIAATWK--PHLKALHTC-----SPT 406
 DB 347 YATNLSRTDLHSTWQYERTVYPMYRLIPLNQLELLRLNLSKSGLTFRKEPQPEPSP 405
 OY 407 NOKLSFERVRMASPGOSIKSROASVGD--RRSPDTITAEGSPRTVKOKSMSPNDRTRE 464
 DB 406 SOKVSLKADNV-FSSPGMAKKGSPQAOQTVRRSPADOSLSDSPSKVPSMSGDSKRT 464
 OY 465 RSLRLKSSQPKPVYIDADTALGTDVYDEKGCOCODVSEDLTPRLKTVIRAIRIMKTHVA 524
 DB 465 RSLRLKSSQPKPVYIDADTALGTDVYDEKGCOCODVSEDLTPRLKTVIRAIRIMKTHVA 524
 OY 525 KKKFKETLAPYDKVIEQYSAGHLDMLSRKISLQSRIDMVGPPRSTPRHKKYPTKGP 584
 DB 525 KKKFKETLAPYDKVIEQYSAGHLDMLSRKISLQSRIDMVGPPRSTPRHKKYPTKGP 584
 OY 561 -----RVDOILGQITSDKSKREKITAHEHTDDLSMLGRVNVKEKOVOSIE 608
 DB 585 TAPRSRPOYSRPVDDIVGRPTITD-KDRTKGAPELELPEDPSMGRGLGVEKOVLSME 643
 OY 609 SKLDCLDIYQOVLKRGASALALASFOIPPEFC-----EOTS DYOSPVDSKDLISG 659
 DB 644 KKLDFLVSYITQ--RMG-----IPPAETEAFFGAKEPPAPYHSPEDSRD--- 687
 OY 660 SAONSGC-----LSNSTANISRGLOFILTTPNEFSAGTYALSPTMHSATQVPIQS 712
 DB 688 HADKHGCIKIYVSTSS-----TGQRNYAAPRAL--PPACCPSTPS 726

RESULT 6

OY 0923N6 PRELIMINARY; PRT: 747 AA.
 AC 0923N6;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE BM401L17.3.10 (potassium voltage-gated channel, subfamily O, member 2 (isoform 10)).
 GN KCNQ2.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Wall M.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL450341; CAC40726.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF03520; KCNQ1_channel_1.
 DR SEQUENCE 747 AA; 83118 MW; E5714B98A18A7E60 CRC64;

Query Match 37.0%; Score 1753; DB 11; Length 747;
 Best Local Similarity 51.0%; Pred. No. 3.3e-118;
 Matches 389; Conservative 77; Mismatches 170; Indels 126; Gaps 18;

OY 21 GAAAAAGGRLSGMKDVGSGRGLVLSAARGDGLLGLTRAATLGGGGGLRESRR 80
 DB 9 GYPTSEKRLKLVFVGLDPGA-----PDSTRDGLALLIAGEAAR---RGSVLSPRT 59
 OY 81 GKGARMSLGRPLSTSSQCRNVKRYRNVNYLVNERPGMAFIYHAEVLLVFGC 140
 DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFVLEPRGMFIYHAEVLLVFGC 106
 OY 141 LILSVFTIPHTKLASSCLLLEFMYVFGLEFIIRIMSAGCCCRYRMOGRLEPARK 200
 DB 107 LVLSEFTIKEYEKSEGLTYLEIYIVFGEYEVRIWMAACCCCRKRWGRGLPARK 166
 OY 201 PFCVIDIYLVASIVASAKTOGNIFATSLNSLRLOILRMVMDRGGTWMKLLGSVY 260
 DB 167 PFCVIDIYLVASIVASAKTOGNIFATSLNSLRLOILRMVMDRGGTWMKLLGSVY 226
 OY 261 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTITIGYGDPTL 286
 OY 321 TWLGRLLSAGFALLIGISFPALPAGILGSGFALKVQEOHROKHREKRNPAANTLQCVWRS 380
 DB 287 TWNGRLAATFTLLIGVSFPALPAGILGSGFALKVQEOHROKHREKRNPAANTLQCVWRS 346
 OY 381 YAAD-----EKVSIAATWK--PHLKALHTCSPNOK--LSFERVR--MAS 420
 DB 347 YATNLSRTDLHSTWQYERTVYPMYRLIPLNQLELLRLNLSKSGLTFRKEPQPEPSP 406
 OY 421 PRGOSIKSROASVGD--RRSPDTITAEGSPRTVKOKSMSPNDRTRE 478
 DB 407 PRGMAKKGSPQAOQTVRRSPADOSLSDSPSKVPSMSGDSKRTQAFRIGASARON 466
 OY 479 IDADTALGTDVYDEKGCOCODVSEDLTPRLKTVIRAIRIMKTHVAKRKETLRPDYK 538
 DB 467 SEASLPGEDIVEDNKCNCDEFYTEDTLPLKYSIRAVCYMRPLVSKRKESLRPDYK 526
 OY 539 DVIEQYSAGHLDMLSRKISLQSRIDMVGPPRSTPRHKKYPTKGPAPRSRPOYSRPV 586
 DB 527 DVIEQYSAGHLDMLSRKISLQSRIDMVGPPRSTPRHKKYPTKGPAPRSRPOYSRPV 586
 OY 563 DOILGQITSDKSKREKITAHEHTDDLSMLGRVNVKEKOVOSIEKDLDCLDIYQOVL 622
 DB 587 DOIVGRPTITD-KDRTKGAPELELPEDPSMGRGLGVEKOVLSMEKDLDFLVSYITQ-- 643
 OY 623 RKGASALALASFOIPPEFC-----EOTS DYOSPVDSKDLISGSAONSGC--LSRS 670
 DB 644 RMG-----IPPAETEAFFGAKEPPAPYHSPEDSRD---HADKHGCIKIYVRS 689
 OY 671 TSANISRGLOFILTTPNEFSAGTYALSPTMHSATQVPIQS 712
 DB 690 TSS-----TGQRNYAAPRAL--PPACCPSTPS 714

RESULT 7

0923N0
AC 0923N0 PRELIMINARY; PRT: 623 AA.
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BM401L17.3.5 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 5)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN NCBINucleotide
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL450341; CAC40732.1; -
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF03520; KCNQ1_channel.1.
SO SEQUENCE 623 AA; 69764 MW; C05D2F023DA32D26 CRC64;

Query Match 34.1%; Score 1614; DB 11; Length 623;
Best Local Similarity 57.3%; Pred. No. 2.9e-108;
Matches 333; Conservative 66; Mismatches 122; Indels 60; Gaps 10;

QY 21 GAAAAAGGRLGSGMKDVESSGRVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
DB 9 GYPTSGEKKLKVGFGLDPGA-----PDSTRDGLALLGSEAPK--RGSVLSKPR 59
QY 81 GKQAGARSLGKPLSTYSOSCRNRYRVRVNYLVNLRPRGAFYHAFFLVFPGC 140
DB 60 GGAGA-----GKP-----PKRNATYKLNFLVNLPRGMAFYHAFFLVFPGC 106
QY 141 LILVSTIPEHRTKLASSCLLLEFVMIYVGEFIIRIWSAGCCCRYRGMOGRLEFARK 200
DB 107 LVLSVESTIKEYEKSESGALYILEYIVVGEYEVFVMAAGCCCRYRGMRGLKFAK 166
QY 201 PCVIDITVLASIAVSATQGNIFATSAIRSLRFLOILNVRMDRGRGTWKLGSVY 260
DB 167 PCVIDIMVLASIAVSATQGNIFATSAIRSLRFLOILNVRMDRGRGTWKLGSVY 226
QY 261 AHSKELITAMYGIFLVLIFFSFLVYLVLEKDNKFEFSTYADALMNGITLTIGYDRTPL 320
DB 227 AHSKELITAMYGIFLVLIFFSFLVYLVLEKDNKFEFSTYADALMNGITLTIGYDRTPL 286
QY 321 TWLGRLLSAGFALLGISFEPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIOCVR 380
DB 287 TWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEOHROKHFEKRRNPANLIOCVR 346
QY 381 YAAD-----EKSVSIAATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRLDHTSWOYERTVPMYRLIPNLQLELLRLNLSKSGLTFRKEPPEPSP- 405
QY 407 NOKLSFEKRVMAASPRGOSITKSROASVGD--RRSPSTDIITAEGSPTKVQKSMSEFNDRT 464
DB 406 SOKVSLKDRY--FSSPRGMAAKGKSPQAGVVRSPADQSLDSDPSKVPKSMSEFNDRT 464
QY 465 RPSRLKSSQKRPVADADALGTDVYDEKGCOCVSVEDLTPLKTVIRAIKMFHVA 524
DB 465 ROAFRIKGAASRONSEASLPGEDIVEDNKSCEFEYEDLTPLKTVIRAIKMFHVA 524
QY 525 KRKFETLRPYDVYKDIYEOYSAGHLDMLCRISLQTRVDQI 565
DB 525 KRKFETLRPYDVYKDIYEOYSAGHLDMLCRISLQTRVDQI 565

RESULT 8
0923N3 PRELIMINARY; PRT: 570 AA.

AC 0923N3
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BM401L17.3.3 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 3)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN NCBINucleotide
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL450341; CAC40729.1; -
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF03520; KCNQ1_channel.1.
SO SEQUENCE 570 AA; 68335 MW; 6BEDA2953C1C7178 CRC64;

Query Match 34.1%; Score 1613; DB 11; Length 570;
Best Local Similarity 57.7%; Pred. No. 3e-108;
Matches 333; Conservative 64; Mismatches 120; Indels 60; Gaps 10;

QY 21 GAAAAAGGRLGSGMKDVESSGRVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
DB 9 GYPTSGEKKLKVGFGLDPGA-----PDSTRDGLALLGSEAPK--RGSVLSKPR 59
QY 81 GKQAGARSLGKPLSTYSOSCRNRYRVRVNYLVNLRPRGAFYHAFFLVFPGC 140
DB 60 GGAGA-----GKP-----PKRNATYKLNFLVNLPRGMAFYHAFFLVFPGC 106
QY 141 LILVSTIPEHRTKLASSCLLLEFVMIYVGEFIIRIWSAGCCCRYRGMOGRLEFARK 200
DB 107 LVLSVESTIKEYEKSESGALYILEYIVVGEYEVFVMAAGCCCRYRGMRGLKFAK 166
QY 201 PCVIDITVLASIAVSATQGNIFATSAIRSLRFLOILNVRMDRGRGTWKLGSVY 260
DB 167 PCVIDIMVLASIAVSATQGNIFATSAIRSLRFLOILNVRMDRGRGTWKLGSVY 226
QY 261 AHSKELITAMYGIFLVLIFFSFLVYLVLEKDNKFEFSTYADALMNGITLTIGYDRTPL 320
DB 227 AHSKELITAMYGIFLVLIFFSFLVYLVLEKDNKFEFSTYADALMNGITLTIGYDRTPL 286
QY 321 TWLGRLLSAGFALLGISFEPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIOCVR 380
DB 287 TWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEOHROKHFEKRRNPANLIOCVR 346
QY 381 YAAD-----EKSVSIAATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRLDHTSWOYERTVPMYRLIPNLQLELLRLNLSKSGLTFRKEPPEPSP- 405
QY 407 NOKLSFEKRVMAASPRGOSITKSROASVGD--RRSPSTDIITAEGSPTKVQKSMSEFNDRT 464
DB 406 SOKVSLKDRY--FSSPRGMAAKGKSPQAGVVRSPADQSLDSDPSKVPKSMSEFNDRT 464
QY 465 RPSRLKSSQKRPVADADALGTDVYDEKGCOCVSVEDLTPLKTVIRAIKMFHVA 524
DB 465 ROAFRIKGAASRONSEASLPGEDIVEDNKSCEFEYEDLTPLKTVIRAIKMFHVA 524
QY 525 KRKFETLRPYDVYKDIYEOYSAGHLDMLCRISLQTRVDQI 561
DB 525 KRKFETLRPYDVYKDIYEOYSAGHLDMLCRISLQTRVDQI 561

RESULT 9
0923M9 PRELIMINARY; PRT: 473 AA.
AC 0923M9
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE BM401L17.3.7 (potassium voltage-gated channel, subfamily Q,
 member 2 (isoform 7)).
 GN KCNO2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Wall M.;
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL450341; CA040733.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans. 1.
 DR SEQUENCE 473 AA; 52682 MW; 3AFC95E6946FA57 CRC64;

Query Match 26.1%; Score 1234; DB 11; Length 473;
 Best Local Similarity 58.2%; Pred. No. 6.4e-81;
 Matches 235; Conservative 51; Mismatches 98; Indels 34; Gaps 9;

OY 21 GAAAAAGGGRGCGMKVDSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESRR 80
 DB 9 GYVPGTSGEKKLVGFGLDGA-----PDSTRDGAALLINGSEAPK---RGSVLSKRPRT 59
 OY 81 GKOGAKMSLLGKPLSTYSOSGCRNRNRYRYRYQNTLYNLEPRRGMAFYHAFFVLLVFGC 140
 DB 60 GGAGA-----GKP-----PKRNAFYRKLNFLNLYLERPRGMAFYHAFFVLLVFGC 106
 OY 141 LILSVSTIPEHTKLIASSCLLLEFVMIYVGFLEFIRIWSAGCCCRYGMRGRLPARK 200
 DB 107 LVLSVSTIPEHTKLIASSCLLLEFVMIYVGFLEFIRIWSAGCCCRYGMRGRLPARK 166
 OY 201 PFCVIDTIVLIASIVASAKTQGNIFATSLRSLRFLQILRMVMDRGGTCKLLGVSYY 260
 DB 167 PFCVIDTIVLIASIVASAKTQGNIFATSLRSLRFLQILRMVMDRGGTCKLLGVSYY 226
 OY 261 AHSKELITANYIGLVLISSFLVLYVEKDKANKESTYADALMWGTITLTITGYGDKTFL 320
 DB 227 AHSKELITANYIGLVLISSFLVLYVEKDKANKESTYADALMWGTITLTITGYGDKTFL 286
 OY 321 TWIGRLSAGPALGISFFALPAGILSGFALKVOEOROKHFEKRRNPAAMLIOCVMRS 380
 DB 287 TWIGRLSAGPALGISFFALPAGILSGFALKVOEOROKHFEKRRNPAAMLIOCVMRS 346
 OY 381 YAADEKSVSI-ATWKPMLKALHTCSPTNOKLSFKERVMASPRGO-----SIKSRQASVG 434
 DB 347 YATNLSTDLHSTQWYERVTVPWYSSQOTQYGAS-RLIPPLNQLLELLRLNLSK-SGLT 404
 OY 435 DRSPSTDTAEGSPTKY 452
 DB 405 FRKEPQ---PEPSPRV 418

RESULT 10

ID Q967F8 PRELIMINARY; PRT; 692 AA.
 AC Q967F8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE C25B8.1 protein.
 GN C25B8.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peioderineae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;

RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA W11cox L.;
 RT "The sequence of C. elegans cosmid C25B8."
 RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41556; AAK39192.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNO1_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF03520; KCNO1_channel. 1.
 DR SEQUENCE 692 AA; 77486 MW; 6A69D9B21D059BF8 CRC64;

Query Match 25.9%; Score 1226; DB 5; Length 692;
 Best Local Similarity 41.1%; Pred. No. 4.3e-80;
 Matches 276; Conservative 121; Mismatches 184; Indels 90; Gaps 17;

OY 75 LRSRRGKQKARMSLLGKPLSTYSOSGCRNRNRYRYRYQNTLYNLEPRRGMAFYHAFFV 133
 DB 54 LHDSEBGR--KMSLVKPLTY--KNYRDFRRMKNHNLPRGRGMAFYHAFFV 108
 OY 134 FLVFGCLISVSTIPEHTKLIASSCLLLEFVMIYVGFLEFIRIWSAGCCCRYGMRGW 193
 DB 109 LPMVIMCLALSVSTIPEHTKLIASSCLLLEFVMIYVGFLEFIRIWSAGCCCRYGMRGW 168
 OY 194 RLFPARRPFCVIDTIVLIASIVASAKTQGNIFATSLRSLRFLQILRMVMDRGGTCKLL 253
 DB 169 RLFPARRPFCVIDTIVLIASIVASAKTQGNIFATSLRSLRFLQILRMVMDRGGTCKLL 228
 OY 254 LLSGVYAAHSEKELITANYIGLVLISSFLVLYVEKDKANKESTYADALMWGTITLTIT 313
 DB 229 LLSGVYAAHSEKELITANYIGLVLISSFLVLYVEKDKANKESTYADALMWGTITLTIT 288
 OY 314 YGDKTPTLWIGRLSAGPALGISFFALPAGILSGFALKVOEOROKHFEKRRNPAAML 373
 DB 289 YGDKTPTLWIGRLSAGPALGISFFALPAGILSGFALKVOEOROKHFEKRRNPAAML 348
 OY 374 IQCVWRSYAADEKSVSIATWKPMLKALHTCSPTNOKLSFKERVMASPRGO----- 427
 DB 349 IQCVWRSYAADEKSVSIATWKPMLKALHTCSPTNOKLSFKERVMASPRGO----- 408
 OY 428 SROASVDRRS-----PSDTITAEGSTTKYKQKSMFSDRTFRPSLR-- 469
 DB 409 SROASVDRRS-----PSDTITAEGSTTKYKQKSMFSDRTFRPSLR-- 468
 OY 470 ----LKSQKRPV---IDADTALCTDVIDYDEKGGCCDVSDVLTPLTVIRAIRIMFH 522
 DB 469 DSVLQSRMLAPSAHDEEAVG---YQPO-----TIEFPTALNCVVAIRIOLL 518
 OY 523 VAKRKEKTLRPYVVKVYIEOYSAGHLDMLCRISLQTRVQIILGQOTISKKREKIT 582
 DB 519 VAKRKEKTLRPYVVKVYIEOYSAGHLDMLCRISLQTRVQIILGQOTISKKREKIT 570
 OY 583 AEHTTDDLSMLGVVYVEKOVOSTESKLDLIDYQOVLLRKGASALATLASFQIIPPEC 642
 DB 571 PK-----ISMFTTALILETTVGKMDKDLDMVENLM-----GRASQRFESQNSP--- 616
 OY 643 EGTSDYOSPVDSKDLSSAQNCSLSNSTANISRGLOFILTPNFSAQTLYALSPTHMS 702
 DB 617 --RGFESEPTSAQ-----DLTRSRSMVSTDMEM-----YTARSH---SPGYHG 656
 OY 703 QATVPPISSQSD 713

Db 657 DARP1-IAQID 666

RESULT 11

0923M8 PRELIMINARY; PRT: 347 AA.

AC 0923M7;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)

DE BM401117.3.6 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 6)).

GN KCNO2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA Wall M.;

RP SEQUENCE FROM N.A.

Query Match

Best Local Similarity 25.3%; Score 1199; DB 11; Length 347;

Matches 237; Conservative 33; Mismatches 63; Indels 22; Gaps 4;

21 GAAAAAGGRLGSGMKDVGSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESRR 80

9 GYVPGTSGEKKLVGVGLDPGA-----PDSTRGALLIAGEAPK---RGSVLSKPT 59

81 KGOGARMSLKGPLSTSSQCRNRVRYRQNYLVLEPRGMATFYHAFVFLVFGC 140

60 GGAGA-----GKP-----PKRNAFYRKQNLNLYNLEPRGMATFYHAYVFLVFGC 106

141 LLSVFTIPERTKLASSCLLLEFVMIVFGLFEIIRMSAGCCCRGRMGRRLRFARK 200

107 LVLSVFTIKETKESSEGALYILEYIVFGEYFVRIMAAAGCCCRGRMGRRLRFARK 166

201 PCVVIDIVLIASIAVYSAKTQGNIPATSLRSRLFLQILRMVMDRGRGTWKLGSVY 260

167 PCVVIDIVLIASIAVYSAKTQGNIPATSLRSRLFLQILRMVMDRGRGTWKLGSVY 226

261 AHSKELITWYIGFLVLIFFSFLVLYVEKANKERSTVADALMWGITLTITIGYDKPTL 320

227 AHSKELITWYIGFLVLIFFSFLVLYVEKANKERSTVADALMWGITLTITIGYDKPTL 286

321 TWLGRLLSAGFALLGISFPALPAGILGSGFALKVOEORHOKHFEKRNPANLIQ 375

287 TWNGRLAATFTLLIGVSFFALPAGILGSGFALKVOEORHOKHFEKRNPANLIQ 341

RESULT 12

0923M8 PRELIMINARY; PRT: 349 AA.

AC 0923M8;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)

DE BM401117.3.2 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 2)).

GN KCNO2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA Wall M.;

RP SEQUENCE FROM N.A.

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL450341; CAC40734.1; -

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR000636; M+channel_nlg.

DR Pfam: PF00520; Ion_trans; 1.

SQ SEQUENCE 349 AA; 38683 MW; A35A50C777C54EC2 CRC64;

Query Match

Best Local Similarity 25.3%; Score 1199; DB 11; Length 349;

Matches 237; Conservative 33; Mismatches 63; Indels 22; Gaps 4;

21 GAAAAAGGRLGSGMKDVGSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESRR 80

9 GYVPGTSGEKKLVGVGLDPGA-----PDSTRGALLIAGEAPK---RGSVLSKPT 59

81 KGOGARMSLKGPLSTSSQCRNRVRYRQNYLVLEPRGMATFYHAFVFLVFGC 140

60 GGAGA-----GKP-----PKRNAFYRKQNLNLYNLEPRGMATFYHAYVFLVFGC 106

141 LLSVFTIPERTKLASSCLLLEFVMIVFGLFEIIRMSAGCCCRGRMGRRLRFARK 200

107 LVLSVFTIKETKESSEGALYILEYIVFGEYFVRIMAAAGCCCRGRMGRRLRFARK 166

201 PCVVIDIVLIASIAVYSAKTQGNIPATSLRSRLFLQILRMVMDRGRGTWKLGSVY 260

167 PCVVIDIVLIASIAVYSAKTQGNIPATSLRSRLFLQILRMVMDRGRGTWKLGSVY 226

261 AHSKELITWYIGFLVLIFFSFLVLYVEKANKERSTVADALMWGITLTITIGYDKPTL 320

227 AHSKELITWYIGFLVLIFFSFLVLYVEKANKERSTVADALMWGITLTITIGYDKPTL 286

321 TWLGRLLSAGFALLGISFPALPAGILGSGFALKVOEORHOKHFEKRNPANLIQ 375

287 TWNGRLAATFTLLIGVSFFALPAGILGSGFALKVOEORHOKHFEKRNPANLIQ 341

RESULT 13

09BX08 PRELIMINARY; PRT: 409 AA.

AC 09BX08;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)

DE BA358D14.1.1 (Potassium voltage-gated channel, KQT-like subfamily, member 2, isoform 1) (Fragment).

GN KCNO2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RA LLOYD D.;

RP SEQUENCE FROM N.A.

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL353658; CAC36009.1; -

DR HSSP: Q54397; 1BL8.

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR003091; K channel.

DR InterPro: IPR000636; M+channel_nlg.

DR Pfam: PF00520; Ion_trans; 1.

DR PRINTS: PR00169; KCHANNEL.

FT NON_TER

FT NON_TER

SQ SEQUENCE 409 AA; 45645 MW; 5D828C0EFA31649A CRC64;

Query Match

Best Local Similarity 25.0%; Score 1181; DB 4; Length 409;

Matches 238; Conservative 40; Mismatches 61; Indels 64; Gaps 6;

134 FLVFGCLLSVFTIPERTKLASSCLLLEFVMIVFGLFEIIRMSAGCCCRGRMGR 193

1 FLVFGCLLSVFTIPERTKLASSCLLLEFVMIVFGLFEIIRMSAGCCCRGRMGR 60

```

QY 194 RLRFARKPCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAK 253
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RLRFARKPCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAK 120
QY 254 LIGSVVYAHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIG 313
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LIGSVVYAHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIG 180
QY 314 YGKRTPLTWIGRLISAGFALLGISFFALPAGILGSGFALKVOEOROKHFEKRRRPAANL 373
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 YGKRTPLTWIGRLISAGFALLGISFFALPAGILGSGFALKVOEOROKHFEKRRRPAANL 240
QY 374 IGVWRSYAAD-----EKSVSIATWK-----PHLKALHT----- 402
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 IGVWRSYAAD-----EKSVSIATWK-----PHLKALHT----- 300
QY 403 -----CSP--TNQKLSFEKRYVMASPRCOSIKRQAS 432
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KSGIAFRKDDPPPPSPKSGSPCRGPGCCGPRSSQKVKSLKDRV-FSSPRGVAAKGGKSP 359
QY 433 VGD--RRSPSTDTAEKSPTRKVKQSMSPNDTRFRPRLKSS 473
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 QAOCTVRRSPSADSDLEDSFSKVPKSMSPGDRSRARQAFRIKA 402

```

RESULT 14

```

Q9BX07 PRELIMINARY: PRT: 294 AA.
ID 09BX07
AC 09BX07
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE BA35BD14.1.2 (Potassium voltage-gated channel, KQT-like subfamily,
member 2, isoform 2) (Fragment).
GN KCNQ2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL353658; CAC36010.1; -.
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR000636; M-channel_nlg.
DR Pfam: PF00520; Ion_trans.1.
DR PRINTS: PR00169; KCHANNEL.
FT NON_TER
SQ SEQUENCE 294 AA; 33649 MW; 6A680F1BEC05FB45 CRC64;

```

Query Match 22.5%; Score 1064.5; DB 4; Length 294;
 Best Local Similarity 76.3%; Pred. No. 5.8e-69;
 Matches 200; Conservative 24; Mismatches 37; Indels 1; Gaps 1;

```

QY 134 FLVFGCLLISVFSTIPEHTKLASSCLLIEFMVIVGLETITIRMSAGCCCRKGMG 193
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 FLVFGCLLISVFSTIPEHTKLASSCLLIEFMVIVGLETITIRMSAGCCCRKGMG 60
QY 194 RLRFARKPCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAK 253
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RLRFARKPCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAK 120
QY 254 LIGSVVYAHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIG 313
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LIGSVVYAHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIG 180
QY 314 YGKRTPLTWIGRLISAGFALLGISFFALPAGILGSGFALKVOEOROKHFEKRRRPAANL 373
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 YGKRTPLTWIGRLISAGFALLGISFFALPAGILGSGFALKVOEOROKHFEKRRRPAANL 240

```

```

QY 374 IGVWRSYAADKESVSI-ATWK 394
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 IGVWRSYAADKESVSI-ATWK 262

```

RESULT 15

```

Q923M6 PRELIMINARY: PRT: 338 AA.
ID 0923M6
AC 0923M6
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE BM401IL17.3.4 (Potassium voltage-gated channel, subfamily O,
member 2 (isoform 4)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL450341; CAC40736.1; -.
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR000636; M-channel_nlg.
DR Pfam: PF00520; Ion_trans.1.
SQ SEQUENCE 338 AA; 37483 MW; 82520B7C1C01FA2F CRC64;

```

Query Match 22.0%; Score 1040; DB 11; Length 338;
 Best Local Similarity 63.8%; Pred. No. 4.3e-67;
 Matches 206; Conservative 33; Mismatches 62; Indels 22; Gaps 4;

```

QY 21 GAAAAAGGGRILSGMKDVGSGRGRVLLNSAARDGGLITRAATLGGGGGLREGSR 80
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 GVPYGTSGEKKLVGVGLDPA-----PDSTDGALLINGSEAPK---RGSVLSKRT 59
QY 81 GKGQARMSLIGKPLSYTSSQSCRNNVYRRQVLYLVLEPRGMATYHAEVFLVFGC 140
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GGAGA-----GKP-----PKRNAYRKQNFYLVNLEPRGMATYHAEVFLVFGC 106
QY 141 LILSVSTIPEHTKLASSCLLIEFMVIVGLETITIRMSAGCCCRKGMGRLRFARK 200
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 107 LILSVSTIPEHTKLASSCLLIEFMVIVGLETITIRMSAGCCCRKGMGRLRFARK 166
QY 201 PCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAKLGSVY 260
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 167 PCVIDITVLIASIAVSAKQNIATFATLSRLSLRFLQILRMVMDRGGTAKLGSVY 226
QY 261 AHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIGYDKTPL 320
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 227 AHSKELITAMVIGFLVLIFFSFLVLYVEKDANKKESTYADALMWGTTLTITIGYDKTPL 286
QY 321 TWIGRLISAGFALLGISFFALPA 343
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 287 TWIGRLISAGFALLGISFFALPA 309

```

RESULT 16

```

Q9XWG9 PRELIMINARY: PRT: 645 AA.
ID 09XWG9
AC 09XWG9
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Y34G9A.3 protein.
GN Y34G9A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peioderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Same R.
 RN Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; AL032648; CAA21699.1; .
 DR HSSP; Q54397; 1BL8.
 DR InterPro: IPR000048; IO_region.
 DR InterPro: IPR001622; Kchannel_pore.
 DR InterPro: IPR003846; KCMOL_channel.
 DR InterPro: IPR003091; K_channel.
 DR Pfam; PF00520; Ion_trans.1.
 DR Pfam; PF00612; IO.1.
 DR Pfam; PF03520; KCMOL_channel.1.
 DR PRINTS; PR00169; KCHANNEL.
 DR SMART; SM00015; IO.1.
 DR SEQUENCE 645 AA; 73569 MW; B30BA20FCOD7AEB8 CRC64;
 SQ
 Query Match 20.1%; Score 950; DB 5; Length 645;
 Best Local Similarity 36.2%; Pred.No.3,7e-60;
 Matches 247; Conservative 92; Mismatches 175; Indels 168; Gaps 22;
 108 YRRVONTLYNVERRGV-AFIYHAFVFLVCGLLISVFSTPEHTKLASSCLLIEFV 166
 3 YRAM---IYNCLERTGKCELYHFSVFLIVLCILSLVSTVEHSHFAELLYIEIV 59
 167 MIYVGFLEFIRISAGCCCRKRGOGRLRFRKPCVT----- 205
 60 LVFFSVFELVRLMSAGCRKTYIGYGRLEKFRKPTLLIGREGRLDLRLHGGPS 119
 206 -----DTI-----VLASTAVS--AKTQGNIFATSA-----L.231
 120 FCGKRDAGDIYASSEDAPRSAGNWEIRISKIPKIEFSLKIGTFENFMNFOQF 179
 232 RSLRFQILR-----MVMEDRGKTWKLKLSGVYVAHSE 265
 180 RKLFEFSKILKNLAGRVHWGSAATPSSGDPDLDVCGFRLHQLASRRLLGSVFTHROE 239
 266 LITAWYIGFLVLISSFLVLYVER-----DANKESTYADALMWGTTTLTIGYDKTPL 320
 240 LITLTYIGFLGLISSYFVLAEKDHIGVDGROAFSTYADALMWGVITMTTIGYGVVPQ 299
 321 TWIGRLISAGFALLGISFPALPAGILGSEFALKVOOHOKHPEKRRNPANLLOCVRS 380
 300 TWIGRIYASCSFIRALISFPALPAGILGSEFALKVOOKHPEKRRNPANLLOCVRS 359
 381 YAADKSVSTATWKRPHLKA--HTCSPTNOKLSFKERVRMA--PRGQSTIKSQAOSVD- 435
 360 HAA-EKRV--ATWNAHIDPLAHETKETHHMMWNGKHAASSMDSNNLTKRQLFKQSSLYNT 417
 436 ---RRSPTITLTAAGSPTKVQKSMSEFNORTFRPRLRLKSSQPKPYIDALGCTD--- 489
 418 FRKKGSTVD-----EMGELOOERLLRHERNSDTDEKR 452
 490 VYDEKGCQCVSV-----DLPPKLTIVRAIRIMFVAKRKKEFET 531
 453 IY-RVAGDIDIDYETPTTPTRPOGHISHYCELDIAIRNAIRLRVYVFAKRRFOQA 511
 512 RKPYADVADVIEYOXGQHLMNMVRIKELORRLDQTLGKGOYDGKSRK---GHPT--- 564
 532 LRPIYKADVIEYOXSAGHLDMLCRISLQTRVQDLIGKQOITSDKRSREKITAHEHTTDL 591
 512 RKPYADVADVIEYOXGQHLMNMVRIKELORRLDQTLGKGOYDGKSRK---GHPT--- 564
 592 SMIGRVYKVKOVQOIESKID---CLLDIYQOYLKRG---SASALALASQIIPPECE 643
 565 -IGSRISRLLEOMSSLDKRVKSSNRTNALYRLMADRNSLTISPSPALISRPVSPAACL 623
 644 QTSYDOSPVDSKDLGSAONGS 665

DB 624 SPRDQLSPT-----SISSQSSG 640
 RESULT 17
 ID 09VSH7 PRELIMINARY; PRT; 343 AA.
 AC 09VSH7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CG12215 protein.
 GN CG12215.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBL_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Ashpayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotler P.,
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brokstein P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dyrin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster K., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svendsen R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003830; AAF5829.1; .
 DR FlyBase; FBgn003494; CG12215.
 DR InterPro; IPR000636; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans.1.
 SQ SEQUENCE 343 AA; 38755 MW; C88BCA56540F4164 CRC64;
 Query Match 14.7%; Score 697; DB 5; Length 343;
 Best Local Similarity 61.3%; Pred.No.3e-42;
 Matches 138; Conservative 33; Mismatches 50; Indels 4; Gaps 3;
 87 MSLGKPLSTYSQGRVKKYRRVONTLYNVERRGV-WAFYHAFVFLVCGLLISV 145
 1 MSLGKPLSTYSQGRVKKYRRVONTLYNVERRGV-WAFYHAFVFLVCGLLISV 58

QY 146 FSTPEHTKLASSCLLLEFEVIVFGLFIRIMSGCCCRYRGMRGRFARKPCVYI 205
 DB 59 FSTIKETEEDAVYLLFRMELLIVIMTFEFGARLMSGCCRSRYOQCLGRLKVKRPFCLII 118
 QY 206 DTIVLASIAVSAKTOGNIPATSLASRLRLQILRMVMDRGGTWWLLGSSVYAH-SK 264
 DB 119 DIVIILASIVYLGMTSGOVFATSLRGLRFFQILRMVMDRGGTWWLLGSSVYAH-RQ 178
 QY 265 ELITAMVIGFLVLFSSFLVYLVEKDANKFESTYDALIMWGITL 309
 DB 179 ELITMVIIGFLGLIFASFLVYMEKDVNDKFSNFAQALMWDHTL 223

RESULT 18

Q96A19 PRELIMINARY; PRT; 392 AA.
 AC 096A19;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Similar to potassium voltage-gated channel, KQT-like subfamily, member 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC017074.1; -
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR00636; K-channel_n19.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF03520; KCNQ1_channel.1.
 FT NON_TER
 SQ SEQUENCE 392 AA; 43727 MW; E0E8CBF2C56FF62C CRC64;

Query Match 11.6%; Score 549.5; DB 4; Length 392;
 Best Local Similarity 34.4%; Pred. No. 1.8e-31;
 Matches 138; Conservative 75; Mismatches 117; Indels 71; Gaps 13;

QY 287 VEKANKFESTYADLMWGTITLTITIGYDRTPLMGLSLGAFLLGSEFALAGTL 346
 DB 4 VNESGRVEFGSADLWMGVYVTTITIGYDQVPTWVGKTIASCFVSFALSPFALPAGIL 63
 QY 347 GSGFALKVOEOHROKHFEKRRNPANLIGQVRSYAADEKSVSIATMKPHLAL--HT- 402
 DB 64 GSGFALKVOQOROKHFNROIPAAASLIOTANRCYAAENPDS--TWKIYIRKAPSHTL 121
 QY 403 CSPTNOKLSFEKERVMASSRGOSIKRQASVGDNRSPSTDTAEGSPTKVQKSW--FN 459
 DB 122 LSPSPKRP--KKSYYVKKKKFKLIDKNGVTPGEKMLTVPHITCDPEERLIDHFSVDGYD 178
 QY 460 DTRRREPLRLKSSQPKPIYIDALGTDVYDEKCCQDQVSYEDLPLP----- 509
 DB 179 SSVKSPPL-LEVSMPH-----FKRTNSFAD-----LDLEGETLTPTHISQLEHH 226
 QY 510 KTVIAIIMKFKVKKRKEKTLRPDVADVIEQYSAGHLDIMCRISLQTRVDILGK 569
 DB 227 RATIVIRMOYFAVAKKROQARKPYDADVIEQYSGHNLNMLVRIKELORLIDQSIGK 286
 QY 570 Q--ITSDDKSRKRTAETHETDLSMLGVAVVKEKOVQSTIESLDCLDLDIYQVY----- 622
 DB 287 SLFISVSEKSKDR-----GSNTIGARLNRVEDVQTOLDRLALITDMLHOLSLHGG 338
 QY 623 -----RKGS-----SALALASFDIPPE 641
 DB 339 STPGSGGPPREGAHITPOCGSGGSDVPELFLPSNTLPTYE 379

RESULT 19

Q9BQ4 PRELIMINARY; PRT; 363 AA.
 AC 09BQ4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE BA261N11.6.1 (Potassium voltage-gated channel, KQT-like subfamily, member 2, isoform 1) (Fragment).
 GN KCNQ2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL121827; CAC36121.1; -
 DR InterPro: IPR003946; KCNQ1_channel.
 DR Pfam: PF03520; KCNQ1_channel.1.
 FT NON_TER
 SQ SEQUENCE 363 AA; 39479 MW; 90862BB0E36097FB CRC64;

Query Match 9.6%; Score 452.5; DB 4; Length 363;
 Best Local Similarity 36.8%; Pred. No. 1.7e-24;
 Matches 130; Conservative 36; Mismatches 94; Indels 93; Gaps 14;

QY 484 ALGTDVYDEKGCOCNVSVDLTPPLKTVIRAIRIMKRVAKRKKEKTLRPDYVDYIQ 543
 DB 2 SLPEEDIVDDKSCCEFEFTEDLTGLKYSIRAVCWRLVSRKPKESLRPYDMDYIQ 61
 QY 544 YSAGHLDIMCRISLQTRVDILGQITSDPKSRKRTAETHETDLSMLGVAVVKEQ 603
 DB 62 YSAGHLDIMCRISLQTRVDILGQITSDPKSRKRTAETHETDLSMLGVAVVKEQ 120
 QY 604 VOSTESKLDCLDIYQVLRKGSASALALASFPDPFC-----EQTSDYQSPVS 654
 DB 121 VLSMEKKLDPLVNIYMQ--RMG-----IPEETEAYFGAKPEPAPPHSPEDS 167
 QY 655 KDLGSAQNSGCLSRSTANISRGLOFLITPNEFSAQTFYALSPYHSQATVPYISQ-- 712
 DB 168 RE--HVDHRHCIVKIVRSSSTG-----QKNFSAAP--AAP-----VCCPSTSMQ 210
 QY 713 -----DGSAAVANTNTIANQINTAPKPAAPTLLQI-----P-- 743
 DB 211 PQSHRQGHGSPVGDHGLVHIPPRAHENSALVGGGNKASMEFLROEDTPGCRPPSG 270
 QY 744 -----PLPAIKHLRPEETLHPNPAGLQESISDYVTCCLVASKENVOAQS 787
 DB 271 NLROSDTISIPSYDH-----FELERSFSGF--SISQ-----SKENLDALNS 310

RESULT 20

Q9CTU2 PRELIMINARY; PRT; 97 AA.
 AC 09CTU2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 9230107005RIK protein (Fragment).
 GN KCNQ5 OR 9230107005RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EPIDIDYMIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stuhl L.F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gillingham S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001)
 DR EMBL: AK020325; BAB32071.1; -;
 DR MGI:1924937; Kcnq5.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10547 MW; 6317ED3AC977B7A CRC64;

Query Match 9.2%; Score 437; DB 11; Length 97;
 Best Local Similarity 88.5%; Pred. No. 3e-24; Mismatches 0; Gaps 0;
 Matches 85; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 827 IRSTELNQLSGSSSGSGSGSODFPKWRRESKLTFTDEVGPEETDTPDAPOPARE 886
 DB 1 IRSTELNQLSGSSSGSGSGSODFPKWRRESKLTFTDEVGPEETDTPDAPOPARE 886
 QY 887 AAFASDSLRTGSRSSOSICKAGESTDALSLPHVKL 922
 DB 61 AAFSSDSLRTGSRSSONICKGTGSDALSLPHVKL 96

RESULT 21
 QY 09GYM8 PRELIMINARY; PRT; 675 AA.
 AC 09GYM8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-JUN-2002 (Tremblrel. 21, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Hypothetical 78.0 kDa protein.
 GN M60.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Stellies L.;
 RT "The sequence of C. elegans cosmid M60.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U39995; AAF99993.2; -;
 KW Hypothetical protein.
 SQ SEQUENCE 675 AA; 77981 MW; 3A5E193769BD1FA2 CRC64;

Query Match 9.1%; Score 430; DB 5; Length 675;

Best Local Similarity 25.0%; Pred. No. 1.8e-22;
 Matches 144; Conservative 103; Mismatches 233; Indels 96; Gaps 15;

QY 103 RRRNKKRVONYLYNLERPPGMAFI-YHAFVLLVFGCLISVSTPEHTRKASSCLL 161
 DB 69 QORNNLRIRIKLVNLEKPLNMAASAPYHFFIFGLIVIANIILGAATN--DNDSTVSKIH 126
 QY 162 ILLEFVIVVGLFEITRWSAGCCORRGWOGRLNFAKRPVIDITVILASAVASAT 221
 DB 127 FLEIFKVFILFLEAVLMSVRADAKYTKGRLLVHPVTLIDILIPATILLIVER- 185
 QY 222 QGNIFATLSALSLFLOILRVNDRRGTYKLLGSVYVANSKELLITAYIGLIFSS 281
 DB 186 -GHVDVOSTDLTLRFIDILRFHVDROMATVKKLLKMIILGQWQMATYIIVLVGSLA 244
 QY 282 FLYV-----LVKDKANKESTYADALMGGITLTITIGYDKTPTLTWGR 325
 DB 245 TIVYSTELAQGIQDNGYGLIVPEGTNATFPTMAHSMWFTAVTVGVDIYPGALTK 304
 QY 326 LLSAGFALLGISFPALPAGILSGFALKVQROHROKHEKRRNPAANLIQCWRSYADE 385
 DB 305 FLVCVLGFIAFCFQOANNTQISVGLTLMMEENKQOTNRRLNLAATIQCWRYHLA-- 362
 QY 386 KSVSIATWKP---HLKALHTC-----SPTNOKLSFKERYMASPROSISROASVD 435
 DB 363 -----TNMKPPRRYTYVHCYKLYVERINQNRVLAKILREKLEKRPICK--SLTH 415
 QY 436 RNSPSTIDITAEG---SPYVOKSWFND-----RTRR-----PSLRKSSQP 475
 DB 416 QNSVTAEILKFGKGMKPMLEKODSFDKERRKISLRTRRVLEFAEARNSSVETSMSS 475
 QY 476 KPIVADDTALGTDVDYDEKQCCQGVSDLLPPLK--TVIRAIRIMKRVAKRKETLR 533
 DB 476 VDVSELETQETINFLQANDVLSKVEDLSLITKIRPLNRYFYVMRFYMKKH---- 531
 QY 534 PYDVKDVIKQYSGHLDL-----CRISLQTRVQDILGKQITSDKRSREKI 581
 DB 532 -----TORIAGQLIMEAIEAERENORQKKLEALILLEGKPTVSFDDSGQK- 582
 QY 582 TAEHETDLSMGRVYKVKQVQSTSKDCLLDI 617
 DB 583 -----LSITIERLECEKRMEDLERKTDALNEI 609

RESULT 22
 QY 09BQ05 PRELIMINARY; PRT; 399 AA.
 AC 09BQ05;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2002 (Tremblrel. 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE BA261N1.6.2 (Potassium voltage-gated channel, KQT-like subfamily,
 DE member 2, isoform 2) (Fragment).
 GN KCNQ2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL121827; CAC36120.1; -;
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR002965; P_rich_extensn.
 DR Pfam: PF03520; KCNQ1_channel; 1.
 DR PRINTS: PRO1217; PRICHEXTENS.
 FT NON_TER 1
 SQ SEQUENCE 399 AA; 43443 MW; ECC9545846F3B969 CRC64;

Query Match 9.0%; Score 424.5; DB 4; Length 399;
 Best Local Similarity 33.4%; Pred. No. 2e-22;
 Matches 130; Conservative 36; Mismatches 94; Indels 129; Gaps 15;

RESULT	23
09V5H6	
ID	09V5H6
AC	09V5H6;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	CG12915 protein.
CN	CG12915
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	Amara R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abrial J.F., Abmayori A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA	Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA	Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hastin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA	Jalili M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasno P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merrulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,

```

QY      438 SPSPDITAESEPTKQKQKMSFNDRFRERPLRLMSQCKPYIADMTAGTDDVDEKCCQ 497
      111      111      :      :      :      :      :      :      :      :
Db      142 SPS-----GSPGSGRTGRFFFAASHF---LETGSSSNPIID-----VANEDEPRC- 185
QY      498 CDVSVEDITPPLKTYIRAIRIMKHFVAKRKPRETLRPDYKVDVTEOYSAGHLDMLCRIS 557

```

```

QY      558  LOTRVDOLILGGQILTSDKKSREKPTAEHETTDUJSLMGRVVKVEKOVOIESKLDCLDLI 617
        | :| |||||          :::::   :| :||||||| || ||| :|
Db      241  LHLRIQDULIGK---QGSKAKDYASK-----ISLARVYKVEQVADIEBKEDLILKA 290
        | :| |||||          :::::   :| :||||||| || ||| :|
QY      618  YOOVLNRKSGASALALASFQIPEPFECEQTSDYQSVPYSKDLSGSAONSCLSKSTSANISR 677
        | :| |||||          :::::   :| :||||||| || ||| :|
Db      291  Y-----MEDRD-----                296
        | :| |||||          :::::   :| :||||||| || ||| :|
QY      678  GLQFLLTNNERSAQCTFYALSPTMH-SQATQVPVISOSDSAV-----AATTINQNT 729
        | :| :|         | :| ||| :| :| :| :| :| :| :| :| :| :|
Db      297  --RFALP-----LPAPKRINHISISHPKRLAHNHLAMIDVWKRTAALSVHDEQVYT 346
        | :| :|         | :| ||| :| :| :| :| :| :| :| :| :| :|
QY      730  AP--KPAPTTLQIPPLPAIKHLRPREFIHNPAGLOESIDVTTCLVASKENYQVQAS 787
        | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      347  TPLNPSADSOSEL-----KSLTAIOTPTTTIDAIAITQI-----PMPPHQHTAT 391
        | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY      788  NLTTRDSMRKSHFDMGGETLLSYCPWVPKDLGSLSVQNILIRSTEE--LNILQSSSESSG 844
        | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      392  N-TKS-SVLNYSQLSSE-----KQHNDVFMTELEDNRTKKRVLTSLHRSTSEP-- 437
        | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY      845  SRGSODFTPKMFRESKLFITDEVEGEETETDFDAQPQ 883
        | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      438  -----YSK-OEQRIITPDE-----GASLSDSNAP 461

```

```

RESULT 24
Q9BXD3
ID Q9BXD3 PRELIMINARY; PRT; 911 AA.
AC Q9BXD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Potassium voltage-gated channel, Shab-related subfamily, member
DE 2.
GN KCNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
```



```

Db 277 IFTLESNKSVLOFQONVRRVOIFRIMRLIRILIKLARHSTGLQSLGFTLRSYNELGLTL 336
Qy 271 YIGFLVLFSSFLVYLVEKDA-NKEFSYADALMWGTTLTIGYGDTPPLWGLRLSLA 329
Db 337 FLAMGIMFFSS-LVFFAKEDDDTKFSIPASFMMATTMTVGDIYKPLLGIVGG 395
Qy 330 GFALLGISFFALPAGILGSGFALKVQEOHRQKHFEKRRNPANLLQCWRSTAADEKSYS 389
Db 396 LCCAGLVIALPPIIYVNNSEFYKQKROEKAIKRR-----EALERAKRNS 444
Qy 390 IATKPKHLKALHTCSPTNOKLSFEKERVN-----ASPROGSIKRSQASVDRSPSTDITA 445
Db 445 IVS-----NMKDAFARSYEMMDIYVEKNGENLAKKERKVDONHNSPNWKMT 491
Qy 446 EGSPTKVQKSWSFNDRFRPSLRKSSQPKVYIDADALGDDVYDEKGCOCODSVEDL 505
Db 492 KRTLSSTSSKSFETKEGSGPEKARSSSPQHL-----NVQJLEDIMNKKA----- 537
Qy 506 TPPLKTVIRAIRIMKFNHAKRRKFTLRPYDKVIEOYSAGHLDMLCRKISLQTRVDOI 565
Db 538 -----KTQSQPLYNKKEAAQSKPKLELMESIPS-----PVAPLPRTTEGV 579
Qy 566 LGKQITSDKKSREKITAHEHTTDDLMLGRVYKVEKOVOSIESKLDCLLDIYOVLKRG 625
Db 580 I-----DMRS-----MSSIDSFISCATDF----- 598
Qy 626 SASALALAPQIPPEFECQTSQDYOSPVDS-----KDLSSGANSQGLSRSSANISRLQPL 682
Db 599 -----PEATRRSHSPSLASLPKACGAPBELGWRG-ALGASGGRIVEAN 641
Qy 683 LTPNEFSNQTFVALSPTHSQAOTQVPISQSDSAVAATNTIANQITAPKPAFTLQIP 742
Db 642 PTPASHSGSGFFIESP-KSSKNTNNPLK-----LRALKVFMAGE-----GPIPLPVGMH 692
Qy 743 PPL-----PAIKHLPRPELHPNPAGLOESISPTVTCVASKENVOVAQSNLTKDRSM 795
Db 693 DPLTRGGAAMAAY-----AGIL-ECATLLDKVVLSPESISYTTASARTPPRP 738
Qy 796 RK-----SFDMG-----GFTLLSYCPMVPKDLGKSLSQNLIRSEELNIQL 837
Db 739 EKPAIAPNFEKGVHQYIDATDDEGQLYSVDSPPKSLH----- 779
Qy 838 SGSSSGSGSGSODFFPKWRRESKLTDEVEGPEETETDPAPOPA-----REAAFASD 892
Db 780 GGAPSKCIGAR-----SEKNFESAPLPTSPKFLRQNCIYST 817
Qy 893 SLRTGRSSQSICKAGE--STDALSLP 918
Db 818 EGLTGKSLSGQEKCKLGNHISPDVRLP 845

RESULT 26
Q14193 PRELIMINARY: PRT: 858 AA.
AC Q14193:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE H-DRK1 K(+) channel (DJ791K14.1) (Potassium voltage-gated channel,
SHAB-related subfamily, member 1).
GN H-DRK1 OR KCMB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363205; PubMed=8081723;
RA Albrecht B., Loria C., Stocker K., Pongs O.;
RT "Cloning and characterization of a human delayed rectifier potassium
channel gene.";
RL Recept. Channels 1:99-110(1993).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL (In) Civan M.M. (eds.);
RL The eye's aqueous humor - from secretion to glaucoma, pp 69-104,
RL Academic Press, San Diego (1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; X68302; CAA48374.1;
DR EMBL; AF026005; AAB88808.1;
DR EMBL; AL035685; CAB89417.1;
DR HSSP; Q54397; 1BL8.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001622; K_channel_pore.
DR InterPro; IPR004350; Kv21channel.
DR InterPro; IPR004351; Kv22channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR000636; M_channel_nlg.
DR InterPro; IPR003973; Shab_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF03521; Kv2channel; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1514; KV21CHANNEL.
DR PRINTS; PRO1491; KVCHANNEL.
DR PRINTS; PRO1495; SHABCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel.
SQ SEQUENCE 858 AA; 95877 MW; C4B426174ED0DEE4 CRC64;

Query Match 6.2%; Score 291.5; DB 4; Length 858;
Best Local Similarity 20.2%; Pred. No. 2.8e-12;
Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33;

115 LYVLEPRGMA--FIYHAPVLLVFCGLISVSTPERTKL-----ASSCLLIE 164
175 LMDLEKPNSSVAAKILAIISIMPLVSTIALSL-NTPRELQSLDEFGSTGNPOLAHYE 233
165 FVMIVTGLEPIIRISAGCCRRYRGQGRLEFARKPCVYIDTIVLASIAVSAKTQGN 224
234 AVCIAMFTMEYLLRFLSSP-----KKW-----KFFKGPLNAIDLLAILPYVY-----T 276
225 IFATSAIARSL-----RFLQILRMVRMDRGRGTWKLSSVYVAHAKEL-ITAM 270
277 IFTLESNKSVLOFQONVRRVOIFRIMRLIRILIKLARHSTGLQSLGFTLRSYNELGLTL 336
271 YIGFLVLFSSFLVYLVEKDA-NKEFSYADALMWGTTLTIGYGDTPPLWGLRLSLA 329
337 FLAMGIMFFSS-LVFFAKEDDDTKFSIPASFMMATTMTVGDIYKPLLGIVGG 395
330 GFALLGISFFALPAGILGSGFALKVQEOHRQKHFEKRRNPANLLQCWRSTAADEKSYS 389
396 LCCAGLVIALPPIIYVNNSEFYKQKROEKAIKRR-----EALERAKRNS 444
390 IATKPKHLKALHTCSPTNOKLSFEKERVN-----ASPROGSIKRSQASVDRSPSTDITA 445
445 IVS-----NMKDAFARSYEMMDIYVEKNGENLAKKERKVDONHNSPNWKMT 491
446 EGSPTKVQKSWSFNDRFRPSLRKSSQPKVYIDADALGDDVYDEKGCOCODSVEDL 505
492 KRTLSSTSSKSFETKEGSGPEKARSSSPQHL-----NVQJLEDIMNKKA----- 537
506 TPPLKTVIRAIRIMKFNHAKRRKFTLRPYDKVIEOYSAGHLDMLCRKISLQTRVDOI 565
538 -----KTQSQPLYNKKEAAQSKPKLELMESIPS-----PVAPLPRTTEGV 579
566 LGKQITSDKKSREKITAHEHTTDDLMLGRVYKVEKOVOSIESKLDCLLDIYOVLKRG 625
580 I-----DMRS-----MSSIDSFISCATDF----- 598

```

```

QY 626 SASALALASFOIPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTANISRGIOFILTP 685
D 606 HSPILSLPS-----KTGSTAP--EYGMWALGASG--GRFVEANPS-----P 644
QY 686 NEFSQOTYALSP-----TWHSQATOVPIQSOD-----GSAAVA 719
D 645 DASQHSFEFIESPKSMKTNPLKRLAKYFNMEGDPSPLLPVLMGYHDLPRNRGSAANA 704
QY 720 T-----NTIANQINAPKPAFTLQIPPLPAIKHLPRETELHPN-----PAOLOESIS 769
D 705 VAGLECATLLDRAVSPESISYTTASAKTP-----PRSPKHTATAFNEAGVHOYI- 756
QY 770 DVTTCVLAISKENVQVAQSNMTRDRSMKSGDMGETLLSYCPWPKDLGKSLSYQNLIRS 829
D 757 DADT-----DDEGQLLYSYDSSPPKSLPGSTSPK----- 785
QY 830 TEELNIQISGSSSSSGSQDYFPKWRESKLTITDEVGPEETDTFDAAPOPARAAAF 889
D 786 -----FSTGTREKKNHF-----ESSPLPTSPKFLRQNCI 814
QY 890 ASDSLRTGRSRSSQICKAGE--STDALSIP 918
D 815 YSTEALTKGPGSGQEKCKLENNHISPDVRYLP 845

RESULT 27
ID 018868 PRELIMINARY; PRT; 858 AA.
AC 018868:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Delayed rectifier potassium channel Kv2.1.
GN DRK1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RP [1]
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026006; AAB8809.1; -.
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR004350; Kv21channel.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M-channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF03521; Kv2channel; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1514; KV21CHANNEL.
DR PRINTS: PRO1491; KCHANNEL.
DR PRINTS: PRO1495; SHABCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel.
SQ SEQUENCE 858 AA; 96117 MW; A9E24C3ABE13B491 CRC64;

Query Match 6.1%; Score 287.5; DB 6; Length 858;
Best Local Similarity 19.8%; Pred. No. 5.4e-12;
Matches 173; Conservative 120; Mismatches 307; Indels 275; Gaps 31;

QY 115 LYNVLEPRGWA---FTYHAFVFLVPGCLISVSTPEHKL-----ASSCLLIE 164
D 175 LMDLEPRNSVAAKILAIISIMFTIVSTIALST-NTLPELOSLDEFGQTTPDOLAHVE 233

```

```

QY 165 FVMIVGFEFLIRIRWSAGCCCRFRGMGRURFAPAKPCVIDITVLINIAVYSAKTQCN 224
D 234 AVCIAMFTMYELFELTSSP-----KKW---KFFKGPINADLLALIPVYV-----T 276
QY 225 IFATSAIRSL-----RELOILRMVRMDRRCGTWKLGLSVYAHKEL-ITAM 270
D 277 IFLESKSVSLQGNVRRVQYIFRIMILRLILKLAHSTGLOSLQGLTFLRSYNELGLLL 336
QY 271 YIGFVLVLISSFLVYLVKDA-NKESTYADALMWGITTLTGTIGYDKTPTLWGRLLSA 329
D 337 FLMGIMIFSS-LVFEKEDDDTKFRSIPASFWATTMTTVGDIYKPLLLGIYVG 395
QY 330 GFALLGISFPALPAGLIGSGPALKVOOHORCKHEKRRNPANLIQCWRSYAABEKSVS 389
D 396 LCCIAGVLYALPIPIIVNNSEFPYKQKROEKAIKR----- 433
QY 390 IATWPKHLKALHTCSPNTQKLSFEKERYMASPRGQSIKRSQASVGRDRSPSTDTAE-- 446
D 434 -----EALBRAKRNGSIYSMMKKDAFPRSEIEMMDIYVERKV 469
QY 447 ---GSPTKVO-----KSWGFNDTRFRPRLKSSQKPYIDATLGTDDVDYDEKQO 497
D 470 ENMGQDKYODNHLSPKRWKTKRTLSETS--SKSFEFK-----EQG-- 510
QY 498 CDVSVEDLPPLKTVIRAIRIMKFKVAKRKFKETLRPDYKVDIEQYSGHDMLCRIKS 557
D 511 -----SP-----EKARSSSPQHLNVQLEDMTN-----KM 536
QY 558 LQTRVDOLLGQGITSDKRSREKITAEHETTDLSMLGRVYKV--EKQVQSIESTKIDCLL 615
D 537 AKTQSQPIILNTRKSATQSKPKELEMESIPVAPLFRGTGVIDMRSMSSIDFSICAT 596
QY 616 LIYQVLRKGSABALALASFOIPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTANI 675
D 597 DEPEAT--RFSHSPLA-----SLPSKSGSWAPEVWNG-ALGATG 634
QY 676 SGIQFLIPINPESQAOTFYALSPTHMSQATQVPIQSODGSAVAATNTT-----ANOINT 729
D 635 GRFVEANPTPDASHSTFTIESPK-----SSMKTTNPLKRLAKYFNMEG 679
QY 730 AKPPAAPFTLQIPPLPAIKHLPRETELHPNPAQLOESISDVTC-----LVASKENVO 783
D 680 DSPPLVPVLMGYHDL-----NRRGGAANAVALTECATLLDRVLSPESSY 726
QY 784 VAQSNITKRSNMK-----SFDMG-----GETLLSYCPWPKDLGKSLSYQV 825
D 727 TTASARTPPRSPKHTAIAFNEFAGIHQYIDADTDDEGQVLYSYDSSPPKSLHGSTSPK- 785
QY 826 LIRSTEELNIQISGSSSGSQDYFPKWRESKLTITDEVGPEETDTFDAAPOPAR 885
D 786 -----FSIGTRSEKKNHF-----ESSPLPTSPKFLR 810
QY 886 EAFASDSLRTGRSRSSQICKAGE--STDALSIP 918
D 811 QNCIYSTEALTKGAPGQEKCKLENNHISPDVRYLP 845

RESULT 28
ID 08WNQ3 PRELIMINARY; PRT; 611 AA.
AC 08WNQ3:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Potassium voltage-gated channel (Fragment).
GN KCNB2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RP [1]
SQ SEQUENCE FROM N.A.

```


QY	479	IDADALGTDVVYDERKGCQDVSEVDELPRPLKTVIA-----KIM-----KFNAAKRFKE	530
Db	558	EELKMG-----SIOGPVPMALATHEGFIIDKMSMSISDFICTAEFE	601
QY	531	TLR-----FYVKDYIEQYSAGHDLMLCRKSLQTRVDOILGKQITSPKSKSEKI	581
Db	602	SGRSHSPPLAIIPYRM-NVNSGQNTSHGYESRVRPLSSDV-----SRESF	646
QY	582	TAHEHTTDLMSLGR-----VVVEK-----QVOSIESKLCILD-----	616
Db	647	TEVHPKTD-----LSRHATYILSPKTLVKKVKNPMLRSLKVNPLLEGETSSLPLAPNPLSP	702
QY	617	-----IYQOVLRKKGASALALASFOQPRPECEQ-----	644
Db	703	TSRHQEGSNODTSTFTEHVSQSPETSLEYTTASARPPSSPEKHMMAIDTFTHDANVHKYT	762
QY	645	---TSDYOSPYVDSKDLGSGSAONSGCLS-----RSTSANISIGLOFILPNNEFSAQ	691
Db	763	DADVDDEGQILLDGLDSSPSKELGATMSPRKYNTTKSGHPTQRDWNHGRDKNHELGAPFLSS	822
QY	692	TEFYALSPFMHSQAQVPIISQSDGSAVAALNTLANQNTMP	731
Db	823	SRVYGQNCIYATEGKMTGRQGLLETVYKMKENHISPOVNHLE	862

RESULT	30			
091592				
ID	091592	PRELIMINARY:	PRT:	898 AA.
AC	091592:			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, last annotation update)		
DE	Potassium channel alpha subunit Kv2.2.			
GN	XSHB12.			
OS	Xenopus laevis (African clawed frog).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN-EYE;			
RX	MEDLINE=96225773; PubMed=8778292;			
RA	Burger C., Ribera A.B.;			
RT	"Xenopus spinal neurons express Kv2 potassium channel transcripts			
RL	during embryonic development.";			
RL	J. Neurosci. 16:1412-1421(1996).			
DR	EMBL: U20342; AAC59757.1;			
DR	InterPro: IPR000210; BTB_POZ.			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR004351; Kv22channel.			
DR	InterPro: IPR003968; Kv_channel.			
DR	InterPro: IPR003091; K_channel.			
DR	InterPro: IPR003131; K_tetra.			
DR	InterPro: IPR000636; M+channel_nlg.			
DR	InterPro: IPR003973; Shab_channel.			
DR	Pfam: PF00520; Ion_trans_1.			
DR	Pfam: PF03521; Kv2channel; 1.			
DR	Pfam: PF02214; K_tetra; 1.			
DR	PRINTS: PR00169; KCHANNEL.			
DR	PRINTS: PR01515; KV22CHANNEL.			
DR	PRINTS: PR01491; KCHANNEL.			
DR	PRINTS: PR01495; SHABCHANNEL.			
DR	SMART: SM00225; BTB_1.			
SO	SEQUENCE	898 AA; 102409 MW; 10FFD022CE5078BA CRC64;		

```

Query Match          5.98; Score 280; DB 13; Length 898;
Best Local Similarity 21.88; Pred. No. 2e-11;
Matches 151; Conservative 127; Mismatches 257; Indels 158; Gaps 31

115 LYNNLEPRG-----WAFYHAAVFLVFPCLISVSSTPEHKL-----ASSCLL 161
|:::||||| | | :|| :||: ||: ||: : : : : : : : : : : : : : :

```

```

Db      179J LMDLLEKPPSSVAAKVALI---SILFIYLSTALS-LMLPJLOEIDEFGOPNDNPOLA 234
QY      162I ILEFMIIVAVEGEIIRIRMSAGOCOCYRMOGRLEARRRPFVCIIDITVILASTAVYSAKT 222
Db      235HVEAVCIAMFEIIMTLEIRLSS-----PNMKFEFGKPLNIDIDLALIPYV----- 279
QY      222OGNIFATSALRSL-----RFLQILMVMYMDRGRGTWKLGSVYVAHAKSL-1 267
Db      280--TIFLTASNKSVLQFQNVRRVQVQFPRIMRILITLAKRSTGLOSGLFLRRSYNELGL 337
QY      268TAMVIGFLVLIRSSFLVLYLVEKDAN-KESTYADALAMWGTTITLTIGGKTPLTWLGR 326
Db      338LILFLAMGMIIPSS-LVFEAKDEDEDKTETSPASWMAATITMTTGVGDIYKRTLLGKI 366
QY      337ISAGFALLGISFEFAPAGILGSGFALKVQEOHROKHFEKRRNP-----AANLIQ 375
Db      397IGGLCIAGVLYIALPIPIIIVNNSEFYKQROKQEKAIRRELBEBARNGSTIVSNLKD 456
QY      376CWMRS-----YAAD-----EKSVSITATWKPHLKALHTGSPTNOKLSFEKVR 417
Db      457AFARAMELIDIVADKSESDSNKMEKPSDMLHSFRWK-----WSRRTLSDTSSNKSFDNKYQ 513
QY      418MASPRGQSIKSQASVGVGRRSPSTDIATGASPTKYVQKSMSPFNDRTRFRSLRKLSSQPK 477
Db      514EVSQH-----DSQEOUNNASSPSOHLASQ-----KLEELNETTKAOSHPSVNSFOQAA 564
QY      478VIDA-DTALGTDVDYDEKGCQCDVSVEDTLPLPLTYAIRIIMKFEVAKRKEET-----L 532
Db      565VPPAVEEIEEMEVEVSTK-TQLSVAQKQIDVTVMRSV---SSIDSFASCATDFIETERSPL 620
QY      533RPYDKVDIYOYSA-----GH-----LDMLCRKSL-----QTRVQJLIGKOITSDBKS 577
Db      621TPYPSGSLNIEIRPSYTVPEEGHGANTAOPLPRSPCKGAPKVDVTEFYKLSHPIKNDNET 680
QY      578REKITAHEHTTDDLS-----MLGRVAVKE-KVOYSTEKSUDCLDIYQOVLKRG 625
Db      661-PKILLOQAGNVEVSPERSLKRNPILRSRLSKYVFNKNS-----HSQATATN 728
QY      626SASALALASFOIIPPECQOTS-----DYOSPVDSKDLGSSAONSGCLSRSTANISRGIO 660
Db      729FSSALPVMNIDHPLTLTHLOLSTIFLODYO-----SOEPQSMLOTDSSSDHSRSIQ 778
QY      681FILIPNERSAQTFVLAPTMHSQAOIYOPIRSQD 713
Db      779--VSPKH--NPKLFALSSNMKSSFTLEIGDEED 807

```

RESULT 31			
ID	003717		
AC	003717	PRELIMINARY;	PRT; 857 AA.
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, last annotation update)	
DE	Pocassium channel protein.		
GN	KCNB1 OR SHAB.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE=91162315; PubMed=2002364;		
RA	Pak M.D., Covarrubias M., Ratscliffe A., Salter L.;		
RT	"A mouse brain homolog of the Drosophila Shab K+ channel with		
RT	conserved delayed-rectifier properties.";		
RL	J. Neurosci. 11:869-880(1991).		
DR	EMBL; M64228; AAA40112.1; -.		
DR	HSSP; O54397; 1BL8.		
DR	MED; MGI:96666; KCNB1.		
DR	InterPro; IPR000210; BTB_POZ.		
DR	InterPro; IPR001622; K+channel_pore.		


```

DR InterPro: IPR004350; Kv21channel.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans.1.
DR Pfam: PF03521; Kv2channel.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01514; KV2CHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR SMART: SM00225; BTB.1.
SQ SEQUENCE 857 AA; 95692 MW; 772F1C42C25EF3A5 CRC64;

Query Match 5.94; Score 279; DB 11; Length 857;
Best Local Similarity 20.4%; Pred. No. 2.2e-11;
Matches 181; Conservative 124; Mismatches 280; Indels 304; Gaps 37;

QY 115 LYNVLEPRGMA---FIYHAFVLVFGCLISVFSTIPEHTKL-----ASSCLLIE 164
DB 175 LMDLEKPNSSVAKIILAIISIMFIVSTALSL-NLPELQSDIEFGQSTDPQLAHE 233
QY 165 FVAIVFGLFIIRIRAGCCCRYRGWGRLEFARKPCVCIDTIYLIASIAVSAKTQGN 224
DB 234 AVCIAMFTMYLRLFLSSP-----KKW-----KFFKGPLNADLAILPYV-----T 276
QY 225 IFATSAIRSL-----RFLQILRMVMDRGRGTWKLGSVYVYANSKEL-ITAW 270
DB 277 IFLESNKSVLFQONVRRVVOIFRIMRLIKLASHSTGLQSLGFTLRSYNEIGLILL 336
QY 271 YIGFIVIESFIVYLVKEDA-NKEFSTYADALMGTTTLTGCGDKTPTLTKRLISA 329
DB 337 FLAMGIMFSS-LVFEAKEDDDTKFKSIPASFWMTITTVGDIYPKTLCKIYVG 395
QY 330 GFALLGISFPALPAGIISGFALKVQDQROKHEKRRNPANLIQCWRSYAADEKSVS 389
DB 396 LCCTAGLVYALPIPIIVNNSEFYKREKROKAIKRR-----EALERAKRNS 444
QY 390 IATWPKLALHCTSPNOKISFEKRYRM-----ASPRGOSIKSROASVGRDPSSTDITA 445
DB 445 IVS-----NMKDAFARSIEMMDIIVEKNEGVAKKQVODNHLSPMKMKWT 491
QY 446 EGSPITKQKSMENDRFRPSLRSLKSSQPKRVIDADALGDDVYDEKGCOCOVDEVL 505
DB 492 KRALSETSSSKSFETKEQSGPEKARSSSPQHL-----NVQOLQDMYSK-----MAKTOS 541
QY 506 TPPLKTVIRAIRIMKPFVAKRREKTELRYDVKDVEIQYSAGHLMCLRIKSLQTRVDQI 565
DB 542 QPILNT-----KEMAPQSQPQELKMS-----MPSVVALPRTREBV 579
QY 566 LKGQITSDKKSREKITAHEHTTDDLSMGRVYVKEKOVOSTIESLDCLLDIYOOLRKG 625
DB 580 I-----DMS-----MSSIDSFISCATDR----- 598
QY 626 SASALALASQIIPPECEQTSYQSPYDCKLSSGSAONS-----GCLSTSTANISR 677
DB 599 -----PEATRFSSPLAS--LSGKSGSTAPDEVGMRGLASGGR----- 636
QY 678 GLOFILTPN---EFSAQTFYALSP-----TMHSGATOYFISQSDGSAAVATNTIANO 726
DB 637 ---LMEINPIPEASRSGFVESPSSSMKTHNPKMLRALKVFLBGD----- 679
QY 727 INTPAKPAAPTTLQIPPLPAIKHLPRETILHPN-----AGLQESISDVTTL 775
DB 680 -----PLPAL-----GLYHDLRNNGGARAAVAGL-ECASLIDKDV 717
QY 776 VASKENVOAOSNLTKDSMRK-----SPDMS-----GELLTASCPMVPKDL 817
DB 718 LSPSSITTTASARTPPRSPKHTAIANFEAGVHOYIDTPTDDEGQLLYSDVSLPKSL 777

```

```

QY 818 GKSLSYONLIRSTEELNQLSGSESSGSGSQDFFPKWRKSLFTIDEVGEPEETDTF 877
DB 778 HGSTSPK-----FSLGAR-----TEKNHF 796
QY 878 DAAPQPAR-----EAFASDSIRTGSRSSQSICRAGEST--DALSLP 918
DB 797 ESSPLTPSPKFLRPNVCYASEGL-PGKGPAOEKCKLENTSPDHMLP 844

RESULT 32
Q98SV4 PRELIMINARY; PRT; 816 AA.
AC Q98SV4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Delayed rectifier potassium channel Kv2.
OS Ictalurus punctatus (channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAXILLARY BARBEL;
RX MEDLINE=21136584; Pubmed=11238731;
RA Kang J., Teeter J.H., Brazier S.P., Nguyen N.D., Chang C.C.,
RA Buchalski R.B.
RT "Molecular Cloning and Functional Characterization of a Novel Delayed
RT Rectifier Potassium Channel from Channel Catfish (Ictalurus
RT punctatus): Expression in Taste Buds."
RL J. Neurochem. 76:1465-1474(2001).
DR EMBL: AF319664; AK15623.1;
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003969; Kv6_channel.
DR InterPro: IPR003970; Kv8_channel.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR InterPro: IPR003974; Shab_channel.
DR Pfam: PF00520; Ion_trans.1.
DR Pfam: PF03521; Kv2channel.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01492; KVCHANNEL.
DR PRINTS: PR01493; KVCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR PRINTS: PR01498; SHABCHANNEL.
DR SMART: SM00225; BTB.1.
KW Ionic channel.
SQ SEQUENCE 816 AA; 92092 MW; 0B9B22042CA297E CRC64;

Query Match 5.84; Score 274.5; DB 13; Length 816;
Best Local Similarity 20.5%; Pred. No. 4.4e-11;
Matches 150; Conservative 100; Mismatches 225; Indels 255; Gaps 29;

QY 115 LYNVLEPRGMAFIYHAFVLVFGCLISV---FSTIPE-----HFKLSS 158
DB 180 LMDLEKPNSSVAKIILAIISILF--IILSTIALSLNLPQLQVDFEGQANDPQLAH- 236
QY 159 CILIEFVMIIVFGLFIIRIRAGCCCRYRGWGRLEFARKPCVCIDTIYLIASIAVVS 218
DB 237 ---IEAVCIAMFTMYLRLFLSS-----PKMKWFFFGPLNADLAILPYV--- 280
QY 219 AKTGNIIFATSAIRSL-----RFLQILRMVMDRGRGTWKLGSVYVYANSKE 265

```

```

Db      281 -----TFLTESNKSVALQFQNVRRVQJPRIMKILILKIAKRSSTGLQSGFTLRSYNE 335
QY      266 L-ITAWYIGFLVLIFFSFLVYLVEKDAN-KERSTYADALMWGTTITLTIGYDKTPTLWL 323
Db      336 LGLILFLAMIMIFSS-LVFEAEKDEDATKFTSIPASFWMATITMTVGYGDIYKPTLL 394
QY      324 GRLLSAGFALLGISFFLPAGILSGFALKVOEHROKHFEKRRNP-----AAN 372
Db      395 GKIVGGLCCIAAGLVIALPIPIIVNNSEFYEQKQKAKIKRRELERAKRNGSIYSMN 454
QY      373 LIQCVMSY-----AADEKSVSIATWKPHLKALH-----TCSPTNOKLSFKRRV 417
Db      455 LKDAFASRMELIDVYVEKSEDPNDHLSPSRMGIPKRASDASIRPFDRKVGSRCEFK 514
QY      418 MASPR-----GOSIKRSQASVGDPRSPSTDTITAEQSPTKYOKMSFNDRTFRP 466
Db      515 SSSQHLNVOKLEEMYNOMSKARSLSDLDKN-----NASGPKLEOMNASKGQRNR-- 566
QY      467 SLRLKSSQPKFVIDADTALGTDVYDEKGCQCQSVEDLTPPLKTVIRAIRIMKFHVAKR 526
Db      567 -----PVSDVPRHMASTDSF----- 580
QY      527 KKEETLAPYDVKDIYEQYSAGHLMCLRIKSIQTRVDQLGKQITSDKSKREKITAENE 586
Db      581 -----GSCDELEAKSLTPSSK 598
QY      587 TTDDLMLGRVYKYEKQVOSIESKLDCLLDIYOVLRLKGSASALASLPPEECQOTS 646
Db      599 DDKRSYKNTSLVLESS-NPEYETPLD-----TQOISP-----EQRS 633
QY      647 DYQ-SPVDSKDLGSGA---QNSGLSRSTS---ANISRGLOFLITPNEFSAQFYALSPT 699
Db      634 QFYVAP-----SGHVYNEDEECIVDNTFLIOSINPGMRV---NFLSTDDVPLRTP 683
QY      700 MHSQATQVPS--QSDGSAVATNTIANQINAPKPAFTTQIP-----PPLAIKIH 750
Db      684 STSSAQGLSLSLDDNS-----PROESTPPESVIARIPROGLILSPKLPV-- 732
QY      751 LPRPETLHPN 760
Db      733 -----GDFHPN 738

RESULT 33
Q95L11 PRELIMINARY; PRT; 911 AA.
AC 095L11;
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Voltage-gated potassium channel alpha subunit Kv2.2.
GN KCNB2.
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Malysz J., Farrugia G., Ou Y., Szurzewski J.H., Nehra A.,
RA Gibbons S.J.;
RT "The rabbit Kv2.2 alpha subunit contributes to delayed rectifier K
RT currents in freshly isolated cavernosal myocytes."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037947; AAK84954.1;
DR InterPro: IPR001621; K+channel_pore.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF03521; Kv2channel; 1.
DR Pfam; PF02214; K_tetra; 1.
KW Ionic channel.

```

```

SQ SEQUENCE 911 AA; 102278 MW; 69353D0664C5D689 CRC64;
Query Match 5.8%; Score 274.5; DB 6; Length 911;
Best Local Similarity 22.9%; Pred. No. 5.2e-11;
Matches 170; Conservative 114; Mismatches 308; Indels 151; Gaps 30;

QY 115 LYNVLEPRGWA---FLYHAFVELLVGCGILISVFSTIPE-----HTKLASSC 159
Db 179 LMDLEKPRSSVAKALAIYISILFIVLSTIALSL-NLPELQEDFERQSPDNRLAH-- 235
QY 160 LILFEVMTIVGELFIIRIWSAGCCCRHYGMOGRLPARKPFVIDITVILASTAVVA 219
Db 236 ---VEAVVICAMFMEIYLRFLSS-----PKMKRFKQPLNVLDLALIPYV-- 279
QY 220 KTOGNIFATSLRSL-----REFLOLRMYRMORGGTWTLLGSVYVAHSEL 266
Db 280 -----TFLTESNKSVALQFQNVRRVQJPRIMKILILKIAKRSSTGLQSGFTLRSYNE 335
QY 267 -ITAWYIGFLVLIFFSFLVYLVEKDAN-KERSTYADALMWGTTITLTIGYDKTPTLWL 324
Db 336 LGLILFLAMIMIFSS-LVFEAEKDEDATKFTSIPASFWMATITMTVGYGDIYKPTLL 394
QY 325 RLISAGFALLGISFFLPAGILSGFALKVOEHROKHFEKRRNP-----AANL 373
Db 395 KIVGGLCCIAAGLVIALPIPIIVNNSEFYEQKQKAKIKRRELERAKRNGSIYSMN 454
QY 374 IQCVMSY-----AADEKSVSIATWKPHLKALHSCSPNOKLSFERVMASPRGQSTSR 429
Db 455 KDAFASRMELIDVYVAKAGETANTKOSADNH--LSPSRMKWARKALSESSNKSSTYENK 513
QY 430 QASVGDPRSPSTDTITAEQSP--TKYOK-SWSFNDRTFRP-SLRLKSSQPKFVIDADTAL 485
Db 514 EYSQKDSHQNLNN-TSSSPQHLSAQKLEMLYNEITKQPHSHQAPQCEQP--ERPSAY 570
QY 486 GTDDVYDEKGC---QCDVSEVEDLTPPLKTVIRAIRIMKFHVAKKFEETLAPYDVK 542
Db 571 EEIEMEVEVVCQEQDLAVATQEVYDMKS---TSSIDSFSCATDETER-----SPL 622
QY 543 QYSAGHLMCLRIKSIQTRVDQ-ILGKQITTSKSKREKITAETHETDDLMLGRVYV- 600
Db 623 PPSASHLMKKFTDPFGTEHEQARARPPFL--LIREKPARREGALESPIDITVYLD 679
QY 601 -----EKOVOSIESKLDCLDIYOQVLR-----KGSASALASLFOIIPF 640
Db 680 AGSSQCGLHGLPLOSATSATSPKSLKGNPLKRSILKVNFKENKGSAP-----QPP- 731
QY 641 ECEQTSQSPVDSKDLGSG-----AQNSGLSRSTSANISRGLOFILLPN 686
Db 732 -----STARPLVTTADFSLSTPOHISTILLESPPAGODRLLDLELPAQCQGLAKG 786
QY 687 EFSAQTFYALSPTMHSAQATVPI-----SOSDGSAAVATNTIANQINAPKPA 735
Db 787 RFPKQKLFASFSSRERSRFTIEDTGEDFLELGARADKQADSPNCFAEKPSDARRHLS 846
QY 736 PTTQIPLPPLPAIKHLPRETLH 758
Db 847 EECGSGSSPPPTGHNCRQDSFH 869

RESULT 34
Q97045 PRELIMINARY; PRT; 959 AA.
AC 097045;
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Kv2 channel alpha-subunit.
GN TUKV2.
OC Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyrosidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]

```

RP SEQUENCE FROM N.A.
 RA Ono F., Okamura Y., Katsuyama Y.,
 RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AB018545; BAA75810.1;
 DR InterPro: IPR000210; BTR_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003968; K+channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1491; KCHANNEL.
 DR PRINTS: PRO1495; SHABCHANNEL.
 DR SMART: SM00225; BTR; 1.
 SQ SEQUENCE 959 AA; 108951 MW; D454268687C84394 CRC64;

Query Match 5.6%; Score 267; DB 5; Length 959;
 Best Local Similarity 20.3%; Pred. No. 2e-10; Indels 266; Gaps 39;
 Matches 183; Conservative 131; Mismatches 320;

QY 115 LYNVLEP-----RGNAFYHAFVFLVFGCLLVEFTPE---HTKLASCLLLEF 165
 D 214 LMDLEKPGSLAKVLAII---SILFVLSVALSL-NLPLDNGENKONEDLAHVES 269
 QY 166 VMIVFGLFETIRIMSGACCCRYRGWGRLPARKPCVIDTI-VLISIAVSAKTQGN 224
 D 270 VCIAMFMEYELRLVSA-----PNKWFEPKPLNIIDLAVLPYVVFELFESNQ 320
 QY 225 IFATSAIRSL---RFLQILRMVRMDRGWTKLGSVYVAHSEL-ITAWYIGFLVLF 279
 D 321 ILQONVRRVQVQIRIMIRILKIAHSTGLQSLGYLRKSYNEGLMLFLANGIMVF 380
 QY 280 SSFLVLYVEKDANK-ESTYADALMWGITLTITIGYDKPTPLTWLGRLSAGFALGISF 338
 D 381 SS-LAYFAEKENEMENFNSIPASFWMATITMTVGYGDIPTVGLKLVAGCCITGVLV 439
 QY 339 PALPAGLIGSFALKVOEQRHOKHEKRRNPANLIQCWRSYAADKSVSATWPKPLK 398
 D 440 IALPPIIVNFSFEYKQKROKRAIKRREALENA-----KANGELVNNMRDYPVAK 491
 QY 399 ALHFCSPF--NOKLSFKERVMASSRGOSIKSRQSVGDRSP---SDTITAEGSTKYQ 453
 D 492 SLELVDTKSNKELDDRD-----EKKKDDSESPALIAETLADGKEVERQ 538
 QY 454 KSMFNDRTREPRSLRLKSSQPKPVIDATLGTDDVYDEKGCQCDVSVEDLTPPLKTVI 513
 D 539 SSEKRN--TNF-----ISDRQSSIKE---GRK-----EVTSP----- 568
 QY 514 RAIIMKFEVAKKRFKETLRPYDKVDIEQYSAGHLMCLRIKSQTQVQTL-GKQIT 572
 D 569 NIAMAPDHSAEFLSRSHYLSDDSDIV-----FADKTVVPGNNSKE 609
 QY 573 SDKSREKITAHEHTDLSMLGRVYKVE-----KQVQISEKIDCLL-- 615
 D 610 GRNSNTNQNNSHERYD-----REYKISLPYPPYDEHEHPDYERREYRDALDSVTEY 664
 QY 616 ----DIQOVLKRSASALALASFOIPPEECQTSYDOS-PYDSKDLG-----S 660
 D 665 KEHNDYDDMLR-----SISCASF-VF--ETDGMADHSSYNDRDKDDYSMTSSVYS 716
 QY 661 AQNSGCCISRTSANISRGLOFLTP-----NEFSAQTFYALSTPHSQTQVPI 709
 D 717 GKHHDLNVSTSSGISVDAGSIQSEPTLDSNLKGGDSGIFNDQSPASS-----TKADL 769
 QY 710 --SOSDGSAAVATNI-----ANQINTAPKPAAPTTLQI 741
 D 770 LGSITKEGSDISTNSVQTVVINSITLEDAGSEYSSNTHESVKNRLOOLQALPALVS 829
 QY 742 PPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASK-----ENVQVQSNLTCKDRSMR 796

D 830 P-----TEYIDQVNCRIAKKYIDYPELLPRASS----- 858
 QY 797 KSPDMGGETLISVCPMPKDLGKLSYQNLIRSEBELNIQSGSESSSSRSQDFPKR 856
 D 859 -----GGNT-----KTPYRQRKRLN-EMDCDNNCTTLAQOQDEVTYR 894
 QY 857 ESKLFTIDEVGPETEITDFDAAPQPARAEAFSDSLRTGRSSSSQSCAKGSESTALS 916
 D 895 RNR-----NSNNNSNTIDIELLDTTPPLLSRDKLSNPLRENNQNCSESEITDLC 945

RESULT 35

0900U4 PRELIMINARY; PRT; 575 AA.
 AC 0900U4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE K+ channel, DRK1 (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxID=10118;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92156897; PubMed=1740690;
 RA Drewe J.A., Verma S., Frech G., Joho R.H.;
 RT "Distinct spatial and temporal expression patterns of K+ channel mRNAs
 from different subfamilies";
 RT J. Neurosci. 12:538-548(1992).
 RL HSSP: O54397; 1BL8.

DR InterPro: IPR000210; BTR_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004351; Kv22channel.
 DR InterPro: IPR003968; K+channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF03521; Kv2channel; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1491; KCHANNEL.
 DR PRINTS: PRO1495; SHABCHANNEL.
 DR SMART: SM00225; BTR; 1.
 FT NON_TER
 SQ SEQUENCE 575 AA; 65808 MW; 67FAA0E214138C58 CRC64;

Query Match 5.5%; Score 262.5; DB 11; Length 575;
 Best Local Similarity 23.3%; Pred. No. 1.9e-10;
 Matches 102; Conservative 74; Mismatches 145; Indels 117; Gaps 16;

QY 115 LYNVLEPGRWA---FYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLIE 164
 D 175 LMDLEKPNSSVAKAILAISIMFIVLSTLSL-NLPELQSLDEFGQSTNPPDLAIVE 233
 QY 165 FMIVFGLFETIRIMSGACCCRYRGWGRLPARKPCVIDTIYVLISIAVSAKTQGN 224
 D 234 AVCIAMFTMEYLRLFLSSP-----KKW-----KFEKGPLNADLLAILPYVV-----T 276
 QY 225 IFATSAIRSL-----RFLQILRMVRMDRGWTKLGSVYVAHSEL-ITAW 270
 D 277 IFLTESNKSVALQONVRRVQVQIRIMIRILKIAHSTGLQSLGFETLRSSYNEGLLIL 336
 QY 271 YIGFLVIFSSFLVLYVEKDA-NKEFSTYADALMWGITLTITIGYDKPTPLTWLGRLSA 329
 D 337 FLAMGIMIFSS-LVFEAKDEDDQTKFSIPASFWMATITMTVGYGDIPTLGLGIYGV 395
 QY 330 GPALLGISFPALPAGLIGSFALKVOEQRHOKHEKRRNPANLIQCWRSYAADKSVS 389
 D 396 LCCIAGVLVIALPPIIVNFSFEYKQKROKRAIKR-----EALERAKRNGS 444

ID 09H1V6 PRELIMINARY; PRT; 606 AA.
 AC 09H1V6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE DJ10032.3.2 (Potassium voltage-gated channel, Shaw-related subfamily, member 4) (Fragment).
 DE KCNC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark G.;
 RL Submitted (0CT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL137790; CAC19684.1; -
 DR HSP; Q63734; 127N.
 DR InterPro; IPR000210; BTB_P02.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR000636; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PRO0169; KCHANNEL.
 DR PRINTS; PRO1583; KV34CHANNEL.
 DR SMART; SM00225; BTB; 1.
 FT NON TER 606
 SQ SEQUENCE 606 AA; 66698 MW; 50D8C15487F70E40 CRC64;

Query Match 5.4%; Score 254; DB 4; Length 606;
 Best Local Similarity 23.2%; Pred. No. 8.5e-10;
 Matches 111; Conservative 70; Mismatches 195; Indels 102; Gaps 17;

29 GGRGSGKNDVSGGRVUNSAARGDGLLGLTAAALGGGGGGRSGRKGARMS 88
 166 GGGGAGGSDAGDDERELALQRLGPHG-----GAGHGAGSGC---KGMQPMWA 214
 89 LAGPLSTSSQSCRRNVKRVQNVLYNLEPRGMAFYHAFVFLVFGCL----- 141
 215 LFEDPYSSRA-----RVAFASLFLVLTITTE-CLETHAEN 252
 142 -----ILVSFTIPEHTKL---ASSCLLLEFYVIVFGLFIRIMSAGCCRRYRW 191
 253 IDRWNTLEIRVGNITSVHFRREVETEPILTYEGVCVLTLEFLVRI-----VCC----- 303
 192 QGRLEFAPKPCVDTIVLI-----ASTAVSAKTOGNIPTASLSLRLOLLRWYMD 246
 304 PDLTDFVKNLNTIDFAVILPPEYEVGLSGLSKKAARDVL--GELRVVRVRLIRIFKLT 361
 247 RRGSTWKLGSVYVANSKE-LITAWYIGFLVLFSSFLVLYLEK-----DANKEF 295
 362 RHFGVGLAVLGLTASTNEFLILITFLALGVILFAT-MIYARIGARSDPPGNDHTDF 420
 296 STTADALMWGTIVLTIGYGDKTPTLWGRLLSAGFALLGISFALPAGILSGFALKVO 355
 421 KNIPIGFWMAVVVTLTIGYGMYPKTMGMLGALCALAGVLTIAMVPVIVANNFGMYS 480
 356 -EQHROKHFEKRRRNPANLLOCVMSRYAADEKSVSIATKPKHKLALHTSPTOKISFKE 414
 481 LAMAKOKLPPKRRKKNVPRPAQLESPPMYCKSEET-----SPRDSSTCSPPAREGME 534
 415 RVMAASPGOSIKRSQASVGDSPSTDTITAE-----SPTKYOKSMSPNDRTFR 465
 535 RKRADSKN-----GNANVLSDEBAGLITQPLASSPTPEERRALLRSTTDR 582

RESULT 41
 ID P91256 PRELIMINARY; PRT; 528 AA.
 AC P91256;
 DT 01-JAN-1999 (TREMBLrel. 09, Created)

DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE EXP-2 protein.
 GN F12F3.1 AND EXP-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OC NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Fulton B., Wohlmann P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: STRONG, TO C. ELEGANS C53C9.3.
 DR EMBL; U80022; AAC25887.1; -
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR000636; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PRO0169; KCHANNEL.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 341 361 POTENTIAL.
 FT TRANSMEM 413 433 POTENTIAL.
 FT TRANSMEM 441 461 POTENTIAL.
 FT TRANSMEM 472 492 POTENTIAL.
 SQ SEQUENCE 528 AA; 59574 MW; 3CB3B576697B17D9 CRC64;

Query Match 5.3%; Score 248.5; DB 5; Length 528;
 Best Local Similarity 23.5%; Pred. No. 1.7e-09;
 Matches 72; Conservative 61; Mismatches 117; Indels 57; Gaps 8;

110 RVQNTLYNLEP-----RGMAFYHAFVFLVFGCLISVFSTIP----- 150
 226 KLRMRWTLERBGSSMOAKAFELSTLFAISVNG--LS-FGITDPQYTHLMPHNE 281
 151 -----EHTKASSCLLLEFYVIVFGLFIRIMSAGCCRRYRW 195
 282 TVVLPNGTVVQVQVOMREHAPFETERICIAFFVEYCLREFAA-----PRKL 332
 196 REARKPCVYDIT-----VLASIAVSAKTOGNIPTASLSLRLOLLRWYMD 247
 333 RRLKPLNVDLAIYPTIELLITLTCGVDRKLRDLMALVYRILRVLRITIKGR 392
 248 RGGTWKLGSVYVANSKE-LITAWYIGFLVLFSSFLVLYLEK--ANKEFTYADALMWGT 306
 393 FSSGLQTFEMTLORSQKOLQOMTIVLLTGVPFSTMTIYFEKDEGTPFTSIPAYWICI 452
 307 ITLTITIGYDKTPTLWGRLLSAGFALLGISFALPAGILSGFALKVO 355
 453 VMTTVGVGDVAVPATMGKRIASAAIMCVLALPTIIVDNF-IRVADDEQDAEQOKN 511
 367 RNPANL 373
 512 DQGSQEL 518

RESULT 42
 ID Q95XD1 PRELIMINARY; PRT; 609 AA.
 AC Q95XD1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical 70.4 kDa protein.
 DE Y73B6BL.19.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OC NCBI_Taxid=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Graves T.;
 RT "The sequence of *C. elegans* cosmid Y73B6B.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084197; AAF68591.1; -
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003131; K-tetra.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K-tetra; 1.
 DR Hypothetical protein.
 KW SEQUENCE 609 AA; 70370 MW; 707C39BEE115821A CRC64;

Query Match 5.2%; Score 246; DB 5; Length 609;
 Best Local Similarity 24.2%; Pred. No. 3.3e-09;
 Matches 72; Conservative 64; Mismatches 106; Indels 56; Gaps 11;

QY 103 RRVKRYRNVLYNLE---RPRGMAFYH-----AFVLLVGCGL-----LSVST 148
 DB 150 QERLOEERVENADSTLKLSEKMMAFENPHSTSLVFEYVIGFIAVSVMCNIVET 209
 QY 149 IP--EHKRLASSC-----LLLEFVIVVEGLEFIIRMSAGCCCRMGRLRFR 199
 DB 210 IPCGIEDNVSTGCEAVEGFVIDTACVITITFYFLRLSA-----PDRIKFR 260
 QY 200 KPCVIDTIVLI---ASIAVVSARTQGNIFATSLRSLRFLQILRMVDRRGRTWKL 256
 DB 261 SIMSVIVIAIMPYVSLVLTDNKDVSGLFVT---LRVFRFLFKFSRHSQGLRLIG 315
 QY 257 SVYAHSEKELTANYIGLV-----LIFSSFLVLYVEKANKESFYADLWGTITL 309
 DB 316 YTLKSCASEL-----GFLVFSLAMALIFATIMYAEKKVDATRTSPSAFWYITVL 369
 QY 310 TTIGGKPTLWGLRLISAGFALIGSFALPAGILGSGFALKVOEHRKHFEKR 367
 DB 370 TTLGGMVSTIMGKIVGCVSLGVLYIALPVPVIVSNFS---RIYHONRADKRK 424

RESULT 43

Q26344 PRELIMINARY; PRT; 905 AA.
 AC Q26344;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Action potential broadening potassium channel.
 GN SHAB.
 OS *Aplysia* sp. (Sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_Taxid=6504;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94121918; PubMed=8292361;
 RA Quatrocki E.A., Marshall J., Kaczmarek L.K.;
 RT "A Shab potassium channel contributes to action potential broadening
 in peptidergic neurons.";

RL Neuron 12:73-86(1994).
 DR EMBL: S68356; AAC60504.2; -
 DR HSSP: Q54397; 1BL8
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K-tetra.
 DR InterPro: IPR000636; M-channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K-tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01495; SHABCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel.
 KW SEQUENCE 905 AA; 100050 MW; 2437F102167E6451 CRC64;

Query Match 5.2%; Score 245.5; DB 5; Length 905;
 Best Local Similarity 27.6%; Pred. No. 6.5e-09;
 Matches 76; Conservative 53; Mismatches 107; Indels 37; Gaps 9;

QY 115 LYNVLEP-----RGMAFYHAFVFLVFCGLLSVFSSTIPERTKLA-----SSCL 161
 DB 301 VMDLEKPTSMARVVAIISLFIIVL-----STALFTLNTIPALQDRADPSLNDQMDIA 356
 QY 162 ILFEVIVVVEGLEFIIRMSAGCCCRMGRLRFRAPKPCVIDTIVLISIAVSAKT 221
 DB 357 VVEAVCVGWFTLEIARFNAS-----PNKRFEGPLNVLD-LIAIMPEFISGLT 406
 QY 222 QGNIFATSLRSL-----RFLQILRMVDRRGRTWKLGSVYVYASKEK-TYAWYIG 273
 DB 407 ETNKSTEQONVRRVQIRIMRLILKLARSTGLQSLCYTLQSRKELGMLMTLA 466
 QY 274 FLVLISSFLVLYVEK-ANKESFYADALWGTITLTITIGDKTPLTWGLRLISAGFA 332
 DB 467 IFLLFSS-LAYFAEKDEPEKYSIPETFWMAITMTVVGDIYPTVLGKVGVSVC 525
 QY 333 LIGISFPALPAGILGSGFALKVQEOHRKHFEKR 367
 DB 526 ICGVLYIALPPIIVNFAEYKQDMREKAKFR 560

RESULT 44

Q22012 PRELIMINARY; PRT; 484 AA.
 AC Q22012;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE R186.5 protein.
 GN R186.5.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z78016; CAB01442.1; -
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003968; Kv_channel.

```

DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M_channel_nlg.
DR InterPro: IPR003974; Shaw_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01491; KYCHANNEL.
DR PRINTS: PR01498; SHAWCHANNEL.
DR SMART: SM00225; BTB; 1.
SQ SEQUENCE 484 AA; 55471 MW; 39F02D8F26705609 CRC64;

```

Query Match	5.2%	Score 245;	DB 5;	Length 484;
Best Local Similarity	24.28;	Pred. NO. 2.7e-09;		
Matches 72; Conservative	59;	Mismatches 117;	Indels 50;	Gaps 8

QY 108 YRRQNYLYNLERP---RGWAFITHAVFELLFEGCLI-----LSVFSTIPE 15
 148 WQTKPRIMRLFDENSSRSQAFOIAISVFELITAIYVCLTHPGLRIPELAPFGNFSR 207
 QY 152 HTKLAAS-----CLLLEFVMIVGLEGLEITIRIWSAGCCRYGMWG 193
 208 NHRSTSRINHPAQINDKANSRPHETPMYIETICIMWFIETL-----ARESSCP 258
 QY 194 RLRRARRPFCVIDITVLASIAVVSAKTQGNIFANLSALRSLFLOILRMVBMRRGGTWK 253
 259 REFELRRAPVNIID---IYATILFTYIDLLSSMGATADLEFFSTIRIMRLPKLTHNHSGLK 315
 QY 254 LIGSVVYASHKEL-ITAWYIGFVLVLIFFSFLVYL--VEKDANKRSTYADALMWTITLT 310
 316 ILMTFPRASAKELMLVEFVLIGVVFASLVYVARSVESENEDNQFVSIPLGLMVALVTMT 375
 QY 311 TIGGDKTPLTWLGRLLSAGFALLGISFAPLAPAGLIGSFALKVDE-QHRKHFEKRR 367
 376 TIGVGTITPHTYLRLLGISICALGCVLTALDEVPVIVSFAFMYSHTQARSKMPKRR 433

RESULT	45
09NSA2	
ID	09NSA2
AC	09NSA2;
DT	01-OCT-2000 (TReMBLrel. 15, Created)
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT	01-MAR-2002 (TReMBLrel. 20, last annotation update)
DE	Shal-type potassium channel (Kv4.1).
GN	KCND1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HEART;
RA	Makita N., Shirai N., Sawa H., Sasaki K., Nagashima K., Yoshida M.C.
RA	Kitabatake A.;
RL	"Homo sapiens mRNA for shal-type potassium channel KCND1 (Kv4.1).";
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL AB021865; BA96454.1; -
DR	InterPro: IPR000210; BTF; POZ.
DR	InterPro: IPR001622; K+channel_pore.
DR	InterPro: IPR004054; Kv4channel.
DR	InterPro: IPR003091; K_channel.
DR	InterPro: IPR003131; K_tetra.
DR	InterPro: IPR000636; M+channel_nlg.
DR	Pfam: PF00520; Ion_trans; I.
DR	Pfam: PF02214; K_tetra; I.
DR	PRINTS; PRO0169; KCHANNEL.
DR	PRINTS; PRO1516; KV4CHANNEL.
DR	SMART; SM00225; BTF; 1.
KW	Ionic channel.
SEQUENCE	647 AA; 71371 MW; 464326308398CC3A CRC64;

Query Match 5.28; Score 245; DB 4; Length 647;

Best Local Similarity 22.7%; Pred. No. 4, 2e-09;
Matches 108; Conservative 79; Mismatches 171; Indels 118; Gaps 22

```

OY 115 LYNNLERR-----GWAFTYHAFVFLVYGCILLSEFTIP-----EHKTL 155
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 LMRAFENHSTAAALVEFYVYTGFFLAV--SYIANVETIIPCGSARRBSRBPCEGRPQ 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 156 ASSCLLIEFWAVIVEGLEFTIRIWSAGCCCRYRGMGRRLRFPARRPCVIDITVILA-SI 214
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 AFFC---MDTACVLLTEGYELLRLEFA-----PSCRFLRSVMSLIDIVALLPYII 277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 215 AVSAKTCGNIFATSAIILRLEJOTLRNVRBDRGCTKKILGSVYAAHSEKITMYIGF 274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 278 GLVYK---NDVSAEYVTLRFKFRFRLEPKSRHSQGLRIIGYLLKSCASEL-----GF 328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 275 L-----VLISSELYLVLEKEDANK--EFSTYADALIMWGTITLTITGYDKPTWLGRL 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 LFLSLTMAIIIFATVMEY-AEKGTKTKTFNTINPAFWTITVMTLIGGDWVPSITACKI 387
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 327 LSAGFALLGIFFPALPACILGSGFALKVQEOHROKHFEKRRNPANLIQC----- 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 388 FGSICSLSGVLYIALPPIIVSNFS--RIYHONDRACKR--AOQKRLARILRILAKSGT 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 377 -----VMRSYADEKSVSI--ATMKRLKALH-----TQSPNOKLSFKER 415
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 TNAFLQYKONGNGLEBSGSEGCALCYNRKSAFEQOHNLHLLCLETTHFEFLDELTFESA 502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 416 VRMASPRGOSIKSRQAS--VG-----DRNSPTDITAEGSPTRVOKWSMSEFNDRTR 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 503 LGAVSPGRTSRSTSVSQPVGPGSLSSCCPRRAKRAIRLANSTASVSRG-SMQELDM 561
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 464 FRPSLRKSSQPKPIVADTALGTDVDDYDEKGGQD-----VSVEDLRRPLKT 511
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 562 LAGLRSHAPORSKSLNAKP-----HSDLDLNDGSDQVAAITISIP--TPPANT 608
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT	46.		
ID	075671		
AC	075671	PRELIMINARY;	PRT; 647 AA.
DT	01-NOV-1998	(TREMBLrel. 08, Created)	
DT	01-NOV-1998	(TREMBLrel. 08, last annotation update)	
DT	01-MAR-2002	(TREMBLrel. 20, last annotation update)	
DE	Shal-type potassium channel (Voltage-gated potassium channel Kva.1).		
GN	KCNKD1.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RA	Strom T.M., Miyakura G., Hellebrand H., Drescher B., Rosenthal A.,		
RA	Meindl A.,		
RT	"Transcription map in Xp11.23."		
RL	Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA, AND KIDNEY;		
RC	MEDLINE=20195625; PubMed=10729221;		
RA	Isbrandt D., Lelcher T., Walschutz R., Zhu X., Luhmann U., Michel U.		
RA	Salter K., Pongs O.;		
RT	"Gene structures and expression profiles of three human KCND (Kv4)		
RT	potassium channels mediating A-type currents I(TO) and I(SA)."		
RL	Genomics 64:144-154 (2000).		
DR	EMBL; AJ005898; CAA06755.1; -		
DR	EMBL; AF166006; AAF65617.1; -		
DR	EMBL; AF166004; AAF65617.1; JOINED.		
DR	EMBL; AF166005; AAF65617.1; JOINED.		
DR	EMBL; AF166003; AAF65516.1; -		
DR	InterPro; IPR000210; BTB_P0Z.		
DR	InterPro; IPR001622; K+channel_pore.		


```

QY 123 -RGMAFIYHAEVFLVFG-----CL-----ILSVSTIPEHTKLASSCLLI 162
DB 225 SRAAFIFAFSLFFLIVSTTTCLEHFAFNKYKNTKEPIYNGSVLQYEIEDPALTY 284
QY 163 LEFVIAVFGLEFIRIMSAGCCCRYRGMOGRLEFARKPECVDTIVLI-----ASIAV 217
DB 285 VEGVCVWFTEFLVRIYS-----PNKLEFIKNLNIIDFVALPPELVGLSGL 335
QY 218 SAKOQNFATSLRSLRLOILRMVMDRSGTAKLGSVVAHSE-LITAVYIGFLV 276
DB 336 SSKAKADV--GELNVRFRILRIFKLRHVEGLRVLGHTRASTNEFLLLIFLALGV 393
QY 277 LIFSSFLVLYEK-----DANKFSTYADALMWGTTITLTIGYDTPLTWLGRL 326
DB 394 LIFAT-MIYIAERVAQOPNDPSASEHTQFNIPIGFWMVAVYMTTIGYDMYPTQWSGL 452
QY 327 LSGFALLIGISFPALPAGIL----GSGFALKVOEQ----HROKH 362
DB 453 VGALCALAGVLTAMPVPVIVNNFGMYSLAMAKOKLPRKRKH 496

```

RESULT 49

```

Q96PRL PRELIMINARY; PRT; 638 AA.
AC 096PRL;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Voltage gated potassium channel Kv3.2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Vega-Saenz de Miera E.C., Lau D.H.P., Mathew S., Miller A.C.,
RA Kucherlapati R., Rudy B.;
RT "Localization of the Voltage-Gated Potassium Channel Gene KCNC2 to
RT Human Chromosome 12q21 and Cloning of Two of Its Alternatively-Spliced
RT Transcripts, Kv3.2a and Kv3.2b."
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF208896; AAL27272.1; -
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR01581; KV3CHANNEL.
DR Ionic channel.
SQ SEQUENCE 638 AA; 70225 MW; 211CAF8395A58C5D CRC64;

```

Query Match 5.1%; Score 243; DB 4; Length 638;

Best Local Similarity 23.8%; Pred. No. 5.8e-09; Mismatches 109; Indels 88; Gaps 13;

```

QY 65 AATLGGGGGGRSGRGRGAGMSLLGKPLSTYSOSCCRNVYRYRYNYLVLRP-- 122
DB 195 AAGIGGPD-----GKSG-----RMRRLOQPMMLAFEDPYS 224
QY 123 -RGMAFIYHAEVFLVFG-----CL-----ILSVSTIPEHTKLASSCLLI 162
DB 225 SRAAFIFAFSLFFLIVSTTTCLEHFAFNKYKNTKEPIYNGSVLQYEIEDPALTY 284
QY 163 LEFVIAVFGLEFIRIMSAGCCCRYRGMOGRLEFARKPECVDTIVLI-----ASIAV 217
DB 285 VEGVCVWFTEFLVRIYS-----PNKLEFIKNLNIIDFVALPPELVGLSGL 335
QY 218 SAKOQNFATSLRSLRLOILRMVMDRSGTAKLGSVVAHSE-LITAVYIGFLV 276
DB 336 SSKAKADV--GELNVRFRILRIFKLRHVEGLRVLGHTRASTNEFLLLIFLALGV 393
QY 327 LIFSSFLVLYEK-----DANKFSTYADALMWGTTITLTIGYDTPLTWLGRL 326

```

```

DB 394 LIFAT-MIYIAERVAQOPNDPSASEHTQFNIPIGFWMVAVYMTTIGYDMYPTQWSGL 452
QY 327 LSGFALLIGISFPALPAGIL----GSGFALKVOEQ----HROKH 362
DB 453 VGALCALAGVLTAMPVPVIVNNFGMYSLAMAKOKLPRKRKH 496

```

RESULT 50

```

Q9XND1 PRELIMINARY; PRT; 490 AA.
AC 09XND1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Y48A6B.6 protein.
GN Y48A6B.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
DE none.
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RL EMBL; AL023844; CAI19530.1; -.
DR HSSP; 054397; 1BL8.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
SQ SEQUENCE 490 AA; 55361 MW; 7DFA90EBD58C261 CRC64;

```

Query Match 5.1%; Score 242.5; DB 5; Length 490;

Best Local Similarity 27.1%; Pred. No. 4.2e-09; Mismatches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

```

QY 104 RNKRYRYRYNYLVLRP----RGMAFIYHAEVFLV-FGCLISVSTIPEHTKLASS 158
DB 192 KTLRFGELIRCVWNIIEEPASSGKAQFAVCSVYFVLISGLVGLSLEIQAATKORNN 251
QY 159 -----CLILIEFVMTIVFGLFIRIMSAGCCCRYRGMOGR--FARKP 201
DB 252 LIGEEFTEPMPIILGIEYICVIMFMEGLKMLVS--ARSKTFKOLLNIIDILALIP 309
QY 202 FCVIDITIVLIASIAVYSAKTQNFATSLRSLRLOILRMVMDRSGTAKLGSVYA 261
DB 310 F-IIEMLLIFIGISTQLRLDKAFV--VIRILVLRVIRVLRKIGRYSGLQMFEXTLKA 366
QY 262 HSKELITAMTIGVLVLIFFSFLVLYVKD--ANKFSTYADALMWGTTITLTIGYDTP 319
DB 367 SFRQLQMMAMVAVTGVIFSTLAVFLFKEDPAK--FHSIPAAQWCIVTMTTVGGLDP 425
QY 320 LFWLRLSLAGFALLIGISFPALPAGIISGFPALKVOEQHR 359
DB 426 VIVPGKLVATGALACGVLYALPITITIVDNF-MKVAETER 464

```

Search completed: June 14, 2003, 17:44:21

Job time : 111 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:44:26 ; Search time 54 Seconds
(without alignments)
1827.466 Million cell updates/sec

Title: US-09-825-147-2

Perfect score: 4733
Sequence: 1 MPRHAGGEGAGAGIWMKS.....SICKAGESTDALSLPHVKK 923

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4733	100.0	923	10	US-09-825-147-2
2	4713.5	99.6	932	10	US-09-813-148-2
3	4547	95.1	888	10	US-09-810-796-5
4	4527.5	95.7	897	10	US-09-810-796-4
5	1991	42.1	695	10	US-09-810-796-15
6	1991	42.1	696	10	US-09-813-148-6
7	1793	37.9	844	10	US-09-813-148-4
8	1793	37.9	844	10	US-09-810-796-14
9	1792.5	37.9	722	9	US-10-128-870-23
10	1792.5	37.9	722	9	US-10-131-685-20
11	1788.5	37.8	871	9	US-10-128-870-20
12	1788.5	37.8	871	9	US-10-131-685-20
13	1620.5	33.2	872	10	US-09-813-148-5
14	1603.5	33.9	854	9	US-10-128-870-27
15	1603.5	33.9	854	9	US-10-131-685-27
16	1207.5	25.5	300	9	US-10-128-870-4
17	1207.5	25.5	300	9	US-10-128-870-6
18	1207.5	25.5	300	9	US-10-131-685-4
19	1207.5	25.5	300	9	US-10-131-685-6

20	1102	23.3	676	9	US-10-138-316-2	Sequence 2, Appl1
21	1102	23.3	676	10	US-09-840-125-2	Sequence 2, Appl1
22	1102	23.3	676	10	US-09-813-148-3	Sequence 3, Appl1
23	1100.5	23.3	605	9	US-10-128-870-24	Sequence 24, Appl1
24	1100.5	23.3	605	9	US-10-131-685-24	Sequence 24, Appl1
25	1085	22.9	310	9	US-10-128-870-18	Sequence 18, Appl1
26	1085	22.9	310	9	US-10-131-685-18	Sequence 18, Appl1
27	1081.5	22.9	570	9	US-10-138-316-114	Sequence 114, App
28	993.5	21.0	245	9	US-10-128-870-8	Sequence 8, Appl1
29	993.5	21.0	245	9	US-10-131-685-8	Sequence 8, Appl1
30	957	20.2	298	9	US-10-128-870-2	Sequence 2, Appl1
31	957	20.2	298	9	US-10-131-685-2	Sequence 2, Appl1
32	905.5	19.1	430	9	US-10-128-870-21	Sequence 21, Appl1
33	905.5	19.1	430	9	US-10-131-685-21	Sequence 21, Appl1
34	898.5	19.0	376	9	US-10-138-316-113	Sequence 113, App
35	485.5	10.3	137	9	US-10-128-316-109	Sequence 109, App
36	255	5.4	446	10	US-09-864-761-37011	Sequence 37011, A
37	250	5.3	539	9	US-10-325-891-13	Sequence 13, Appl1
38	245	5.2	646	9	US-10-121-746-10	Sequence 10, Appl1
39	243	5.1	601	9	US-10-121-746-4	Sequence 4, Appl1
40	243	5.1	638	9	US-10-024-623-11	Sequence 11, Appl1
41	242	5.1	638	9	US-10-024-623-33	Sequence 33, Appl1
42	232.5	4.9	635	12	US-10-062-879-2	Sequence 2, Appl1
43	230	4.9	511	9	US-10-192-116A-7	Sequence 7, Appl1
44	229	4.8	636	12	US-10-062-879-4	Sequence 4, Appl1
45	224	4.7	477	9	US-10-121-746-18	Sequence 18, Appl1
46	223	4.7	499	9	US-10-121-746-8	Sequence 8, Appl1
47	223	4.7	500	9	US-09-999-220B-5	Sequence 5, Appl1
48	206.5	4.4	494	9	US-10-325-891-4	Sequence 4, Appl1
49	206.5	4.4	494	12	US-10-143-002-4	Sequence 4, Appl1
50	206.5	4.4	532	9	US-09-875-321-13	Sequence 13, Appl1
51	206.5	4.4	532	9	US-10-162-012-13	Sequence 13, Appl1
52	206.5	4.3	532	10	US-09-993-811-6	Sequence 6, Appl1
53	204.5	4.3	456	10	US-09-974-712-2	Sequence 2, Appl1
54	204.5	4.3	490	9	US-10-121-746-6	Sequence 6, Appl1
55	204.5	4.3	491	9	US-09-999-220B-3	Sequence 3, Appl1
56	203.5	4.3	446	9	US-09-875-321-8	Sequence 8, Appl1
57	203.5	4.3	446	9	US-10-162-012-8	Sequence 8, Appl1
58	201.5	4.3	454	10	US-09-993-811-12	Sequence 12, Appl1
59	201.5	4.3	456	10	US-09-989-920-175	Sequence 175, App
60	201.5	4.3	456	10	US-09-993-811-2	Sequence 2, Appl1
61	199.5	4.2	513	9	US-10-325-891-2	Sequence 2, Appl1
62	199.5	4.2	513	12	US-10-143-002-2	Sequence 2, Appl1
63	198.5	4.2	579	9	US-09-922-364A-19	Sequence 19, Appl1
64	198.5	4.2	579	9	US-09-254-590-19	Sequence 19, Appl1
65	198.5	4.2	579	9	US-10-115-695-19	Sequence 19, Appl1
66	198.5	4.2	579	9	US-10-116-561-19	Sequence 19, Appl1
67	198.5	4.2	579	9	US-10-115-671-19	Sequence 19, Appl1
68	198.5	4.2	579	9	US-10-115-415-19	Sequence 19, Appl1
69	198.5	4.2	579	9	US-10-116-260-19	Sequence 19, Appl1
70	198.5	4.2	579	9	US-10-115-688-19	Sequence 19, Appl1
71	198.5	4.2	847	9	US-09-875-321-2	Sequence 2, Appl1
72	198.5	4.2	847	9	US-10-162-012-2	Sequence 2, Appl1
73	193	4.1	491	9	US-09-999-220B-4	Sequence 4, Appl1
74	192.5	4.1	580	9	US-09-922-364A-2	Sequence 2, Appl1
75	192.5	4.1	580	9	US-09-254-590-2	Sequence 2, Appl1
76	192.5	4.1	580	9	US-10-115-695-2	Sequence 2, Appl1
77	192.5	4.1	580	9	US-10-116-561-2	Sequence 2, Appl1
78	192.5	4.1	580	9	US-10-115-671-2	Sequence 2, Appl1
79	192.5	4.1	580	9	US-10-115-415-2	Sequence 2, Appl1
80	192.5	4.1	580	9	US-10-116-260-2	Sequence 2, Appl1
81	192.5	4.1	580	9	US-10-115-688-2	Sequence 2, Appl1
82	188	4.0	115	10	US-09-925-297-612	Sequence 612, App
83	186	3.9	425	9	US-10-016-647-2	Sequence 2, Appl1
84	174	3.7	61	9	US-10-138-316-108	Sequence 108, App
85	174	3.7	545	9	US-09-999-220B-2	Sequence 2, Appl1
86	174	3.7	545	9	US-09-999-220B-34	Sequence 34, Appl1
87	174	3.7	545	9	US-09-999-220B-36	Sequence 36, Appl1
88	174	3.7	545	9	US-09-999-220B-116	Sequence 116, App
89	174	3.7	545	9	US-09-999-220B-118	Sequence 118, App
90	174	3.7	545	9	US-09-999-220B-120	Sequence 120, App
91	174	3.7	561	9	US-09-922-364A-1	Sequence 1, Appl1
92	174	3.7	561	9	US-09-254-590-1	Sequence 1, Appl1

93	174	3	7	561	9	US-10-115-695-1
94	174	3	7	561	9	US-10-116-561-1
95	174	3	7	561	9	US-10-116-671-1
96	174	3	7	561	9	US-10-115-415-1
97	174	3	7	561	9	US-10-116-260-1
98	174	3	7	561	9	US-10-115-688-1
99	166.5	3.5	215	9	US-10-555-532-4	
100	163.5	3.5	223	9	US-09-875-321-9	
101	163.5	3.5	223	9	US-10-162-012-9	
102	163.5	3.5	557	9	US-09-922-364A-20	
103	163.5	3.5	557	9	US-09-922-364A-47	
104	163.5	3.5	557	9	US-09-922-364A-47	
105	163.5	3.5	557	9	US-10-115-695-20	
106	163.5	3.5	557	9	US-10-116-561-20	
107	163.5	3.5	557	9	US-10-115-671-20	
108	163.5	3.5	557	9	US-10-115-415-20	
109	163.5	3.5	557	9	US-10-116-260-20	
110	163.5	3.5	557	9	US-10-115-688-20	
111	163.5	3.5	736	9	US-09-922-364A-47	
112	163.5	3.5	736	9	US-09-922-364A-47	
113	163.5	3.5	736	9	US-10-115-695-47	
114	163.5	3.5	736	9	US-10-116-561-47	
115	163.5	3.5	736	9	US-10-115-671-47	
116	163.5	3.5	736	9	US-10-115-415-47	
117	163.5	3.5	736	9	US-10-116-260-47	
118	160.5	3.4	458	9	US-10-115-688-47	
119	160.5	3.4	458	9	US-09-922-364A-47	
120	160.5	3.4	458	9	US-09-922-364A-47	
121	160.5	3.4	458	9	US-10-115-695-47	
122	160.5	3.4	458	9	US-10-116-561-47	
123	160.5	3.4	458	9	US-10-115-671-47	
124	160.5	3.4	458	9	US-10-115-415-47	
125	160.5	3.4	458	9	US-10-116-260-47	
126	159.5	3.4	553	9	US-10-115-688-43	
127	159.5	3.4	553	9	US-09-922-364A-43	
128	159.5	3.4	553	9	US-09-922-364A-43	
129	159.5	3.4	553	9	US-10-115-695-43	
130	159.5	3.4	553	9	US-10-116-561-43	
131	159.5	3.4	553	9	US-10-115-671-43	
132	159.5	3.4	553	9	US-10-115-415-43	
133	159.5	3.4	553	9	US-10-116-260-43	
134	159.5	3.4	732	9	US-10-115-688-43	
135	159.5	3.4	732	9	US-09-922-364A-43	
136	159.5	3.4	732	9	US-09-922-364A-43	
137	159.5	3.4	732	9	US-10-115-695-43	
138	159.5	3.4	732	9	US-10-116-561-43	
139	159.5	3.4	732	9	US-10-115-671-43	
140	159.5	3.4	732	9	US-10-115-415-43	
141	159.5	3.4	732	9	US-10-116-260-43	
142	159.5	3.4	732	9	US-10-115-688-43	
143	153	3.2	2344	10	US-09-815-242-12713	
144	153	3.2	120	9	US-10-128-870-28	
145	153	3.2	890	9	US-10-131-685-28	
146	151	3.2	890	9	US-10-158-684-4	
147	146.5	3.2	890	9	US-10-158-711-4	
148	144.5	3.1	335	9	US-09-738-628-4367	
149	141	3.0	189	10	US-09-864-761-35104	
150	141	3.0	328	9	US-09-922-364A-27	
			328	9	US-09-254-590-27	

ALIGNMENTS

RESULT 1
 US-09-825-147-2
 : Sequence 2, Application US/09625147
 : Patent No. US20020042505A1
 : GENERAL INFORMATION:
 : APPLICANT: Hu, Yi
 : APPLICANT: Kieke, James Alvin
 : APPLICANT: Turner, C. Alexander Jr
 : APPLICANT: Nehls, Michael C.
 : APPLICANT: Friedrich, Glenn

[illegible]

```

: APPLICANT: Zambrowicz, Brian
:
: TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
:
: TITLE OF INVENTION: Polynucleotides Encoding the Same
:
: FILE REFERENCE: LEX-0160-USA
:
: CURRENT APPLICATION NUMBER: US/09/825,147
:
: CURRENT FILING DATE: 2001-04-03
:
: PRIOR APPLICATION NUMBER: US 60/194,255
:
: PRIOR FILING DATE: 2000-04-03
:
: NUMBER OF SEQ. ID NOS: 3
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 2
:
: LENGTH: 923
:
: TYPE: PRT
:
: ORGANISM: homo sapiens
:
: US-09-825-147-2

```

Query Match	100.0%	Score 4733;	DB 10;	Length 923;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 923;	Conservative 0;	Mismatches	0;	Gaps 0

Query Match	100.0%;	Score 4733;	DB 10;	Length 923;
-------------	---------	-------------	--------	-------------

Matches 923; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MPRHHAGGEEGGAAGLWVKSAAAAAAGGGRLGSGMKDVEESGRVLLNSAARGDLL 60

1 MPRHHAGGEEGGAAGLWVKSAAAAAAGGGRLGSGMKDVESGRGRVLLNSAARGDGLL 60

61 LGTRAATLGGGGGGLRESRRGKOGARMSLGKPLSYTSSOSCIBRNKYRBYONYI.YNYI.F 120

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

100 11M 11N 12M 12N 13M 13N 14M 14N 15M 15N 16M 16N 17M 17N 18M 18N 19M 19N 20M 20N 21M 21N 22M 22N 23M 23N 24M 24N 25M 25N 26M 26N 27M 27N 28M 28N 29M 29N 30M 30N 31M 31N 32M 32N 33M 33N 34M 34N 35M 35N 36M 36N 37M 37N 38M 38N 39M 39N 40M 40N 41M 41N 42M 42N 43M 43N 44M 44N 45M 45N 46M 46N 47M 47N 48M 48N 49M 49N 50M 50N 51M 51N 52M 52N 53M 53N 54M 54N 55M 55N 56M 56N 57M 57N 58M 58N 59M 59N 60M 60N 61M 61N 62M 62N 63M 63N 64M 64N 65M 65N 66M 66N 67M 67N 68M 68N 69M 69N 70M 70N 71M 71N 72M 72N 73M 73N 74M 74N 75M 75N 76M 76N 77M 77N 78M 78N 79M 79N 80M 80N 81M 81N 82M 82N 83M 83N 84M 84N 85M 85N 86M 86N 87M 87N 88M 88N 89M 89N 90M 90N 91M 91N 92M 92N 93M 93N 94M 94N 95M 95N 96M 96N 97M 97N 98M 98N 99M 99N

121 NFGWAF I IHAH VF LUVFGLLSVFSIPEHIKLASSCLLLEFVMI VFGLEELIRIW 180

181 SAGCCCRYRGWQRLRFARKPFVCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQIL 240

181 SAGCCCRYGWQGLRFARKPECVIDTIVLLASIAVVSAKTQGNIFATSALRSLRFLQIL 240

Y 241 RMVRMDRGCTWKLGSVVAHskELITAMyIGFLVLIffSFLVYLVEKDANKEfESTYAD 300

b 241 RMVRMDRGGTWWKLLGSSVVAHSEKITAWYIGFLVLTSSFLVYLVEKPAKKEESTYAD 300

301 A T W G T T T T T T C Y C D K T B I T W I G B I S A C E A I C I S E E A I D A C T I C C C E A I K V A E O U R C A 360

[illegible]

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

001 RNF ENNNFANL IQ VWKS IAADEASVSIATWPHLKALHTCS PINQKLSFKERVMAS 420

361 KHEKRRNPANLIQCVMRSYADEKSVSIAIWKPHLKALHTCSPTNQKLSFEKERVMS 420

```

421 PRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTFRFPSLRLKSSQPKPVID 480

```

421 PRGSIKSRQASVGDRRSPSTIDITAEGSPTKVQKSWSEFNDRTFRFRLKSSQPKPVID 480

481 ADTALGTDVYDEKGCQCDVSVDLTPLKTVIRAIRIMKFHVAKRKEETLRPYDKDV 540

481 ADTALGTDVYDEKGCOCPSVEDLTPLKTVIBAIRIMKFNHVAKRREKETI.PRYDYKDY 540

541 TEVVSACHT DWT CBTVCT OBPYDOTT CVCSTECNVCNNVTM; WUTEMNT OVET QVVTTT... 600

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

[illegible]

601 EKQVQSIKLPCLDIQQVLRKGSASALALASFQIPFECEQTSIDYQSPVDSKDLSS 660

601 EKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPECEQTSQSPVDSKDLGS 660

661 A Q N S G C L S R S T S A N I S R G L Q F I L T P N E F S A Q T F Y A L S P T M H S Q A T Q V P I S Q S D G S A V A A T 720

661 A Q N S G C L S R S T S A N I S R G L Q F I L T P N E F S A Q T F Y A L S P T M H S O A T O V P I S O S D G S A V A A T 720

721 NTAHOTNTAPKPAДTITOTPBPI.PATKH.I.PPETH.KPNPACIOECTSDIVETTCIVASKE 780

[illegible]

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

QY 781 NVQAQSNLTDRSMRKSFDMDGETLLSVCPMPVKDGLKSLSVONLIRSTEELIOLSGS 840
|||||
Db 781 NVQAQSNLTDRSMRKSFDMDGETLLSVCPMPVKDGLKSLSVONLIRSTEELIOLSGS 840
QY 841 ESSGSRGSDQDFPKWRESKLFITDEEVGPETETDTPDAAPQAPARAFAASDLRTGRSR 900
|||||
Db 841 ESSGSRGSDQDFPKWRESKLFITDEEVGPETETDTPDAAPQAPARAFAASDLRTGRSR 900
QY 901 SSOSICKAGESTDALSLPHVKLK 923
|||||
Db 901 SSOSICKAGESTDALSLPHVKLK 923
RESULT 2
US-09-813-148-2
; Sequence 2, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHER, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF CEN
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-2
Query Match 99.6%; Score 4713.5; DB 10; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 922; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 1 MPRHHAGEEGGAALWYKSGAAAAAGGGRGSGMKDVESEGRVLLNSAARGGLL 60
|||||
Db 1 MPRHHAGEEGGAALWYKSGAAAAAGGGRGSGMKDVESEGRVLLNSAARGGLL 60
QY 61 LGTRATATGGGGGGLRESRGRKOGARMSLLGKPLSTYSSOSCRNNKYRRVQVLYLVLE 120
|||||
Db 61 LGTRATATGGGGGGLRESRGRKOGARMSLLGKPLSTYSSOSCRNNKYRRVQVLYLVLE 120
QY 121 RPRGMAFYHAFVFLVFGCLLSVFTIPEHTKLASSCLLLEFVMIIVVGELEFIIRIW 180
|||||
Db 121 RPRGMAFYHAFVFLVFGCLLSVFTIPEHTKLASSCLLLEFVMIIVVGELEFIIRIW 180
QY 181 SAGCCCRRRGNGRLRPAKPCVVDITVLIASIAVSAKQONITATSLRSLRQITL 240
|||||
Db 181 SAGCCCRRRGNGRLRPAKPCVVDITVLIASIAVSAKQONITATSLRSLRQITL 240
QY 241 RNVRRDRRGGTWKLGLSVYVAHSHKELITAMVIGFLVLISSEFVYVLEKANKFEFTYAD 300
|||||
Db 241 RNVRRDRRGGTWKLGLSVYVAHSHKELITAMVIGFLVLISSEFVYVLEKANKFEFTYAD 300
QY 301 ALMMGTITLTITIGYDGTPTLWLGRLLSAGFALLGISFPALPAGILGSGFALKVQEOHRQ 360
|||||
Db 301 ALMMGTITLTITIGYDGTPTLWLGRLLSAGFALLGISFPALPAGILGSGFALKVQEOHRQ 360
QY 361 KHEEKRRNPAANLQCVMSYAADEKSVSIATWKPPLKALHTCSPT-----NOKLS 411
|||||
Db 361 KHEEKRRNPAANLQCVMSYAADEKSVSIATWKPPLKALHTCSPT-----NOKLS 411
QY 412 FKERVMASSPRGOSIKRSQASVGDRRSPSTDTAEGSPPTVKQKSWSFNDRTFRFSLRLK 471
|||||

Db 421 FKERVMASSPRGOSIKRSQASVGDRRSPSTDTAEGSPPTVKQKSWSFNDRTFRFSLRLK 480
|||||
QY 472 SSQPKPIYIDATFALCTDQVYDEKGCQCCVSVEDLTPPLKTYIRAIRIKKFNHAKRKRET 531
|||||
Db 481 SSQPKPIYIDATFALCTDQVYDEKGCQCCVSVEDLTPPLKTYIRAIRIKKFNHAKRKRET 540
QY 532 LRPYDVADVIEQYAGHLDMLCRITSLQTRDQILGKQITSDKSKREKTEAHEHTDOL 591
|||||
Db 541 LRPYDVADVIEQYAGHLDMLCRITSLQTRDQILGKQITSDKSKREKTEAHEHTDOL 600
QY 592 SMLGRVYKVEKQVQVIESKLDCLDIYQVLRKGSASALALASFQIPPECEQTSIDYQSP 651
|||||
Db 601 SMLGRVYKVEKQVQVIESKLDCLDIYQVLRKGSASALALASFQIPPECEQTSIDYQSP 660
QY 652 VDSKDLGSAQNSGCLSRSTANISRGLOFILTPEHFAQCTFYALSPTHMSQATVPISQ 711
|||||
Db 661 VDSKDLGSAQNSGCLSRSTANISRGLOFILTPEHFAQCTFYALSPTHMSQATVPISQ 720
QY 712 SDGSAAVATNTIANQINTAPKPAFTTQIPPLPAIKHLPPETLHPNAGLOESISDV 771
|||||
Db 721 SDGSAAVATNTIANQINTAPKPAFTTQIPPLPAIKHLPPETLHPNAGLOESISDV 780
QY 772 TTCLVASKENYQVQSNLTDRSMRKSFDMDGETLLSVCPMPVKDGLKSLSVONLIRSTE 831
|||||
Db 781 TTCLVASKENYQVQSNLTDRSMRKSFDMDGETLLSVCPMPVKDGLKSLSVONLIRSTE 840
QY 832 ELNLTQSGSESSGSDQDFPKWRESKLFITDEEVGPETETDTPDAAPQAPARAFAAS 891
|||||
Db 841 ELNLTQSGSESSGSDQDFPKWRESKLFITDEEVGPETETDTPDAAPQAPARAFAAS 900
QY 892 DSLRTGRSSOSICKAGESTDALSLPHVKLK 923
|||||
Db 901 DSLRTGRSSOSICKAGESTDALSLPHVKLK 932
RESULT 3
US-09-810-796-5
; Sequence 5, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGen, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNO5-2
US-09-810-796-5
Query Match 96.1%; Score 4547; DB 10; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 MKDVESSGGRVLLNSAARGDGLLIGTRAAFLGGGGGLRSRRKQOGARMSLLKPLS 95
|||||
Db 1 MKDVESSGGRVLLNSAARGDGLLIGTRAAFLGGGGGLRSRRKQOGARMSLLKPLS 60
QY 96 YTSOSCRNNKYRRVQVLYLVLEPRGMAFYHAFVFLVLEGCILLSVFTIPEHTKL 155
|||||
Db 61 YTSOSCRNNKYRRVQVLYLVLEPRGMAFYHAFVFLVLEGCILLSVFTIPEHTKL 120
QY 156 ASSCLLLEFVMIIVVGELEFIIRIWSAGCCCRYRGWGRRLRPAKPCVVDITVLIASIA 215
|||||

```

121 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRKMGOGRLFAKRPFCVIDITVILASIA 180
216 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTAKLIGSVYAHSKELITAMVIGFL 275
181 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTAKLIGSVYAHSKELITAMVIGFL 240
276 VLISSFLVYLVEKDANKKESTYADALMWGTITLTITIGYDGTPLTWLGRLLSAGFALLG 335
241 VLISSFLVYLVEKDANKKESTYADALMWGTITLTITIGYDGTPLTWLGRLLSAGFALLG 300
336 ISFEPALPAGILSGFALKVOEHRQKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 395
301 ISFEPALPAGILSGFALKVOEHRQKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 360
396 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAEKSPKVKOKS 455
361 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAEKSPKVKOKS 420
456 WSFNDRTFRPSLRKSSQPKPVADTALGTDVYDEKGCQCDVSEDLTPPLKTVIRA 515
421 WSFNDRTFRPSLRKSSQPKPVADTALGTDVYDEKGCQCDVSEDLTPPLKTVIRA 480
516 IRIMEFHAARKKFKETLRPYDKVIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 575
481 IRIMEFHAARKKFKETLRPYDKVIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 540
576 KSREKITAEHETTDLSMLGRVYKVEKQVOSIESKLDCLDIYQOVLKRSASALALASF 635
541 KSREKITAEHETTDLSMLGRVYKVEKQVOSIESKLDCLDIYQOVLKRSASALALASF 600
636 QIPPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTPNEFSAQTFYA 695
601 QIPPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTPNEFSAQTFYA 660
696 LSPTHMSOATQVPIQSODGSAVAATNTIANQINTAPKPAPTLQIPPLPAIHLPRPE 755
661 LSPTHMSOATQVPIQSODGSAVAATNTIANQINTAPKPAPTLQIPPLPAIHLPRPE 720
756 TLHPNPAGIQESISDVTTCVLVASKENVQVAAQSNLTKDRSMKRSFDMGGETLLSYCPMPVK 815
721 TLHPNPAGIQESISDVTTCVLVASKENVQVAAQSNLTKDRSMKRSFDMGGETLLSYCPMPVK 780
816 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDQPYPKWRESKLFITDEBVGPEETED 875
781 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDQPYPKWRESKLFITDEBVGPEETED 840
876 TFDAAPOPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 923
841 TFDAAPOPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 888

```

```

; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(640)
; OTHER INFORMATION: conserved region of KCNQ5-1
US-09-810-796-4

Query Match      95.7%; Score 4527.5; DB 10; Length 897;
Best Local Similarity 98.9%; Pred. No. 1.8e-318;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

36 MCVESGRGNVLLNSAARGDGLLLGTRAAITLGGGGGGLRBSRKGQKQAGARMSLLGKPLS 95
1 MKVYESGRGHVLLNSAARGDGLLLGTRAAITLGGGGGGLRBSRKGQKQAGARMSLLGKPLS 60
96 YTSQSCRNVKRRVQNYLNVLERPRGMAFIYHAFVFLVFGCLLSVESTIEPHTL 155
61 YTSQSCRNVKRRVQNYLNVLERPRGMAFIYHAFVFLVFGCLLSVESTIEPHTL 120
156 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRKMGOGRLFAKRPFCVIDITVILASIA 215
121 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRKMGOGRLFAKRPFCVIDITVILASIA 180
216 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTAKLIGSVYAHSKELITAMVIGFL 275
181 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTAKLIGSVYAHSKELITAMVIGFL 240
276 VLISSFLVYLVEKDANKKESTYADALMWGTITLTITIGYDGTPLTWLGRLLSAGFALLG 335
241 VLISSFLVYLVEKDANKKESTYADALMWGTITLTITIGYDGTPLTWLGRLLSAGFALLG 300
336 ISFEPALPAGILSGFALKVOEHRQKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 395
301 ISFEPALPAGILSGFALKVOEHRQKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 360
396 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAEKSPKVKOKS 455
361 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAEKSPKVKOKS 420
456 WSFNDRTFRPSLRKSSQPKPVADTALGTDVYDEKGCQCDVSEDLTPPLKTVIRA 515
421 WSFNDRTFRPSLRKSSQPKPVADTALGTDVYDEKGCQCDVSEDLTPPLKTVIRA 480
516 IRIMEFHAARKKFKETLRPYDKVIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 575
481 IRIMEFHAARKKFKETLRPYDKVIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 540
576 KSREKITAEHETTDLSMLGRVYKVEKQVOSIESKLDCLDIYQOVLKRSASALALASF 635
541 KSREKITAEHETTDLSMLGRVYKVEKQVOSIESKLDCLDIYQOVLKRSASALALASF 600
636 QIPPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTPNEFSAQTFYA 695
601 QIPPEECQOTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFTLTPNEFSAQTFYA 660
696 LSPTHMSOATQVPIQSODGSAVAATNTIANQINTAPKPAPTLQIPPLPAIHLPRPE 755
661 LSPTHMSOATQVPIQSODGSAVAATNTIANQINTAPKPAPTLQIPPLPAIHLPRPE 720
756 TLHPNPAGIQESISDVTTCVLVASKENVQVAAQSNLTKDRSMKRSFDMGGETLLSYCPMPVK 815
721 TLHPNPAGIQESISDVTTCVLVASKENVQVAAQSNLTKDRSMKRSFDMGGETLLSYCPMPVK 780
816 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDQPYPKWRESKLFITDEBVGPEETED 875
781 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDQPYPKWRESKLFITDEBVGPEETED 840
876 TFDAAPOPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 923
841 TFDAAPOPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 888

```

```

US-09-810-796-4
; Sequence 4, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegaia, Timothy James
; APPLICANT: ICAGEN, INC.
; TITLE OF INVENTION: KCNQ5, A NO. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated

```

```

US-09-810-796-15
RESULT 5

```

```

: Sequence 15, Application US/09810796
: Patent No. US20020102677A1
: GENERAL INFORMATION:
: APPLICANT: Jeggia, Timothy James
: APPLICANT: IChogen, Inc.
: TITLE OF INVENTION: KCNO5, a No. US20020102677A1a1 Potassium Channel
: FILE REFERENCE: 018512-005010US
: CURRENT APPLICATION NUMBER: US/09/810,796
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 60/190,954
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 15
: LENGTH: 695
: TYPE: PR
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human KCNO4
: US-09-810-796-15

```

Query Match 42.1%; Score 1991; DB 10; Length 695;

Best Local Similarity 57.8%; Pred. No. 1,7e-135;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

```

Qy 25 AAAGGRLSGMKDVEGSGRVLNSAARGDGLLLGTRAAATLGGGGGGLRESRRGKG 84
Db 2 AEAPRRRLGGLPPGDARAEIALTAVOSEG-----EAGGGSPR----- 43
Qy 85 ARMSLLGKPL-----SYSSQSCRNVKRYRNVNYLYNLERPGMAFIYH 130
Db 44 -RLGLSSPLPGALPPLPGSGSGSAGCGRSSAAKRRYRLQNMVYNLERPGMAFIYH 102
Qy 131 AFVFLVFGCLLSVFTIPEHTKLASSCLLLEFVMIVFGLFIIRIRMSGCCRRYG 190
Db 103 VFILVFSCLVSLSTIOHQLANECCLLLEFVMIVFGLFIIRIRMSGCCRRYG 162
Qy 191 WQRLRFARKPCFYIDITVLIASIAVSAKTQGNIFATSALRSRLRQLILRMVMDRGG 250
Db 163 WQGRFRARKPCFYIDITVLIASIAVSAKTQGNIFATSALRSRLRQLILRMVMDRGG 222
Qy 251 TWKLLGSVVAHAKSKELITAWYIGFLVLIFFSFLVYLVERDANKESTYADALMWGTTTLT 310
Db 223 TWKLLGSVVAHAKSKELITAWYIGFLVLIFFSFLVYLVERDANKESTYADALMWGTTTLT 282
Qy 311 TIGGDKPTLWGLWGLSAGFALLGISFPALPAGILGSGFALKVOQHOKHEKRRMPA 370
Db 283 TIGGDKPTLWGLWGLSAGFALLGISFPALPAGILGSGFALKVOQHOKHEKRRMPA 342
Qy 371 ANLIQCVWRSYAAD-EKSVSIATW----- 393
Db 343 ANLIQAAARLXSTDMRAVLTATWYYDILSPRELALFEHVORARNGGLRPLEVRA 402
Qy 394 -----KPHLKLHT-----CSPINOKLSFEKERVMAASPRGOSIKSRQ--ASVGR 436
Db 403 PVPDGAAPSRYPVATCHRPSTSPCGESSRNGIKDRIMGSSQRTGTGSKQDLAPPTMP 462
Qy 437 RSPSTDIATAG-SPTKVOKSMGFNDRTFRPSLRKSSQPKPVITADTALGTDDVDEKG 495
Db 463 TSPSEQVGEATSPTRKVOKSMGFNDRTFRASRLR-----KPTSAEDA-PSEVEAEKS 516
Qy 496 CQCDVSVEDLTPPLKTVIRAIRIMKFKVAKRKFETLRPYDVKVDIEYSAGHLMICRI 555
Db 517 YOCELTVDDIMPAVYTVIRSIIRILKFLVAKRKKEFLRPYDVADVIEQYSAHGLDMLGRI 576
Qy 556 KSLQTRVVOIIGKQITSDKRSRE---KITAEHETDDLSMGRVYKVEQVOYSIESKLD 612
Db 577 KSLQTRVVOIIGKQITSDKRSRE---KITAEHETDDLSMGRVYKVEQVOYSIESKLD 612
Qy 613 CLLDYVOOVLKRGSAALALASFOIPEPCEOTSDVQSVDSKDLGSAQNSCLSRSTS 672
Db 635 LILGYSKRLMSGSTA---SLGAVQVPLFPDITSDHSFVDDHEDISVSAQTLS-ISRVS 691

```

```

Qy 673 ANI 675
Db 692 TMN 694

```

RESULT 6

US-09-813-148-6

: Sequence 6, Application US/09813148

: Patent No. US20020076809A1

: GENERAL INFORMATION:

: APPLICANT: STEINMEYER, Klaus

: APPLICANT: LERCHER, Christian

: APPLICANT: SCHERER, Constanze

: APPLICANT: SEEBOHM, Guiscard

: APPLICANT: BUSCH, Andreas E.

: TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF

: FILE REFERENCE: 38005-119

: CURRENT APPLICATION NUMBER: US/09/813,148

: CURRENT FILING DATE: 2001-03-21

: PRIOR APPLICATION NUMBER: DE 100 13 732.6

: PRIOR FILING DATE: 2000-03-21

: PRIOR APPLICATION NUMBER: US 60/194,041

: PRIOR FILING DATE: 2000-04-03

: NUMBER OF SEQ ID NOS: 6

: SOFTWARE: PatentIn version 3.0

: SEQ ID NO 6

: LENGTH: 696

: TYPE: PR

: ORGANISM: Homo sapiens

: US-09-813-148-6

Query Match 42.1%; Score 1991; DB 10; Length 696;

Best Local Similarity 57.8%; Pred. No. 1,7e-135;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

```

Qy 25 AAAGGRLSGMKDVEGSGRVLNSAARGDGLLLGTRAAATLGGGGGGLRESRRGKG 84
Db 2 AEAPRRRLGGLPPGDARAEIALTAVOSEG-----EAGGGSPR----- 43
Qy 85 ARMSLLGKPL-----SYSSQSCRNVKRYRNVNYLYNLERPGMAFIYH 130
Db 44 -RLGLSSPLPGALPPLPGSGSGSAGCGRSSAAKRRYRLQNMVYNLERPGMAFIYH 102
Qy 131 AFVFLVFGCLLSVFTIPEHTKLASSCLLLEFVMIVFGLFIIRIRMSGCCRRYG 190
Db 103 VFILVFSCLVSLSTIOHQLANECCLLLEFVMIVFGLFIIRIRMSGCCRRYG 162
Qy 191 WQRLRFARKPCFYIDITVLIASIAVSAKTQGNIFATSALRSRLRQLILRMVMDRGG 250
Db 163 WQGRFRARKPCFYIDITVLIASIAVSAKTQGNIFATSALRSRLRQLILRMVMDRGG 222
Qy 251 TWKLLGSVVAHAKSKELITAWYIGFLVLIFFSFLVYLVERDANKESTYADALMWGTTTLT 310
Db 223 TWKLLGSVVAHAKSKELITAWYIGFLVLIFFSFLVYLVERDANKESTYADALMWGTTTLT 282
Qy 311 TIGGDKPTLWGLWGLSAGFALLGISFPALPAGILGSGFALKVOQHOKHEKRRMPA 370
Db 283 TIGGDKPTLWGLWGLSAGFALLGISFPALPAGILGSGFALKVOQHOKHEKRRMPA 342
Qy 371 ANLIQCVWRSYAAD-EKSVSIATW----- 393
Db 343 ANLIQAAARLXSTDMRAVLTATWYYDILSPRELALFEHVORARNGGLRPLEVRA 402
Qy 394 -----KPHLKLHT-----CSPINOKLSFEKERVMAASPRGOSIKSRQ--ASVGR 436
Db 403 PVPDGAAPSRYPVATCHRPSTSPCGESSRNGIKDRIMGSSQRTGTGSKQDLAPPTMP 462
Qy 437 RSPSTDIATAG-SPTKVOKSMGFNDRTFRPSLRKSSQPKPVITADTALGTDDVDEKG 495
Db 463 TSPSEQVGEATSPTRKVOKSMGFNDRTFRASRLR-----KPTSAEDA-PSEVEAEKS 516
Qy 496 CQCDVSVEDLTPPLKTVIRAIRIMKFKVAKRKFETLRPYDVKVDIEYSAGHLMICRI 555

```



```

QY 201 PCVIDITVLIASIAVYSAKTOGNIENFATSALRSLEFLOILRMVDRMGCTKLLGSVY 260
Db 167 PCVIDITVLIASIAVYSAKTOGNIENFATSALRSLEFLOILRMVDRMGCTKLLGSVY 226
QY 261 AHSKELITWAMYIGFLVLISSFLVLYVEKDANKKESTFADALMWTITLTITIGYDGPPL 320
Db 227 AHSKELITWAMYIGFLVLISSFLVLYVEKDANKKESTFADALMWTITLTITIGYDGPPL 286
QY 321 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEORHOKHFEKRRNPANLIQCWRS 380
Db 287 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEORHOKHFEKRRNPANLIQCWRS 346
QY 381 YAAD-----EKSYSIATWK--PHLKALHTC-----SPT 406
Db 347 YATNLSRTDLHSTMOYERYIVTPMYRLIPLNQLELLRNLSKSGGLFRKRPDPSP- 405
QY 407 NOKLSFERVMAASRGOSIKSROASVGD--RRSPSTDTTAEAGSPTKYOKSMSEFDRTRF 464
Db 406 SOKVSLKDRV-FSSPRGVAAGKGSPOQOTVARSPSADQSLDPSKVPKSMSEFDRSRA 464
QY 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVDLTPLKTVIRAIRIMKFNVA 524
Db 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVDLTPLKTVIRAIRIMKFNVA 523
QY 525 KRKFKETLRPYDVADVTEQYSGHIDMLCRISLOTRODILGKOITSDKKSREKTTAE 584
Db 524 KRKFKETLRPYDVADVTEQYSGHIDMLCRISLOTRODILGKOITSDKKSREKTTAE 582
QY 585 HETTDLSMLGRVYVKEKOVOSIESKLDCLDIYOQVLKSGASALALASFOIIPREC-- 642
Db 583 AELPEDESMGRIGLVEKQVLSMEKKDLFLVITYMQ--RMG-----IPPEETA 629
QY 643 -----EQTSDYOSPVDSKIDSGSAONSGCLSRSTANISRGLOITLPNESAQTFFA 695
Db 630 YFGAKEPPAPPYHSPEDSRD--HYDRHGCTIVKIVRSSSTG-----QKNSSAP-A 678
QY 696 LSPMHQSQTQVPISSO-----DGSVAATNTTIANINTAPKPAAPLTQI----- 741
Db 679 APP-----VOCPESTSQPOSHPRQGHGTSVYDGHSLVIRPPRAHERSLAYSAGNR 732
QY 742 -----PP-----PLPAIKHLPRPETLHPNAGLOESISDVTTCL 775
Db 733 ASMEFLROEDTPGCRPPETLHSDTSTISIPSVH-----EELERSPSGF--SISQ----- 781
QY 776 VASKENVOAOS 787
Db 782 --SKENIDLANS 791

RESULT 9
US-10-128-870-23.
; Sequence 23, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blauhar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DCS8adiv
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

```

```

; LENGTH: 722
; TYPE: PRF
; ORGANISM: MOUSE
US-10-128-870-23
Query Match 37.9% Score 1792.5; DB 9; Length 722;
Best Local Similarity 53.4%; Pred. No. 4,1e-121;
Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;

QY 21 GAAAAAGCGRLSGMKDVESGRGRVILNSAAAGDGLLLGTRATYGGGGGRLRESR 80
Db 9 GYVPGTSGEKKLKGFFGLDPGA-----PDSTRGALLIGSEAPK--RGSVLSKPT 59
QY 81 GKOGARSLGKPLSTYSSGCRNRVYRRONYLYNLYNLEPRGAFIYHAFVFLVFGC 140
Db 60 GGAGA-----GKP-----PKRNAFYRKQNLNLYNLEPRGAFIYHAFVFLVFGC 106
QY 141 LLSVSTPIBHTKLASSCLLLEFVMIIVGFELEIRIIMSAGCCCRYRGWGRLPARK 200
Db 107 LVLSVFSTIKEREKSEBGLTYLEIVTVGVEYFVRIMAGCCCRYRGWRGRLPARK 166
QY 201 PCVIDITVLIASIAVYSAKTOGNIENFATSALRSLEFLOILRMVDRMGCTKLLGSVY 260
Db 167 PCVIDITVLIASIAVYSAKTOGNIENFATSALRSLEFLOILRMVDRMGCTKLLGSVY 226
QY 261 AHSKELITWAMYIGFLVLISSFLVLYVEKDANKKESTFADALMWTITLTITIGYDGPPL 320
Db 227 AHSKELITWAMYIGFLVLISSFLVLYVEKDANKKESTFADALMWTITLTITIGYDGPPL 286
QY 321 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEORHOKHFEKRRNPANLIQCWRS 380
Db 287 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEORHOKHFEKRRNPANLIQCWRS 346
QY 381 YAAD-----EKSYSIATWK--PHLKALHTC-----SPT 406
Db 347 YATNLSRTDLHSTMOYERYIVTPMYRLIPLNQLELLRNLSKSGGLFRKRPDPSP- 405
QY 407 NOKLSFERVMAASRGOSIKSROASVGD--RRSPSTDTTAEAGSPTKYOKSMSEFDRTRF 464
Db 406 SOKVSLKDRV-FSSPRGVAAGKGSPOQOTVARSPSADQSLDPSKVPKSMSEFDRSRA 464
QY 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVDLTPLKTVIRAIRIMKFNVA 524
Db 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVDLTPLKTVIRAIRIMKFNVA 523
QY 525 KRKFKETLRPYDVADVTEQYSGHIDMLCRISLOTRODILGKOITSDKKSREKTTAE 584
Db 524 KRKFKETLRPYDVADVTEQYSGHIDMLCRISLOTRODILGKOITSDKKSREKTTAE 582
QY 585 HETTDLSMLGRVYVKEKOVOSIESKLDCLDIYOQVLKSGASALALASFOIIPREC-- 642
Db 583 TELPEDESMGRIGLVEKQVLSMEKKDLFLVITYMQ--RMG-----IPPEETA 629
QY 643 -----EQTSDYOSPVDSKIDSGSAONSGCLSRSTANISRGLOITLPNESAQTFFA 695
Db 630 YFGAKEPPAPPYHSPEDSRD--HYDRHGCTIVKIVRSSSTG-----QKNSSAP-A 678
QY 696 LSPMHQSQTQVPISSO-----DGSVAATNTTIANINTAPKPAAPLTQI----- 741
Db 679 APP-----VOCPESTSQPOSHPRQGHGTSVYDGHSLVIRPPRAHERSLAYSAGNR 732
QY 742 -----PP-----PLPAIKHLPRPETLHPNAGLOESISDVTTCL 775
Db 733 ASMEFLROEDTPGCRPPETLHSDTSTISIPSVH-----EELERSPSGF--SISQ----- 781
QY 776 VASKENVOAOS 787
Db 782 --SKENIDLANS 791

RESULT 10
US-10-131-685-23
; Sequence 23, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blauhar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

```

```

; FILE REFERENCE: DC58aCON
; CURRENT APPLICATION NUMBER: us/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 722
; TYPE: PRF
; ORGANISM: MOUSE
US-10-131-685-23

Query Match      37.9%; Score 1792.5; DB 9; Length 722;
Best Local Similarity 53.4%; Pred. No. 4,1e-121;
Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19,

QY 21 GAAAAAGGRLSGMKDVGSGRGVLLNSAARGDGLLGLTRATLGGGGGLRESR 80
DB 9 GYVPGTSGEKKLKVGVLDPGA-----PDSTRDGLALLGSEAPK---RGSVLSKPR 59
QY 81 GKQARMSLLGKPLSTYSQSCRNVKRYRVQNTLYNLERPRGMATYAAVFLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKQNFYLVLERPRGMATYAAVFLVESC 106

QY 141 LILVSTIPEHRTKLASSCLLLEFVIVYFGEFIIRIMSGACCCYRGMOGRLEFR 200
DB 107 LVLSVFSTIKETKESGALYILEYTVYVGEYEVPRIMAAAGCCCRGMGRGLKFAK 166
QY 201 PCVVIDITVLASIAVSAKTQGNIFATSALRSRLFQILRMVMDRGRGTWKLGSVY 260
DB 167 PFCVIDIMVLASIAVLAAGSGNVFATSALRSRLFQILRMVMDRGRGTWKLGSVY 226
QY 261 AHSKELITAMYGFLVLISSFLVLYVEKDANKFEFTYADALMWGTTTLTIGYDKT 320
DB 227 AHSKELITAMYGFLVLISSFLVLYVEKDANKFEFTYADALMWGTTTLTIGYDKT 286
QY 321 TWLGRLLSAGFALLGISFALPAGILSGFALKVQBOHOKHFEKRRNPANLLOCVRS 380
DB 287 TWNGRLLAATFTLLIGVSFPALPAGILSGFALKVQBOHOKHFEKRRNPANLLOCVRS 346
QY 381 YAAD-----EKSVSIATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRDLHSTWQYERVTVPWYRLPLNOLLELLNLKSKGLTFEKEPQEPS 405
QY 407 NOKLSFERVMASSPRGOSIKSROASVGD--RRSPSTDLTAEGSPTRKVKQWSFNDR 464
DB 406 SOKVSLADRV-FSSPRGMANKGKSPQAOQTVARSPADSDLDSPSKVPKSWMSFGDSRT 464
QY 465 RPSLRLLSSOPRPVIDADTALGTDVYDEKGCOCVDVSDLPPLTVIRAIRIMHVA 524
DB 465 ROAFRIRINGAASRONSEASLP--GEDIVEDNKSCEVETEDLTPGLKAVSTIACV 523
QY 525 KRRKRELRLRPDVADVYEQYSAGHLDMLCRISLQTRVDQILGKOITSDKSKREK 584
DB 524 KRRKRELRLRPDVADVYEQYSAGHLDMLCRISLQTRVDQILGKOITSDKSKREK 582
QY 585 HETDDLSMLGRVAVKVEKOVOSIESKLDCLDIYQOVLRKGSASALALASFOLEPFC 642
DB 583 TELPDESSMGRKLGVEKQVLSMEKKDLFLVSIYQ--RMG-----PPAPETEA 629
QY 643 -----EQNSDYOSPVDSKDLGSAONSGC---LSRSTANISRLQOIFLTPNESA 692
DB 630 YFGAKEPEBPAPYHSPEDSRD---HADKHGCIKIVRSTSS-----TGQR 671
QY 693 FYALSPTMHSAQOVPIQS 712
DB 672 NYAAPPAI--PPAQCPESTS 689

```

```

US-10-128-870-20
; Sequence 20, Application US/10128870
; Patent No. US2002016872A1
; GENERAL INFORMATION:
; APPLICANT: Blana, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aDIV
; CURRENT APPLICATION NUMBER: us/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 871
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-128-870-20

Query Match      37.8%; Score 1788.5; DB 9; Length 871;
Best Local Similarity 46.8%; Pred. No. 1e-120;
Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAAAGGRLSGMKDVGSGRGVLLNSAARGDGLLGLTRATLGGGGGLRESR 80
DB 9 GYVPGTSGEKKLKVGVLDPGA-----PDSTRDGLALLGSEAPK---RGSVLSKPR 59
QY 81 GKQARMSLLGKPLSTYSQSCRNVKRYRVQNTLYNLERPRGMATYAAVFLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKQNFYLVLERPRGMATYAAVFLVESC 106
QY 141 LILVSTIPEHRTKLASSCLLLEFVIVYFGEFIIRIMSGACCCYRGMOGRLEFR 200
DB 107 LVLSVFSTIKETKESGALYILEYTVYVGEYEVPRIMAAAGCCCRGMGRGLKFAK 166
QY 201 PCVVIDITVLASIAVSAKTQGNIFATSALRSRLFQILRMVMDRGRGTWKLGSVY 260
DB 167 PFCVIDIMVLASIAVLAAGSGNVFATSALRSRLFQILRMVMDRGRGTWKLGSVY 226
QY 261 AHSKELITAMYGFLVLISSFLVLYVEKDANKFEFTYADALMWGTTTLTIGYDKT 320
DB 227 AHSKELITAMYGFLVLISSFLVLYVEKDANKFEFTYADALMWGTTTLTIGYDKT 286
QY 321 TWLGRLLSAGFALLGISFALPAGILSGFALKVQBOHOKHFEKRRNPANLLOCVRS 380
DB 287 TWNGRLLAATFTLLIGVSFPALPAGILSGFALKVQBOHOKHFEKRRNPANLLOCVRS 346
QY 381 YAAD-----EKSVSIATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRDLHSTWQYERVTVPWYRLPLNOLLELLNLKSKGLTFEKEPQEPS 405
QY 407 NOKLSFERVMASSPRGOSIKSROASVGD--RRSPSTDLTAEGSPTRKVKQWSFNDR 464
DB 406 SOKVSLADRV-FSSPRGMANKGKSPQAOQTVARSPADSDLDSPSKVPKSWMSFGDSRT 464
QY 465 RPSLRLLSSOPRPVIDADTALGTDVYDEKGCOCVDVSDLPPLTVIRAIRIMHVA 524
DB 465 ROAFRIRINGAASRONSEASLP--GEDIVEDNKSCEVETEDLTPGLKAVSTIACV 523
QY 525 KRRKRELRLRPDVADVYEQYSAGHLDMLCRISLQTRVDQILGKOITSDKSKREK 584
DB 524 KRRKRELRLRPDVADVYEQYSAGHLDMLCRISLQTRVDQILGKOITSDKSKREK 582
QY 585 HETDDLSMLGRVAVKVEKOVOSIESKLDCLDIYQOVLRKGSASALALASFOLEPFC 642
DB 583 TELPDESSMGRKLGVEKQVLSMEKKDLFLVSIYQ--RMG-----PPAPETEA 629
QY 643 -----EQNSDYOSPVDSKDLGSAONSGC---LSRSTANISRLQOIFLTPNESA 692
DB 630 YFGAKEPEBPAPYHSPEDSRD---HADKHGCIKIVRSTSS-----TGQR 671
QY 693 FYALSPTMHSAQOVPIQS 712
DB 672 NYAAPPAI--PPAQCPESTS 689

```

Db 584 LOSRVDOIVGPAITD-KDRTKGPAEALPEPDSMMGRGLGVEKOVLSMEKKLDELVNI 642
 QY 618 YOQVLRKGSASALALASFOIPPEFC-----EOTS DYOSPVSKDLGSAONSGCLS 668
 Db 643 YMO--RNG-----IPTEEATFGAKEPEPAPYHSPEDSRE---HYDRGCIY 686
 QY 669 RSTSANISRGLOFLTPNEFSAOTFYALSPTMHSAOTVPIQS-----DGSVAAT 720
 Db 687 KIVSSSSSTG-----QKNFSAP--AAP-----VOCPPSTMQPOSHPRGHGTSPIV 732
 QY 721 NTIANQINTAPKPAFTLQI-----PP-----PLPAI 748
 Db 733 GDHGSILVRIPPPAHERSLAYGGGNRASMEFLROEDTPGCRPPETGLRDSITSISIPSV 792
 QY 749 KHLRPELHPNPAGLOESIDVTTCIYASKEKNOVAOS 787
 Db 793 DH----EELERSFSGF--SISO-----SKENLALNS 818

RESULT 12

US-10-131-685-20
 ; Sequence 20, Application US/10131685
 ; Publication No. US20030044912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauar, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauber, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ACON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; PRIOR FILING DATE: 1997-08-12
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-131-685-20

Query Match 37.8%; Score 1788.5; DB 9; Length 871;

Best Local Similarity 46.8%; Pred. No. 1e-120;

Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAAAGGRLGSGMKDVEGGRVLLNSAARGDILLGTRATLGGGGGLRESRR 80
 Db 9 GVGPGSEKKLKVGVLDPGA-----PDSTROGALLIASSEAK---RGSILKPPRA 59
 QY 81 GKQGRMSLGLKPLSTYSOSCRNNVKKRYONYLYNVLEPRGMAFYHAFFLLVFGC 140
 Db 60 GGAGA-----GKP-----PKRNAFYKLIQNFLYNVLEPRGMAFYHAFFLLVESC 106
 QY 141 LILSVFTPIPHRTKLIASSCLLLEFVMIVVPEGLFIRIRWSAGCCCRRYGMORLFAK 200
 Db 107 LVLVSFTIKKEKSESGALYLLVTVIVFVGVFVRIMAGCCCRRYGMORLFAK 166
 QY 201 PFCVIDTIVLILASIVVSAKTGNIFFATSLRFLQILIRVMDRGRGTWKLGSVYV 260
 Db 167 PFCVIDIVILASIVVLAAGSGNVFATSLRFLQILIRVMDRGRGTWKLGSVYV 226
 QY 261 AHSKELTAWYIGFLVLFSSFLVYLVKDKANKPESTYADALWGTITLTIGYGDKPTL 320
 Db 227 AHSKELTAWYIGFLVLFSSFLVYLVKDKANKPESTYADALWGTITLTIGYGDKPTL 286
 QY 321 TWLGLSAGFALGISFPAIAGLIGSGFALKVGOHQHOKHEKRRNPAANIQCWMS 380
 Db 287 TWNGRLAATYTLIGVSPFALPAGILIGSGFALKVGOHQHOKHEKRRNPAAGLIGSAMP 346

QY 381 YAAD-----EKSVIATWK-----PHIKALHT----- 402
 Db 347 YATNLSTDLHSTWQYERVIVTVMYSQOTQYCASRLIPLNLQELLRLNLSKSGLAER 406
 QY 403 -----CSP--TWOKLSFKERVAMASPRGSISSRQASVGD--RR 437
 Db 407 KDPPEPSPKSGPCRGPLCGCCPGRSSQKVSCLKRV-FSSRGVAAAGKSPQAOQYVR 465
 QY 438 SPSTDIATGSPPTVOKMSFNDRTFRPSPRLKSSQPKPYADATLGTDDVYBEKGO 497
 Db 466 SPADQSLBDSPPKVPKWSFSGDSRANQARIKAASRQ--NSRASILGEDIYVDKSP 523
 QY 498 CDVSDEDLTPPLKTVIRAIRMKFHVAKRKRETLRPYDKVIBOYSAGHIDMLCRKS 557
 Db 524 CEVTEEDTLPLKVISIRAVCMRFLVSKRKRESLRPYDVMVIBOYSAGHIDMLSRKS 583
 QY 558 LOTRVDOILKGQOTSDSKSREKITAHEETDDLSMLGRVYKVEKOVOSIESKLDCLDI 617
 Db 584 LOSRVDOIVGPAITD-KDRTKGPAEALPEPDSMMGRGLGVEKOVLSMEKKLDELVNI 642
 QY 618 YOQVLRKGSASALALASFOIPPEFC-----EOTS DYOSPVSKDLGSAONSGCLS 668
 Db 643 YMO--RNG-----IPTEEATFGAKEPEPAPYHSPEDSRE---HYDRGCIY 686
 QY 669 RSTSANISRGLOFLTPNEFSAOTFYALSPTMHSAOTVPIQS-----DGSVAAT 720
 Db 687 KIVSSSSSTG-----QKNFSAP--AAP-----VOCPPSTMQPOSHPRGHGTSPIV 732
 QY 721 NTIANQINTAPKPAFTLQI-----PP-----PLPAI 748
 Db 733 GDHGSILVRIPPPAHERSLAYGGGNRASMEFLROEDTPGCRPPETGLRDSITSISIPSV 792
 QY 749 KHLRPELHPNPAGLOESIDVTTCIYASKEKNOVAOS 787
 Db 793 DH----EELERSFSGF--SISO-----SKENLALNS 818

RESULT 13

US-09-813-148-5

; Sequence 5, Application US/09813148
 ; Patent No. US20020076809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHER, Christian
 ; APPLICANT: SEEBOHM, Guisard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813,148
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/194,041
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 872
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-813-148-5

Query Match 34.2%; Score 1620.5; DB 10; Length 872;

Best Local Similarity 42.2%; Pred. No. 1.4e-108;

Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;

QY 7 GGEAGGAAGLWVKSAAAAAGGRLGSGMKDVEGGR-----VLNSAARGDILL 60
 Db 14 GGGGGGGG-----GGAANPAGGDAAGADEKRGGLAGVDEOYTLALGAGADKDTLL 68
 QY 61 LGTRAAATLGGGGGLRESRRKQAGRMSLGLK-PLSTYSOSCRNNVKKRYONYLYNV 119

Db 726 RPTVLPILTLLDSRSCH--SQADLOGPYSD-----RISPRQ-----RRSIT 765
 QY 801 MGGETLLSVCMPVPKDLKSLISVONLIRNTEELINQLSGSESSGSGSODFPY----KMR 856
 Db 766 RDSOTPLSL-----MSVNH-----EELERSPSGFSISODRDDYVFGNGSSWM 809
 QY 857 ESKLEFIDEEVGEPEETDTF 877
 Db 810 REKRYLAE---GETDTDTDPF 827

RESULT 15

US-10-131-685-27
 ; Sequence 27, Application US/10131685
 ; Publication No. US20030044912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauar, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubaer, Michael G.
 ; APPLICANT: Yang, Wen-pin
 ; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58aCON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; PRIOR FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 854
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-131-685-27

Query Match 33.9%; Score 1603.5; DB 9; Length 854;
 Best Local Similarity 42.7%; Pred. No. 2,4e-107;

Matches 393; Conservative 109; Mismatches 252; Indels 167; Gaps 29;

QY 20 SGAAAGAGG--GRGSGMKDYESGGRVILNSAARGDILLIGRAATLGGGGGLRE 77
 Db 11 AGGDAAAAGDEDERKTVGLAGDVEQ---VTLAAGAGDKDCTLL-----EGGGDEG 59
 QY 78 SRRGQAGMSLLGR-PLSYTSSQSCRNVKRYRNVNYLVLERPRGMAFIYHAEVLL 136
 Db 60 QRRTPQG--IGLAKTPLSRPVK---RNNAKYRIQTLIYDALERPRGMAFIYHAEVLL 114
 QY 137 VEGCLLSVFSITPIRHTKLASSCLLLEFVMIVFGLFIRIWSAGCCCRYGWGRRLR 196
 Db 115 VGLCATLLAVLTFFKETEVSQWLLLETFALFIFGAEPALRLWAAGCCCRYGWGRRLR 174
 QY 197 FARKPFVCDITVLIVLASIVASAKTQGNIFATSLSLFQLILRWVRMDRGSTWKL 256
 Db 175 FARKPLMDIVLLASVVAVANGNVLAIS-LRSLRLQLILRLMRDRRGSTWKL 233
 QY 257 SVVYHAKSKELLTAWYIGFLVLIFFSFLVLYVEKDA-----NKESTYADALWGT 306
 Db 234 SAICAHKSKELLTAWYIGFLVLIFFSFLVLYVEKDA-----NKESTYADALWGT 293
 QY 307 ILLTIGGDKTPLMWGLLSAGFALLIGSFALPAGLIGSGFALKVQBOHROKHREKR 366
 Db 294 ILLTIGGDKTPLMWGLLSAGFALLIGSFALPAGLIGSGFALKVQBOHROKHREKR 353
 QY 367 RNPANLILQCVRSYNADEKSVS-IATWK-----PHKALHTCSPTQOKLSFKRRVR 417
 Db 354 RNPANLILQCVRSYNADEKSVS-IATWK-----PHKALHTCSPTQOKLSFKRRVR 413
 QY 418 MASPGQSTKSRQASVGDRRSPSTDTTAECSPTKVKQSMGFNDTRRPSIRLK-----471
 Db 414 LSNPGRSNRK-----GKLTPLNVDAIESPSKEPKPVGILNNKERRFRTAFRMKAYAFWQ 467

QY 472 SSQPKPVYADATGTDVDYDEKGGQCVSEEDLTPPLKTVYAIRIMKFAVKKRREKET 531
 Db 468 SSE-----DACTG---DPMADRGYGNDFPLEDMPTLKAIRAYRITLQFLYKKKKFET 519
 QY 532 LRPYDVADVIEOYSAGHLMCLRIKSLQTRVDQILGKQITSDKSR-----578
 Db 520 LRPYDVADVIEOYSAGHLMCLRIKSLQTRVDQILGKQITSDKSR-----579
 QY 579 -----EKITAEHETT--DDLMSGRYVYKQVQOISLESKLDCLLDIYQVLR-----623
 Db 580 SPRNEPYVARPSTSEIEQSMGKFKVVEROVQDGKKLDFLVDMQHMERLQVQVTEY 639
 QY 624 ---KGSASALALASQRIPEFCQTSQSPVDSKDLGSAQNSGCLSRSTANISRGHQ 680
 Db 640 YPTKGTSS-----PAERKEDNRYS-DLKTICNYSETGPPEPFYF-----682
 QY 681 FILTPNERSAOTFYALSPTHMSQATQVPIQSOSGSAVATNTIANQINTAPPAFTTQ 740
 Db 683 -QVITDKSPYGFFAHDF-----VNLPRGSPSGKQVQAT-----PRSATTYVE 725
 QY 741 IPPPLPAIKHLPREPTLPNPAQLOESISDYTTCLVASKENYQVQSNLTKRSMKSPD 800
 Db 726 RPTVLPILTLLDSRSCH--SQADLOGPYSD-----RISPRQ-----RRSIT 765
 QY 801 MGGETLLSVCMPVPKDLKSLISVONLIRNTEELINQLSGSESSGSGSODFPY----KMR 856
 Db 766 RDSOTPLSL-----MSVNH-----EELERSPSGFSISODRDDYVFGNGSSWM 809
 QY 857 ESKLEFIDEEVGEPEETDTF 877
 Db 810 REKRYLAE---GETDTDTDPF 827

RESULT 16

US-10-128-870-4
 ; Sequence 4, Application US/10128870
 ; Patent No. US20020168724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubaer, Michael G.
 ; APPLICANT: Yang, Wen-pin
 ; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58aDIY
 ; CURRENT APPLICATION NUMBER: US/10/128,870
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 300
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-128-870-4

Query Match 25.5%; Score 1207.5; DB 9; Length 300;
 Best Local Similarity 74.7%; Pred. No. 2,2e-79;

Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

QY 91 GKPLSYTSSQSCRNVKRYRNVNYLVLERPRGMAFIYHAEVLLVFGCLLSVSTIP 150
 Db 5 GRP-----PKRNFYKTLQNFILNVLERPRGMAFIYHAEVLLVSTLVSVSTIK 56
 QY 151 EHTKLASSCLLLEFVMIVFGLFIRIWSAGCCCRYGWGRRLRPAKPFVCDITVL 210
 Db 151 EHTKLASSCLLLEFVMIVFGLFIRIWSAGCCCRYGWGRRLRPAKPFVCDITVL 210

```

Db 57 EYEKSEGLALYILEIYIVVEGVYVIRMAAGCCCRGRGRGLKFAKREPCVIDIMVL 116
Qy 211 IASIAVSAKTOGNIPTALSRLRFLQILRMVMDRGGTWKLLGSVYVAHASKELITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHASKELITAM 176
Qy 271 YIGFLVLISSFLVYIVVEKDNKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLITIGYDGTPLTWNGRLAAT 236
Qy 331 FALLGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296
Qy 391 -ATW 393
Db 297 HSTM 300

```

```

RESULT 17
US-10-128-870-6
; Sequence 6, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridboff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 300
; TYPE: PRT
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 300 amino acids of murine KCNQ2
US-10-128-870-6

```

```

Query Match 25.5%; Score 1207.5; DB 9; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.2e-79;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

Qy 91 GKPLSTSSQSCRNVKRYRQNYLYNVLEPRGMATFYHAFFLVFGLIISVFSTIP 150
Db 5 GKPLSTSSQSCRNVKRYRQNYLYNVLEPRGMATFYHAFFLVFGLIISVFSTIP 150
Qy 151 EHTKLASCLLIEFVMIIVGEGLEFIIRIMSAGCCCRGRGRGLKFAKREPCVIDITVL 210
Db 57 EYEKSEGLALYILEIYIVVEGVYVIRMAAGCCCRGRGRGLKFAKREPCVIDITVL 116
Qy 211 IASIAVSAKTOGNIPTALSRLRFLQILRMVMDRGGTWKLLGSVYVAHASKELITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHASKELITAM 176
Qy 271 YIGFLVLISSFLVYIVVEKDNKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLITIGYDGTPLTWNGRLAAT 236
Qy 331 FALLGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296

```

```

Qy 391 -ATW 393
Db 297 HSTM 300

```

```

RESULT 18
US-10-131-685-4
; Sequence 4, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 300 amino acids of human KCNQ2
US-10-131-685-4

```

```

Query Match 25.5%; Score 1207.5; DB 9; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.2e-79;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

Qy 91 GKPLSTSSQSCRNVKRYRQNYLYNVLEPRGMATFYHAFFLVFGLIISVFSTIP 150
Db 5 GKPLSTSSQSCRNVKRYRQNYLYNVLEPRGMATFYHAFFLVFGLIISVFSTIP 150
Qy 151 EHTKLASCLLIEFVMIIVGEGLEFIIRIMSAGCCCRGRGRGLKFAKREPCVIDITVL 210
Db 57 EYEKSEGLALYILEIYIVVEGVYVIRMAAGCCCRGRGRGLKFAKREPCVIDIMVL 116
Qy 211 IASIAVSAKTOGNIPTALSRLRFLQILRMVMDRGGTWKLLGSVYVAHASKELITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHASKELITAM 176
Qy 271 YIGFLVLISSFLVYIVVEKDNKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLITIGYDGTPLTWNGRLAAT 236
Qy 331 FALLGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296
Qy 391 -ATW 393
Db 297 HSTM 300

```

```

RESULT 19
US-10-131-685-6
; Sequence 6, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

```

```

: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 676
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-138-316-2

Query Match      23.3%; Score 1102; DB 9; Length 676;
Best Local Similarity 41.9%; Pred. No. 2.9e-71;
Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16

Dy      98  SSOSCRNRVKKR-RQNZLVNVLEPRGW-AFIYAFVLLVFGCLLSVFSTIBETKTL 155
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      92  SYSTRRPVLARTHVQGRVYVLEPRPTMKCVYHFAFLVLYCLLISVSTIBQYAL 151
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      156  ASSCLLLEFMYIVFGLFIIRMSAGCCCCRYRGMQGRFLRPAKRFPCVIDTIVL 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      152  ATGLFWMEIVLVVEFGTEYVYRLMSACGRSKYVGLMGRLEFRARKPDISIIDLI 211
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      216  VVSKATQGNIFATSAKRLRFQLIIRMRMRDROGTNLLSGVVVAHSELTAMVIGL 275
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      212  VLVGSGQGVPTAIRGIRFQLIIRMLHVPOGGTWRLLGSVVEIHRELITTYIGFL 271
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      276  VLISSFVLVYVVEKDA-----NKESTYADALMNGTITLTTCYGDKPFLTWLGRLLSAG 330
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      272  GLIISSTYVYLAEKDAVNESGRVREGSTADALIMGVIYTTTIGYEDKVPQVWKGKTIASC 331
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      332  FSVFAISFPALPAGILGSGFALKVQOKRKHFHQIPAAASLIQTAMRCYAAENPDS- 390
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      391  ATKVPHLKAL--HT-CSPTNOKLSFKERVNRASRGOSIKRKQASVGDGRBSPSDITLAE 446
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      391  -TWKIYIKKAPRSHLLSPSPRP--KKSVAVKKKKFKDKONGVTPGKMLTVPHITD 446
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      447  GSPTRKQVQWS---FNDRTRRPSRLKSSOPKPYADADALGTDDVYDEKGCQCQSVYE 503
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      447  PPERRLDHFESVDGIDSSVKRSPTL-LEVSMPH-----FMRTNSFAD----LDLEE 494
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      504  DLTPPL-----KTVIRAIRIMKEHVAKRKRETLRPYDVKDVIQSYAGHILMLC 553
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      495  TLLRPITRHISLREHNRATIKYIRMQYFAVAKKFOAKRPYDVRDVIQYSGHILMLAY 554
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      554  RIKSLQTRVNDOLKGCQ--TISDKSKREKITAHEHETDLSMLGRVYKVEKQVQSIESKL 611
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      555  RIKELQRLDSDIGRPSLEISVSEKSKR-----GSNTIGARLNRVEDKVTQLDQRL 606
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      612  DCLLDIYQGV-----RKQSA-----SALASFOFPPE 641
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      607  ALITDMLHQLSLHSGSTPGSGGPPREGAHITQPGSGGSVDPELFLPSNTILPYTE 663
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-09-840-125-2
: Sequence 2, Application US/09840125
: Patent No. US20020061524A1
: GENERAL INFORMATION:
: APPLICANT: SPLAWSKI, IGOR
: APPLICANT: Keating, Mark T.
: TITLE OF INVENTION: ALTERATIONS IN THE LONG OF SYNDROME GENES KVLQ71 AND
: FILE REFERENCE: 2323-155
: CURRENT APPLICATION NUMBER: US/09/840.125
: PRIOR FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/634,920
: PRIOR FILING DATE: 2000-08-09
: PRIOR APPLICATION NUMBER: 60/147,488
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 676
: TYPE: PRT

```


US-10-128-870-18

Query Match 22.9%; Score 1085; DB 9; Length 310;

Best Local Similarity 65.3%; Pred. No. 1.6e-70; Mismatches 55; Indels 18; Gaps 3;

Matches 203; Conservative 35; Mismatches 55; Indels 18; Gaps 3;

QY 90 LGRPLSYSSQSCRNVKRYRVONYLVNLEPRGNAPFIYHAFVLLVFGCLLSVFSTI 149

Db 4 LSRPVR-----RNNAKYRRIQTLTYLDALERPRGMALYHALVFLVGLLILAVLTTF 56

QY 150 PEHTLASSCLLILEVMIVVGLLEFIRIRWSAGCCCRIRYMGCRLPFRAPKPCVIDTIV 209

Db 57 KEYETVSGDWMLLETFALIFGAEFALRIWAGCCCRIRYMGCRLPFRAPKPCVIDTIV 116

QY 210 LIASIVAVSAKTQGNIFATSALRSLEFLOILRMVDRMGCTWKLGSVYVAHSELITA 269

Db 117 LIASIPVAVGNGVNLATS-LRSLRFLOILRMVDRMGCTWKLGSVYVAHSELITA 175

QY 270 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTTLTIGYDKTP 319

Db 176 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTTLTIGYDKTP 235

QY 320 LTVGLRLSAGFALLGIFSFALPAGILSGFALKVQDQHQHFKRRRPAANLIQCVNR 379

Db 236 KTWERLLAATFSLIGVSFFALPAGILSGFALKVQDQHQHFKRRRPAANLIQCVNR 295

QY 380 SYADEKSIVI 390

Db 296 YYATNPRIIDL 306

RESULT 26

US-10-131-685-18

Sequence 18, Application US/10131685

Publication No. US20030044912A1

GENERAL INFORMATION:

APPLICANT: Blahar, Michael A.

APPLICANT: Levesque, Paul C.

APPLICANT: Little, Wayne A.

APPLICANT: Neubaer, Michael G.

APPLICANT: Yang, Men-Plin

TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: DC38ACON

CURRENT APPLICATION NUMBER: US/10/131,685

PRIOR FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 09/105,058

PRIOR FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

PRIOR FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 18

LENGTH: 310

TYPE: PR

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: 310 amino acids of human KCNQ3

US-10-131-685-18

Query Match 22.9%; Score 1085; DB 9; Length 310;

Best Local Similarity 65.3%; Pred. No. 1.6e-70;

Matches 203; Conservative 35; Mismatches 55; Indels 18; Gaps 3;

QY 90 LGRPLSYSSQSCRNVKRYRVONYLVNLEPRGNAPFIYHAFVLLVFGCLLSVFSTI 149

Db 4 LSRPVR-----RNNAKYRRIQTLTYLDALERPRGMALYHALVFLVGLLILAVLTTF 56

QY 150 PEHTLASSCLLILEVMIVVGLLEFIRIRWSAGCCCRIRYMGCRLPFRAPKPCVIDTIV 209

Db 57 KEYETVSGDWMLLETFALIFGAEFALRIWAGCCCRIRYMGCRLPFRAPKPCVIDTIV 116

QY 210 LIASIVAVSAKTQGNIFATSALRSLEFLOILRMVDRMGCTWKLGSVYVAHSELITA 269

Db 296 YYATNPRIIDL 306

Db 117 LIASIPVAVGNGVNLATS-LRSLRFLOILRMVDRMGCTWKLGSVYVAHSELITA 175

QY 270 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTTLTIGYDKTP 319

Db 176 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTTLTIGYDKTP 235

QY 320 LTVGLRLSAGFALLGIFSFALPAGILSGFALKVQDQHQHFKRRRPAANLIQCVNR 379

Db 236 KTWERLLAATFSLIGVSFFALPAGILSGFALKVQDQHQHFKRRRPAANLIQCVNR 295

QY 380 SYADEKSIVI 390

Db 296 YYATNPRIIDL 306

RESULT 27

US-10-138-316-114

Sequence 114, Application US/10138316

Publication No. US20030054380A1

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, Igor

TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MIN K WHICH

TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION: KCNE1 AS AN IOT GENE

FILE REFERENCE: 2323-162

CURRENT APPLICATION NUMBER: US/10/138,316

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/444,295

PRIOR FILING DATE: 1999-11-22

PRIOR APPLICATION NUMBER: 09/135,020

PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: 08/921,068

PRIOR FILING DATE: 1997-08-29

PRIOR APPLICATION NUMBER: 08/739,383

PRIOR FILING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 60/019,014

PRIOR FILING DATE: 1995-12-22

PRIOR APPLICATION NUMBER: 60/094,477

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 114

LENGTH: 570

TYPE: PR

ORGANISM: Homo sapiens

US-10-138-316-114

Query Match 22.9%; Score 1081.5; DB 9; Length 570;

Best Local Similarity 41.6%; Pred. No. 7e-70;

Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

QY 112 QNLYNVLEPRGW-AFIYHAFVLLVFGCLLSVFSTIPHTKLASSCLLILEFVIV 170

Db 1 QGRVYNFLRPTGKCFVYHAFVLLVFGCLLSVFSTIPHTKLASSCLLILEFVIV 60

QY 171 FGLFTIRIRWSAGCCCRIRYMGCRLPFRAPKPCVIDTIVLIASIVAVSAKTQGNIFATSA 230

Db 61 FGLFTIRIRWSAGCCCRIRYMGCRLPFRAPKPCVIDTIVLIASIVAVSAKTQGNIFATSA 120

QY 231 LSLRFLQILRMVDRMGCTWKLGSVYVAHSELITAMWIGFLVLISSFLVLYVEKDA 290

Db 121 LSLRFLQILRMVDRMGCTWKLGSVYVAHSELITAMWIGFLVLISSFLVLYVEKDA 180

QY 291 A-----NKEFSTYADALMWGTTTLTIGYDKTPPLTWGLRLSAGFALLGIFSFALPAGI 345

Db 181 AVNESGRVFEFGSYADALMWGTTTLTIGYDKTPPLTWGLRLSAGFALLGIFSFALPAGI 240

QY 346 LGSFALKVQDQHQHFKRRRPAANLIQCVNRSYADEKSIVATWPKPLKAL--HT 402

Db 241 LGSFALKVQDQHQHFKRRRPAANLIQCVNRSYADEKSIVATWPKPLKAL--TWKTYIRAPRSHT 298


```

: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Consensus
: OTHER INFORMATION: amino acid sequence as shown in Fig. 17A-17B
: FEATURE:
: OTHER INFORMATION: Xaa is any amino acid
US-10-128-870-2

Query Match
Best Local Similarity 20.2%; Score 957; DB 9; Length 298;
Matches 189; Conservative 12; Mismatches 79; Indels 2; Gaps 2;

QY 103 RRNVYRRNQNLVNLVLRPRGMAFYHAHFVLLVECLLSVSTIPETHTKLASCLLI 162
DB 9 KRNAVYRXXXQXXXKXLLERPRGMAXXYHAHVFLXVXXCLLXVXXKXEYEXSXXLXX 68

QY 163 LEFVMIIVFGLFEIIRIWSAGCCCRYRGMQGLRFAPKPCVIDITVLIASIAVYSAKTO 222
DB 69 LEXXXIXXFGKXXXKRIWAGCCCRXGMRGLKFAKPKCXKD-IVLIASXXVXAXGXQ 127

QY 223 GNIFATSLRSLRFLQILRMVRMDRGGTWWKLLGSVVAHSEKELITAWYIGFLVLIFFSF 282
DB 128 GNVXATSLRSLRFLQILRMVRMDRGGTWWKLLGSVVAHSEKELITAWYIGFLVLIFFSF 186

QY 283 LVYLVEKANKKEFSTYADALMWGTTITLTIGYGDTPTLWGLRLSGFALLGISFPALP 342
DB 187 LVYLVEKEXDXEFTYADALMWGLITLTIGYGDKPKXTXGRLXATFLLIGVSFPALP 246

QY 343 AGILSGFALKVQEOHROKHFEKRRNPANLIQCWRSYAAD 384
DB 247 AGILSGXALKVQEOHROKHFEKRRNPAXLIQXAMRYATN 288

RESULT 31
US-10-131-685-2
: Sequence 2, Application US/10131685
: Publication No. US20030044912A1
: GENERAL INFORMATION:
: APPLICANT: Blamar, Michael A.
: APPLICANT: Levesque, Paul C.
: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauser, Michael G.
: APPLICANT: Yang, Wen-Pin
: TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: DC58aCON
: CURRENT APPLICATION NUMBER: US/10/131,685
: PRIOR FILING DATE: 2002-07-23
: PRIOR APPLICATION NUMBER: US 09/105,058
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 60/055,599
: PRIOR FILING DATE: 1997-08-12
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Consensus
: OTHER INFORMATION: amino acid sequence as shown in Fig. 17A-17B
: FEATURE:
: OTHER INFORMATION: Xaa is any amino acid
US-10-131-685-2

Query Match
Best Local Similarity 20.2%; Score 957; DB 9; Length 298;
Matches 189; Conservative 12; Mismatches 79; Indels 2; Gaps 2;

QY 103 RRNVYRRNQNLVNLVLRPRGMAFYHAHFVLLVECLLSVSTIPETHTKLASCLLI 162

```

```

DB 9 KRNAVYRXXXQXXXKXLLERPRGMAXXYHAHVFLXVXXCLLXVXXKXEYEXSXXLXX 68

QY 163 LEFVMIIVFGLFEIIRIWSAGCCCRYRGMQGLRFAPKPCVIDITVLIASIAVYSAKTO 222
DB 69 LEXXXIXXFGKXXXKRIWAGCCCRXGMRGLKFAKPKCXKD-IVLIASXXVXAXGXQ 127

QY 223 GNIFATSLRSLRFLQILRMVRMDRGGTWWKLLGSVVAHSEKELITAWYIGFLVLIFFSF 282
DB 128 GNVXATSLRSLRFLQILRMVRMDRGGTWWKLLGSVVAHSEKELITAWYIGFLVLIFFSF 186

QY 283 LVYLVEKANKKEFSTYADALMWGTTITLTIGYGDTPTLWGLRLSGFALLGISFPALP 342
DB 187 LVYLVEKEXDXEFTYADALMWGLITLTIGYGDKPKXTXGRLXATFLLIGVSFPALP 246

QY 343 AGILSGFALKVQEOHROKHFEKRRNPANLIQCWRSYAAD 384
DB 247 AGILSGXALKVQEOHROKHFEKRRNPAXLIQXAMRYATN 288

RESULT 32
US-10-128-870-21
: Sequence 21, Application US/10128870
: Patent No. US2002016872A1
: GENERAL INFORMATION:
: APPLICANT: Blamar, Michael A.
: APPLICANT: Dworetzky, Steven
: APPLICANT: Glibkoft, Valentin K.
: APPLICANT: Levesque, Paul C.
: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauser, Michael G.
: APPLICANT: Yang, Wen-Pin
: TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: DC58aDIY
: CURRENT APPLICATION NUMBER: US/10/128,870
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 09/105,058
: PRIOR FILING DATE: June 26, 1998
: PRIOR APPLICATION NUMBER: 60/055,599
: PRIOR FILING DATE: August 12, 1997
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 21
: LENGTH: 430
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-128-870-21

Query Match
Best Local Similarity 19.1%; Score 905.5; DB 9; Length 430;
Matches 181; Conservative 49; Mismatches 80; Indels 15; Gaps 5;

QY 98 SSOSCRNVKRR-RVQNYLVNLVLRPRGM-AFYHAHFVLLVECLLSVSTIPETHTKL 155
DB 92 SIYSTRPVLARHYVGRVNYFLERPTGWCFCYHFAVFLIVLCLIPSVLSTIQYAL 151

QY 156 ASSCLLIEFVMIIVFGLFEIIRIWSAGCCCRYRGMQGLRFAPKPCVIDITVLIASIA 215
DB 152 ATGTLFWMELIVLVFEGTEVLRWSAGCSKSYVGLMGRLEFAPKPIISIDILIVVAVMY 211

QY 216 VVSAKTOGNIIFATSLRSLRFLQILRMVRMDRGGTWWKLLGSVVAHSEKELITAWYIGFL 275
DB 212 VLVGSGKGVFATSLRSLRFLQILRMVLRMDRGGTWWKLLGSVVAHSEKELITAWYIGFL 271

QY 276 VLIFFSEFLVYLVKDA-----NKEFSTYADALMWGTTITLTIGYGDTPTLWGLRLSG 330
DB 272 GLIFSYFVYLAEKDAVNESGRVFGSYADALMWGVTVTLTIGYGDVPTWVGKTIASC 331

QY 331 FALLGISFPALPAGILSGFALKVQEOHROKHFEKRRNPANLIQCWRSYAADKESYSI 390
DB 332 FSVFALISFPALPAGILSGFALKVQEOHROKHFEKRRNPANLIQTAARCYAENPDSS- 390

QY 391 ATWK-----PHLKALHTCSPTNOK 409

```

PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: 60/019,014

```

Db      391 -TWKTYIRKAPRSHLTLLSPSPKPK 414
| | | | | : | : | : |
US-10-131-685-21
; Sequence 21, Application US/10131685
; Publication No. US20030044912A1
GENERAL INFORMATION:
APPLICANT: Bleaner, Michael A.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubaumer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC58ACON
CURRENT APPLICATION NUMBER: 2002-07-23
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,058
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 430
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-685-21

Query Match          19.1%; Score 905.5; DB 9; Length 430;
Best Local Similarity 55.7%; Pred. No. 2.4e-57;
Matches 181; Conservative 49; Mismatches 80; Indels 15; Gaps 5

QY      98 SSSCSRNVKYR-FVONYLVNLEPRGM-AFIYAFAVLIVFGCLTSVFSTPHXTL 155
| | | | | : | : | | | : | : | | | : | : | | | : | : |
DB      92 SIYSTRPVLARTHQGVKNVFLERPTGKKCVHFAFVLIVLCIFSVLSTIEOYAL 151
| | | | | : | : | | | : | : | | | : | : | | | : | : |

QY      156 ASSCLLLEPMIVVFGLEFIIRIWSAGCCCRYSRMQGRLRPARKPFVIDITVLASIA 215
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      152 ATGLFMEMETVLVVEFTGEYVVRMSACRSKSYKVLGMGRLRARFKRISIIDLIIVVAAMV 211
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      216 VSAKTGGNIFFATSLRSRLFQLIRMYRMDRGSTWKLGSVVYAHSKELTAWYTGL 275
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      212 VLCVSGSGQVFAFNTAIGIRPLQILRMHLHYDRGGTWRLLGSVFLIHROELLITLYIGFL 271
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      276 VLIFSSEVLIVLEKDA-----NKEFSYADALMWGTITLTITIGYGDKPDTLWTGLRLSAG 330
| | | | | : | : | | | : | : | | | : | : | | | : | : |
DB      272 GLIFFSFYVYLAEEDAVNESGRVEFGSYADALLMVGVTVTITIGYGDKVPQTWWGKITASC 331
| | | | | : | : | | | : | : | | | : | : | | | : | : |

QY      331 FALGISGFPLLPAGILSGFALKVOEHRKHFEKRNRNPAAULIQCWMSYADEKSYST 380
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      332 FSFVAISFPFLPAGILSGFALKVQOKORQHFNKPAPAAASLIQTAMRCYAAENPDSS- 390
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      391 ATWK-----PHLKALHTCSEPTNOK 409
| | | | | : | : | | | : | : | | | : | : | | | : | : |
DB      391 -TWKTYIRKAPRSHLTLLSPSPKPK 414
| | | | | : | : | | | : | : | | | : | : | | | : | : |

RESULT 34
US-10-138-316-113
; Sequence 113, Application US/10138316
; Publication No. US20030054380A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguineti, Michael C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING TITLE OF INVENTION: KCNE1 AS AN IQT GENE
FILE REFERENCE: 2323-162
CURRENT APPLICATION NUMBER: US/10/138,316
CURRENT FILING DATE: 2002-05-06

```



```

CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325.891
FILING DATE: 23-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/009.492
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/464.340
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36.134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-325-891-13

Query Match
Best Local Similarity 23.38; Score 250; DB 9; Length 539;
Matches 91; Conservative 77; Mismatches 151; Indels 72; Gaps 13:

115 LYNVLEPRGMA---FIYHAFVFLVFGCLISVFSTIPEHTK-----ASSCLILE 164
173 LMDLEKPRSSVAKLAIISIMEFVLTALSL-NLPELOSLDERGOSTDNQOLAVE 231
165 FMYIVFGLEPIIRISAGCCCRYRGWGRLEFARKPCVYIDTVILASIAVSAKTQGN 224
232 AVCIAMFTMEYLRLFLSSP-----KKW---KFKGPLNADLALIPYV-----T 274
225 IFATSLRSL-----RFLQILRMVMDRGRGTWKLIGSVYVHAKEL-ITAW 270
275 ILTSLNKSVDLOFQNVRRVQVIFRIMRLILKLARHSTGLQSLGFTLRSSYNELGLIL 334
271 YIGFLVLISSFLVYLVKEDA-NKEFSTYADALMWGTTITLTIGYGDPTLWTGRLISA 329
335 FLAMGIMIFSS-LVFEAEKDEDDTKFSTIPASFWMTITMTYIGYGDYIKTLGKIVGG 393
330 GFALLGISFPALPAGLISGFALKVOEQRKHFEKRRNPAANLIQCVMSYADEKSVS 389
394 LCCINGLVIALPIPIYNNSEFEYKORROEKAIRR-----DALEBAKNGS 442
390 IATWPKHALHTGCSPTNOKLSFKERVRM-----ASRSGOSIKRSOASVSGRRSPSTIDTA 445
443 IVS-----MNNKDAFANSIEMADIVYVENGENMGAKDKVQDNHLSPNKWKWT 489
446 EGSPTKVOKSMSFNDRTFRPSLRKSSQPK 476
490 KRLTSETSSSKSFETKEOGSPKARSSSPQ 520

```

RESULT 38
 US-10-121-746-10
 ; Sequence 10, Application US/10121746

```

Publication No. US20030036648A1
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OR INVENTION: No. US20030036648A1 Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/10/121.746
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US/09/336.643A
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/038,262
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 646
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(646)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-121-746-10

Query Match
Best Local Similarity 22.58; Score 245; DB 9; Length 646;
Matches 107; Conservative 81; Mismatches 170; Indels 118; Gaps 22:

115 LYNVLEPRR---GMAFIYAFVFLVFGCLISVFSTIP-----EHRKL 155
172 LWRAFENPHTSTRALVFFYVTGFFIAY--SVIANVETIICRGARSRSREQPCGERPQ 229
156 ASSCLILEFMAIVFVGLFPIIRISAGCCCRYRGWGRLEFARKPCVYIDTVILIA-SI 214
230 AFEC---MDTACVLIPTGELLRLFAA-----PSRCRFLRSVMSLIDVVALIPYI 277
215 AVYSAKTQGNIPATSLRSLRFLQILRMVMDRGRGTWKLIGSVYVHAKELIATYIGF 274
278 GLIVRK---NDVSGAFVTLRVFRVRIEFKSHSGGLRILGYTLKSCASEL-----GF 328
275 L-----VLIFSSFLVYLVKEDANK-EESTYADALMWGTTITLTIGYGDPTLWTGRL 326
329 LIFSILMAIIFATVMEY-AEKGNTKNTFTSIIPAAMWYITVITLTIGYGMVSTINGKI 387
327 LSAGFALLGISFPALPAGLISGFALKVOEQRKHFEKRRNPAANLIQCVMSYADEKSVS 389
368 FGSISLSCGVIALPVPVIVSNFS---RIYHONQPADRR--AQQKVRILARLAKSGT 442
377 -----VMRSYADEKSVS-----ATWPKPLKALH-----TCSPTNOKLSFKER 415
443 TNAFLQYONGNGLEDSGSEBQALCYRNASAEQOHHLHLCLEKTCHEFTDELTFSEA 502
416 VMAASPPOOSIKSRQAS---VG-----DRRSPSTIDTAEGSPTKVOKSMSFNDRTFR 463
503 LGAVSPGGRTSRSTSVSQPVGPGSILSSCCPRRAKRAIRILANSYASVSRG-SMGELDM 561
464 FRPSLRKSSQPKPYIDNATAGTDVYDEKCCQD-----VSVEDITPLPKT 511
562 LAGLRSHAPQSRSSLNKPK-----HDSLDLNCDSRDFVAALISIP--TTPANT 608

```

RESULT 39
 US-10-121-746-4
 ; Sequence 4, Application US/10121746
 ; Publication No. US20030036648A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 601
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-4

Query Match      5.1%; Score 243; DB 9; Length 601;
Best Local Similarity 23.8%; Pred. No. 3e-09; Indels 88; Gaps 13;
Matches 82; Conservative 65; Mismatches 109;

65 AATLGGGGGLRESRKGAGMSLLGKPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
   |||||              |||
   AAGLGGPD-----GKSG-----RWRRLQPRMVALFEDPYS 188
159 AAGLGGPD-----GKSG-----RWRRLQPRMVALFEDPYS 188
   |||||              |||
123 -RGMAFYHAFFVLLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
   |||||              |||
189 SRAAFIAFASLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 248
163 LEPMIVVFGLEFIIRIMSAGCCCRNGRGLRFARKPCVDTIVLI-----ASIAVY 217
249 VEGCVVVFTEFFELVRIYFS-----PNKLEFIKNLNIIDFVALIPFYLEVGISGL 299
218 SAKTQGNIFATSAISSLRFLOILRMVMDRGGTAKLGSVYVANSKE-LITAMYIGELV 276
300 SSKAKDVL--GFLRVRFVRLIRFKLTHFVGLVGLHGLASTNEFLLITLIFLALGV 357
277 LISSFLVLYVER-----DANKFSTYADALMWGTTITLTIGYGDKPTLWLGRL 326
358 LIFFAT-MIYAEKRVGAQPNDSASEHTQKNIPIGFWMAVVTTLTGIDMYPQIWSGML 416
327 LSAGFALLGISFFALPAGIL-----GSGFALKVOEQ-----HROKH 362
417 VGALCALAGVLTITAMPVPVIVNFGMYISLAMAKOKLPRKRKKH 460

RESULT 40
US-10-024-623-11
; Sequence 11, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; FILE REFERENCE: USE THEREOF
; FILE REFERENCE: MNI-21ACP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-623-11

Query Match      5.1%; Score 243; DB 9; Length 638;
Best Local Similarity 23.8%; Pred. No. 3e-09; Indels 88; Gaps 13;
Matches 82; Conservative 65; Mismatches 109;

65 AATLGGGGGLRESRKGAGMSLLGKPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
   |||||              |||
   AAGLGGPD-----GKSG-----RWRRLQPRMVALFEDPYS 224
195 AAGLGGPD-----GKSG-----RWRRLQPRMVALFEDPYS 224
   |||||              |||
123 -RGMAFYHAFFVLLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
   |||||              |||
225 SRAAFIAFASLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 284
163 LEPMIVVFGLEFIIRIMSAGCCCRNGRGLRFARKPCVDTIVLI-----ASIAVY 217
285 VEGCVVVFTEFFELVRIYFS-----PNKLEFIKNLNIIDFVALIPFYLEVGISGL 335
218 SAKTQGNIFATSAISSLRFLOILRMVMDRGGTAKLGSVYVANSKE-LITAMYIGELV 276
336 SSKAKDVL--GFLRVRFVRLIRFKLTHFVGLVGLHGLASTNEFLLITLIFLALGV 393
277 LISSFLVLYVER-----DANKFSTYADALMWGTTITLTIGYGDKPTLWLGRL 326
394 LIFFAT-MIYAEKRVGAQPNDSASEHTQKNIPIGFWMAVVTTLTGIDMYPQIWSGML 452
327 LSAGFALLGISFFALPAGIL-----GSGFALKVOEQ-----HROKH 362
453 VGALCALAGVLTITAMPVPVIVNFGMYISLAMAKOKLPRKRKKH 496

RESULT 41
US-10-024-623-33
; Sequence 33, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; FILE REFERENCE: USE THEREOF
; FILE REFERENCE: MNI-21ACP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-024-623-33

Query Match      5.1%; Score 242; DB 9; Length 638;
Best Local Similarity 24.1%; Pred. No. 3.8e-09; Indels 74; Gaps 14;
Matches 83; Conservative 70; Mismatches 117;

70 GGGGGLRESRKGAGMSL-----LCKPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
   |||||              |||
176 GGGPDEDDELGK--RLGIEDAGLGGPD-----KSGRWKRLQPRMVALFEDPYS 224
123 -RGMAFYHAFFVLLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
225 SRAAFIAFASLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 284

```



```

RESULT 44
US-10-062-879-4
; Sequence 4, Application US/10062879
; Patent No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hui-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: Polypeptides and Uses Therefor
; FILE REFERENCE: ssp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-10-062-879-4

```

```

Query Match 4.8%; Score 229; DB 12; Length 636;
Best Local Similarity 19.7%; Pred. No. 3.3e-08;
Matches 111; Conservative 97; Mismatches 211; Indels 144; Gaps 21;

QY 98 SSOSCRNRYKRYRQNYLVNLEPRGMAFYHAFVFLVFG-----CLILSVSTP-- 150
Db 155 NNOSEMPISLSEFQOT---MKRAEENPHITSL---ALFYVYTGFFIAVSIVTINVEVPCG 208
QY 151 -----EHTKLASSCLILFEFVIVGFEFIRIRMSAGCCCRGMRGRLRPEAR 199
Db 209 TVPGSKELPCGGRYSVAFC---LDTACVAFIVETVILRLFAA-----PERYRIR 256
QY 200 KPFVIDIVILA-SIAVYSAKTOGNIPTALSRLRFLDILNRVDRRGTKKLGSV 258
Db 257 SVMSTIDVVALIMPYITGLVMTNED---VSGAFVTLRFVFRFLFKFSRHSQGLRIIGYT 313
QY 259 VYANSKELITAMYGIFL-----VLIFSSFLVYLVKDKANKERSTYADALMGTITLT 311
Db 314 LKSCASEL-----GFLFSLTMAITITFATVMTYAEKSSASKFTSIPASWTYITVWT 367
QY 312 IGYDKTPTLWLGRLISAGFALLGISFALPACILISGFALKVOEQRKHFEKRR--- 367
Db 368 LGYGDVMEKTIAGKIFGSISSLSGYLVIALPVPVIVSNFS---RIYHONQRADRRRAOK 424
QY 368 -----NPAANLIQCVMRSYADEKSVSIATWPKHLALH 401
Db 425 ARLARIRVAKTGSSNAYLHSKRNGLINELELTGTPEEEMGKTTSL-IESQHHL--LH 481
QY 402 TCSEPTNOLSEKERYRMASSPRGOSIKRSQASVDRSRSPSTD---ITAESPTVKOKSWS 457
Db 482 CLEKTTNHEFIDEQWF---EQNCMESSQONPSTRSPSLSHPLGLTTCCSRKSKTTH 537
QY 458 FNDOTRRPRLKSSQKRPVADATLCTDVTYDEKGCOCODVSVEDLPPPLKTVIRAIR 517
Db 538 LPNSN--LPATRLRMQELSTHIO---GSEQ-----PSLTSSRSLSN 575
QY 518 IMKPHVAKRKFEKTELRPYDVKVIQYSGHDMLCRIKSLQTRVDOILKGGTSSKKS 577
Db 576 L-----KADDGLRPN-----CKTSQITTAIISITPPPALTPGES 610
QY 578 REKITAHEHTTDDLMLGRVAV 600
Db 611 RPPAPSGPMNTNIPSTISNVAV 633

```

```

; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 18
; LENGTH: 477
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-18

```

```

Query Match 4.7%; Score 224; DB 9; Length 477;
Best Local Similarity 23.7%; Pred. No. 5.1e-08;
Matches 84; Conservative 65; Mismatches 139; Indels 66; Gaps 12;

QY 91 GKPLSTSSOSCRNRYKRYRQNYLVNLEPRGMAFYHAFVFLVFGCLILSVSTP 150
Db 163 GQLG-----NFRQL-WLALDNGYSLR-----VFSLISLVVMSITMCLNSLP 210
QY 151 EHTKLASS-----CLILFEFVIVGFEFIRIRMSAGCCCRGMRGRLRPEAR 203
Db 211 DQIPDSQNGPDREIIEHFGIAFTFELVARFAVA-----PDFLKFKNALN 261
QY 204 VIDT-----VLIASIAVSAKTOGNIPTALSRLRFLDILNRVDRRGTKKLGS 256
Db 262 LIDMLSVPTITLVNVLVESTTLNGLVAVQ--LRMRIFRILAKRSTGLRSIG 319
QY 257 SVYANSKELITAMYGIFLIFS-----SFLVYLVKDKANKERSTYADALMGTITLT 310
Db 320 ATEKYSYKE-----GCLLLYLVSGISIFSVAYTEKEENEGLATIPACWMAVTSMT 373
QY 311 TIGYDKTPTLWLGRLISAGFALLGISFALPACILISGFALKVOEQRKHFEKRRPA 370
Db 374 TWGYGVVPEGTIAGKILASACILAGILVVVLPITLIFNKFS-----HYRRQOL 423
QY 371 ANLIQ-CVMRSYADEKSVSIATWPKHLALHTCPTN-----OKLSFKERVR 417
Db 424 ESAMRSCDGDGDKKEVPVNLROYIAHKVSLMSLNMSSSELSLNSLSTR 477

```

```

RESULT 45
US-10-121-746-18
; Sequence 18, Application US/10121746
; Publication No. US20030036648A1

```

```

RESULT 46
US-10-121-746-8
; Sequence 8, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

```

```

? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
? NUMBER OF SEQ. ID NOS: 87
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ. ID NO 8
? LENGTH: 499
? TYPE: PRT
? ORGANISM: H. sapiens
? US-10-121-746-8

```

Query Match	4.7%	Score 223	DB 9	Length 499
Best Local Similarity	28.2%	Pred. No. 6.4e-08		
Matches	80	Conservative	47	Mismatches 107
				Indels 50
				Gaps 10

[illegible]

```

RESULT 47
US-09-999-220B-5
; Sequence 5, Application US/09999220B
; Publication No. US20030059923A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUBUNIT
; TITLE OF INVENTION: K-alpha1, AND VARIANTS THEREOF
; FILE REFERENCE: D0050NP
; CURRENT APPLICATION NUMBER: US/09/999,220B
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/245,383
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/257,780
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/269,854
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-999-220B-5

```

Query Match	4.74;	Score 223;	DB 9;	Length 500;
Best Local Similarity	28.28;	Pred. No. 6,4e-08;		
Matches	80;	Conservative 47;	Mismatches 107;	Indels 50; Gaps 10,
QY	111 VONTLVNVERP-----RGMAFIYHAFVPLVNEGCLLSVFSTIIPETTKAASCLLLE 164 :: :: :: :: :: :: :: :: 192 VRKRLMILTEKPSSSTAARLFEGVISIIIVAAISIIMAIMSA-----ELSWIDLPLEILE 246 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::			
DQ	165 FVIIVVEGFEITIRIMSAGCCCRGRMGWRLEARKFCVIDTIVLLASIAVNSAKTGON 224 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: Db 247 YVCISMFETGEFVRF-----LCVR-----DKREFRKVPNIIDLAALPEFYITLLVESISG 297 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::			

```

OY 225 IFATSAALS-----LRLOLITRWVRMDRRCGTWKLDSVYAHSHKELLITANY--IGFL 275
Db 298 SOTTELENVGRIVOVLLRLLRLRLRMKLGKRNHSTGLSLGMT-----ITOCYEYEGGL 349
OY 276 VL-----IFSSFLVYLVEKDNANKNEFSYADALMNGTITLTITIGYGDKPTLWLGRLLS 328
Db 350 LLEFLSVGISISTVEYFABQSIPTDTETISVPCAMMWATTSMTTVGYGDIRDPDTYTKIVA 409
OY 329 AGFALLGISFPAIGLISGCPA-----LKVOEOH-RKHFEPR 366
Db 410 FMCILSGILVALPRLTAINDRFSACYFTYIKLEAVALKOEALKK 453

```

```

1 RESULT 48
2 US-10-325-891-4
3 : Sequence 4, Application US/10325891
4 : Publication NO. US20030092895A1
5 : GENERAL INFORMATION:
6 : APPLICANT: LI, ET AL.
7 : TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
8 : NUMBER OF SEQUENCES: 13
9 : CORRESPONDENCE ADDRESS:
10 : ADDRESSEE: CECCHI, BYRNE, BAIN, GILFILLAN,
11 : STREET: 6 BECKER FARM ROAD
12 : CITY: ROSELAND
13 : STATE: NEW JERSEY
14 : COUNTRY: USA
15 : ZIP: 07068
16 :
17 : COMPUTER READABLE FORM:
18 : MEDIUM TYPE: 3.5 INCH DISKETTE
19 : COMPUTER: IBM PS/2
20 : OPERATING SYSTEM: MS-DOS
21 : SOFTWARE: WORD PERFECT 5.1
22 :
23 : CURRENT APPLICATION DATA:
24 : APPLICATION NUMBER: US/10/325,891
25 : FILING DATE: 23-Dec-2002
26 : CLASSIFICATION: <Unknown>
27 :
28 : PRIOR APPLICATION DATA:
29 : APPLICATION NUMBER: US/09/009,492
30 : FILING DATE: <Unknown>
31 : APPLICATION NUMBER: 08/464,340
32 : FILING DATE: June 5,1995
33 :
34 : ATTORNEY/AGENT INFORMATION:
35 : NAME: FERRARO, GREGORY D.
36 : REGISTRATION NUMBER: 36,134
37 : REFERENCE/DOCKET NUMBER: 325800-415
38 :
39 : TELECOMMUNICATION INFORMATION:
40 : TELEPHONE: 201-994-1700
41 : TELEFAX: 201-994-1744
42 :
43 : INFORMATION FOR SEQ ID NO: 4:
44 : SEQUENCE CHARACTERISTICS:
45 : LENGTH: 494 AMINO ACIDS
46 : TYPE: AMINO ACID
47 : STRANDEDNESS: <Unknown>
48 : TOPOLOGY: LINEAR
49 :
50 : MOLECULE TYPE: PROTEIN
51 :
52 : SEQUENCE DESCRIPTION: SEQ ID NO: 4:
53 :
54 :
55 :
56 :
57 :
58 :
59 :
60 :
61 :
62 :
63 :
64 :
65 :
66 :
67 :
68 :
69 :
70 :
71 :
72 :
73 :
74 :
75 :
76 :
77 :
78 :
79 :
80 :
81 :
82 :
83 :
84 :
85 :
86 :
87 :
88 :
89 :
90 :
91 :
92 :
93 :
94 :
95 :
96 :
97 :
98 :
99 :
100 :
101 :
102 :
103 :
104 :
105 :
106 :
107 :
108 :
109 :
110 :
111 :
112 :
113 :
114 :
115 :
116 :
117 :
118 :
119 :
120 :
121 :
122 :
123 :
124 :
125 :
126 :
127 :
128 :
129 :
130 :
131 :
132 :
133 :
134 :
135 :
136 :
137 :
138 :
139 :
140 :
141 :
142 :
143 :
144 :
145 :
146 :
147 :
148 :
149 :
150 :
151 :
152 :
153 :
154 :
155 :
156 :
157 :
158 :
159 :
160 :
161 :
162 :
163 :
164 :
165 :
166 :
167 :
168 :
169 :
170 :
171 :
172 :
173 :
174 :
175 :
176 :
177 :
178 :
179 :
180 :
181 :
182 :
183 :
184 :
185 :
186 :
187 :
188 :
189 :
190 :
191 :
192 :
193 :
194 :
195 :
196 :
197 :
198 :
199 :
200 :
201 :
202 :
203 :
204 :
205 :
206 :
207 :
208 :
209 :
210 :
211 :
212 :
213 :
214 :
215 :
216 :
217 :
218 :
219 :
220 :
221 :
222 :
223 :
224 :
225 :
226 :
227 :
228 :
229 :
230 :
231 :
232 :
233 :
234 :
235 :
236 :
237 :
238 :
239 :
240 :
241 :
242 :
243 :
244 :
245 :
246 :
247 :
248 :
249 :
250 :
251 :
252 :
253 :
254 :
255 :
256 :
257 :
258 :
259 :
260 :
261 :
262 :
263 :
264 :
265 :
266 :
267 :
268 :
269 :
270 :
271 :
272 :
273 :
274 :
275 :
276 :
277 :
278 :
279 :
280 :
281 :
282 :
283 :
284 :
285 :
286 :
287 :
288 :
289 :
290 :
291 :
292 :
293 :
294 :
295 :
296 :
297 :
298 :
299 :
300 :
301 :
302 :
303 :
304 :
305 :
306 :
307 :
308 :
309 :
310 :
311 :
312 :
313 :
314 :
315 :
316 :
317 :
318 :
319 :
320 :
321 :
322 :
323 :
324 :
325 :
326 :
327 :
328 :
329 :
330 :
331 :
332 :
333 :
334 :
335 :
336 :
337 :
338 :
339 :
340 :
341 :
342 :
343 :
344 :
345 :
346 :
347 :
348 :
349 :
350 :
351 :
352 :
353 :
354 :
355 :
356 :
357 :
358 :
359 :
360 :
361 :
362 :
363 :
364 :
365 :
366 :
367 :
368 :
369 :
370 :
371 :
372 :
373 :
374 :
375 :
376 :
377 :
378 :
379 :
380 :
381 :
382 :
383 :
384 :
385 :
386 :
387 :
388 :
389 :
390 :
391 :
392 :
393 :
394 :
395 :
396 :
397 :
398 :
399 :
400 :
401 :
402 :
403 :
404 :
405 :
406 :
407 :
408 :
409 :
410 :
411 :
412 :
413 :
414 :
415 :
416 :
417 :
418 :
419 :
420 :
421 :
422 :
423 :
424 :
425 :
426 :
427 :
428 :
429 :
430 :
431 :
432 :
433 :
434 :
435 :
436 :
437 :
438 :
439 :
440 :
441 :
442 :
443 :
444 :
445 :
446 :
447 :
448 :
449 :
450 :
451 :
452 :
453 :
454 :
455 :
456 :
457 :
458 :
459 :
460 :
461 :
462 :
463 :
464 :
465 :
466 :
467 :
468 :
469 :
470 :
471 :
472 :
473 :
474 :
475 :
476 :
477 :
478 :
479 :
480 :
481 :
482 :
483 :
484 :
485 :
486 :
487 :
488 :
489 :
490 :
491 :
492 :
493 :
494 :
495 :
496 :
497 :
498 :
499 :
500 :
501 :
502 :
503 :
504 :
505 :
506 :
507 :
508 :
509 :
510 :
511 :
512 :
513 :
514 :
515 :
516 :
517 :
518 :
519 :
520 :
521 :
522 :
523 :
524 :
525 :
526 :
527 :
528 :
529 :
530 :
531 :
532 :
533 :
534 :
535 :
536 :
537 :
538 :
539 :
540 :
541 :
542 :
543 :
544 :
545 :
546 :
547 :
548 :
549 :
550 :
551 :
552 :
553 :
554 :
555 :
556 :
557 :
558 :
559 :
560 :
561 :
562 :
563 :
564 :
565 :
566 :
567 :
568 :
569 :
570 :
571 :
572 :
573 :
574 :
575 :
576 :
577 :
578 :
579 :
580 :
581 :
582 :
583 :
584 :
585 :
586 :
587 :
588 :
589 :
590 :
591 :
592 :
593 :
594 :
595 :
596 :
597 :
598 :
599 :
600 :
601 :
602 :
603 :
604 :
605 :
606 :
607 :
608 :
609 :
610 :
611 :
612 :
613 :
614 :
615 :
616 :
617 :
618 :
619 :
620 :
621 :
622 :
623 :
624 :
625 :
626 :
627 :
628 :
629 :
630 :
631 :
632 :
633 :
634 :
635 :
636 :
637 :
638 :
639 :
640 :
641 :
642 :
643 :
644 :
645 :
646 :
647 :
648 :
649 :
650 :
651 :
652 :
653 :
654 :
655 :
656 :
657 :
658 :
659 :
660 :
661 :
662 :
663 :
664 :
665 :
666 :
667 :
668 :
669 :
670 :
671 :
672 :
673 :
674 :
675 :
676 :
677 :
678 :
679 :
680 :
681 :
682 :
683 :
684 :
685 :
686 :
687 :
688 :
689 :
690 :
691 :
692 :
693 :
694 :
695 :
696 :
697 :
698 :
699 :
700 :
701 :
702 :
703 :
704 :
705 :
706 :
707 :
708 :
709 :
710 :
711 :
712 :
713 :
714 :
715 :
716 :
717 :
718 :
719 :
720 :
721 :
722 :
723 :
724 :
725 :
726 :
727 :
728 :
729 :
730 :
731 :
732 :
733 :
734 :
735 :
736 :
737 :
738 :
739 :
740 :
741 :
742 :
743 :
744 :
745 :
746 :
747 :
748 :
749 :
750 :
751 :
752 :
753 :
75
```

[illegible]

QY 213 STAVSAKTOGINFATLSRFLQILRMVMDRGGTWMKLGSVYVAHSEL-ITAWY 271
Db 271 TLTHLGARMELTNVOQAVQALRIRIARIFKLARHSSGLQTLTYALKRSFKELGLIMY 330
QY 272 IGEVLVLFSSFLVYLVKEDANKFESTYADALMNGTITLTIGYDKPTLWIGRLLSAGF 331
Db 331 LAVGIFVFALGYTMQSHPELTFKNIPQSFWMATITMTVGYGDYIPKTLTKLMAAIS 390
QY 332 ALLGISFFALPAGILGSGFALKVQEOHQHKEKRR 367
Db 391 FLGCVIAIALPPIHPINNFV-----RYNNKOR 417

RESULT 49

US-10-143-002-4
; Sequence 4, Application US/10143002
; Patent No. US20020132775A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
; CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/143,002
; FILING DATE: 13-May-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,493
; FILING DATE: <unknown>
; APPLICATION NUMBER: US/08/468,533
; FILING DATE: 6 JUNE 1995
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: <unknown>
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-143-002-4
Query Match 4.4%; Score 206.5; DB 12; Length 494;
Best Local Similarity 23.2%; Pred. No. 9.8e-07;
Matches 64; Conservative 57; Mismatches 122; Indels 33; Gaps 6;
QY 107 KYRRQNTLYNVLLEPRGW--FIYHAFVFLVFGCLISVFSTIP-----EHTKLAS 157
Db 160 RWRRCQKCVWFLKPESSCPARVAELSLFLILVSVVCMPTIPLQVLDAEGNVEH 219
QY 158 SCLILEFVMIVFLFIIRIWSAGCCCRYRGMOGRFARRPFCVYIDTVILV-----A 212

Db 220 PLENEVEACIGMETLEYLEILFSS-----PNKILFALSFMNIVDVALILPEVSL 270
QY 213 STAVSAKTOGINFATLSRFLQILRMVMDRGGTWMKLGSVYVAHSEL-ITAWY 271
Db 271 TLTHLGARMELTNVOQAVQALRIRIARIFKLARHSSGLQTLTYALKRSFKELGLIMY 330
QY 272 IGEVLVLFSSFLVYLVKEDANKFESTYADALMNGTITLTIGYDKPTLWIGRLLSAGF 331
Db 331 LAVGIFVFALGYTMQSHPELTFKNIPQSFWMATITMTVGYGDYIPKTLTKLMAAIS 390
QY 332 ALLGISFFALPAGILGSGFALKVQEOHQHKEKRR 367
Db 391 FLGCVIAIALPPIHPINNFV-----RYNNKOR 417

RESULT 50

US-09-875-321-13
; Sequence 13, Application US/09875321
; Publication No. US20030049724A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM
; CHANNEL FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-061001
; CURRENT APPLICATION NUMBER: US/09/875,321
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-321-13

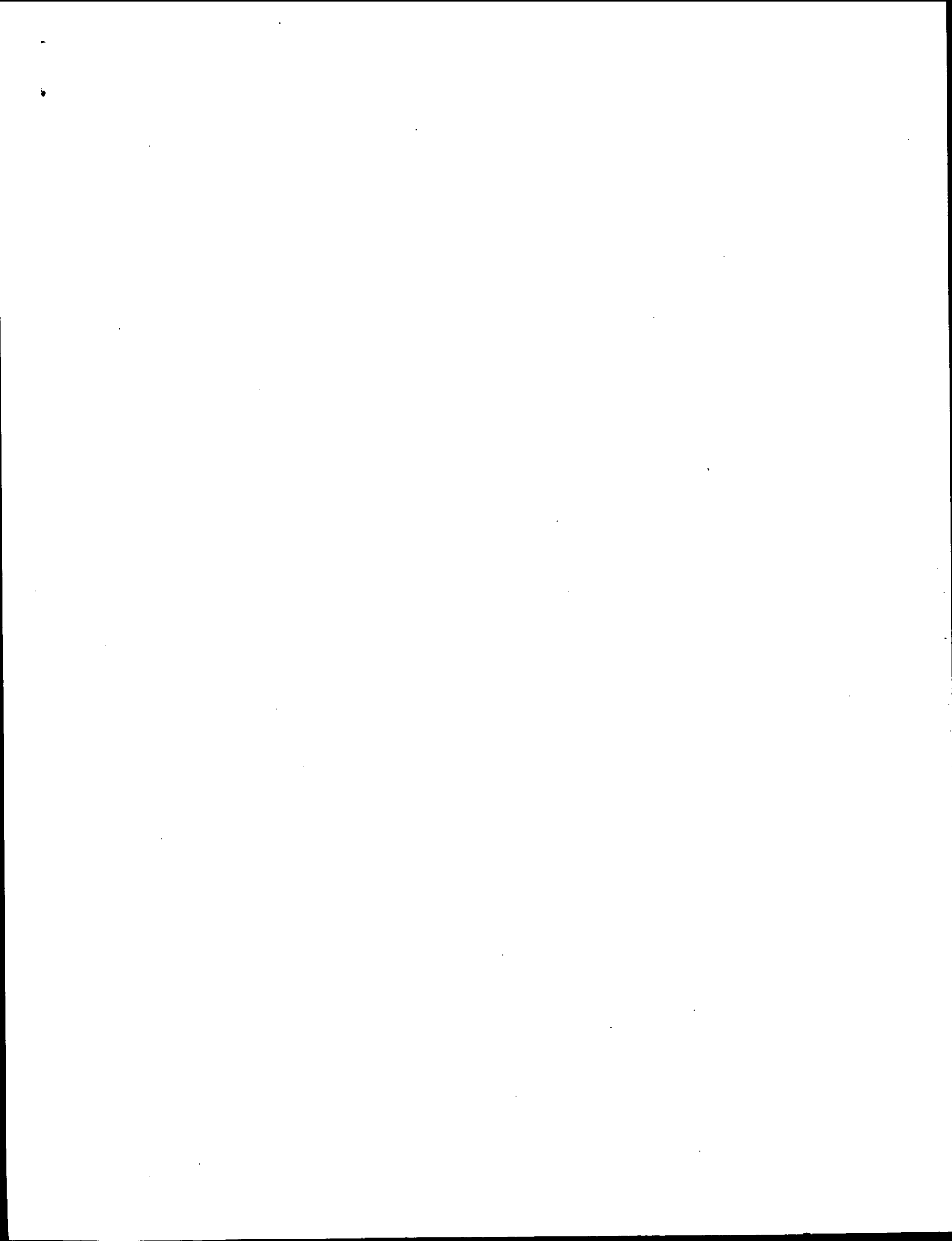
Query Match 4.4%; Score 206.5; DB 9; Length 532;
Best Local Similarity 21.3%; Pred. No. 1.1e-06;
Matches 101; Conservative 74; Mismatches 148; Indels 151; Gaps 19;

QY 3 RHHAGEEGGAGLWYK---SGAAAAAGGRLGSKMKDVSGRGVLLNSGAARGDGL 59
Db 52 RRRRTPDWCG-CGVGATRPPTGRGCRHGAIVPAALRCE---RLVLNVAGLRFE--- 103
QY 60 LGTRATLTGGGGGGLRESRRKOGARM--SLGKPLSYTSQSCRRVRYRQNYLYN 117
Db 104 ---TRATLG-----RFPDTLGDV-----RRSRFYDGAARAEYFF 136
QY 118 VLERPRGMFIYH-----AFVFLVF-----GCLT----- 142
Db 137 DRRHPSEFDALVYYQSGRLRRPAHVPLDVFLEVSFYLGRRLRLREDECAVAERPL 196
QY 143 -----LSVFSTIPEHTKLAS-----SCLILEFVMIVYVGL----- 174
Db 197 PPPFARQWLLEFFPESSQAARVLAVSVIL--VSIVVFCLETLDPDRDDPGLAP 254
QY 175 -----FIIRIMSAG-----CCCRYR-----GMQGRLEPA 198
Db 255 VAAATGSFLARLNGSSPMGPAPRPQPNDFPVVETICIFSEFLLVHIVAPSKAVFF 314
QY 199 RRPFCVYIDTVIL--ASIAVSAKTOG---NIFATLSRFLQILRMVMDRGGTW 252
Db 315 KNVMNLIDFVALPYFVALGTELARQGVGQPAWSLALRLVIRVFRIFKLSHRSKGL 374
QY 253 KLGSVYVAHSELITRMYIGFLVLISSFLYLVEND-AKNEFTYADALMNGTITLT 311
Db 375 QILGQTLRASMRELGLIFLFGVLESSAVYAEVDVDTHTFSIDSEFWAVAYMTT 434
QY 312 IGYGDTPLTWLRLLSAGFALLGISFFALPAGILGSGFALKVQEOHQHKEK 365
Db 435 VGIQMAPYIVGKIVGSLCAIAGVLTISLPVPIVSNFS---YFHHETEEBE 485

'Fri Jun 20 09:08:48 2003

Search completed: June 14, 2003, 17:54:01
Job time : 63 secs

us-09-825-147-2.rapb



GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 10:10:41 ; Search time 376 Seconds
(without alignments)
10818.373 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772

Sequence: 1 atgccccccaccacgcggyg.....ctcatgcaactgaataa 2772

Scoring table: IDENTITY NUC

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_MA:*

1: /cgn2-6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2-6/ptodata/1/pubpna/PC1_NEW_PUB.seq:*
3: /cgn2-6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2-6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2-6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2-6/ptodata/1/pubpna/PC1US_PUBCOMB.seq:*
7: /cgn2-6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2-6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2-6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2-6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2-6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2-6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2-6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2-6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2772	100.0	2772	10	US-09-825-147-1
2	2772	100.0	3111	10	US-09-825-147-3
3	2723.8	98.3	3074	10	US-09-813-148-1
4	2662.2	96.0	2667	10	US-09-810-796-3
5	2635.4	95.1	3071	10	US-09-810-796-1
6	2635.2	94.7	2694	10	US-09-810-796-2
7	478.8	17.3	2169	9	US-10-128-870-22
8	478.8	17.3	2169	9	US-10-131-685-22
9	465.4	16.8	896	9	US-10-128-870-1
10	428.8	15.5	2565	9	US-10-131-685-1
11	428.8	15.5	2565	9	US-10-128-870-26
12	428.8	15.5	3287	9	US-10-131-685-26
13	428.4	15.5	3287	9	US-10-128-870-19
14	428.4	15.5	3287	9	US-10-131-685-19
15	421.4	15.2	900	9	US-10-128-870-3
16	421.4	15.2	900	9	US-10-131-685-3
17	420.6	15.2	900	9	US-10-128-870-5
18	420.6	15.2	900	9	US-10-131-685-5
19	363.8	13.1	930	9	US-10-128-870-17

20	363.8	13.1	930	9	US-10-131-685-17	Sequence 17, Appl
21	334.2	12.1	735	9	US-10-128-870-7	Sequence 7, Appl
22	334.2	12.1	735	9	US-10-131-685-7	Sequence 7, Appl
23	267.8	9.7	2028	10	US-09-840-125-1	Sequence 1, Appl
24	267.8	9.7	3181	9	US-10-138-316-1	Sequence 1, Appl
25	266.6	9.6	2821	10	US-09-880-107-3358	Sequence 3358, Ap
26	130.4	3.7	416	10	US-09-960-352-13343	Sequence 13343, A
27	104.2	3.8	429	10	US-09-783-590-4509	Sequence 4509, Ap
28	90.2	3.3	477	9	US-09-918-995-27819	Sequence 27819, A
29	58.4	2.1	757	9	US-09-989-920-7	Sequence 7, Appl
30	58.4	2.1	1278	9	US-10-016-647-1	Sequence 1, Appl
31	58.4	2.1	1844	9	US-10-016-647-3	Sequence 3, Appl
32	58.4	2.1	2561	12	US-09-976-740-48	Sequence 48, Appl
33	58.4	2.1	2561	12	US-10-023-529-48	Sequence 48, Appl
34	58.4	2.1	2561	12	US-10-023-529-48	Sequence 48, Appl
35	57.6	2.1	12733	9	US-10-032-393-47	Sequence 47, Appl
36	57.6	2.1	12733	9	US-10-032-393-47	Sequence 47, Appl
37	56.4	2.0	1506	10	US-09-963-285-9	Sequence 9, Appl
38	56.4	2.0	3289	10	US-09-963-285-8	Sequence 8, Appl
39	56.4	2.0	4158	10	US-09-963-285-3	Sequence 3, Appl
40	56.4	2.0	6458	10	US-09-963-285-1	Sequence 1, Appl
41	56.2	2.0	440	9	US-10-184-644-202	Sequence 202, App
42	56.2	2.0	440	9	US-10-184-644-202	Sequence 202, App
43	54.6	1.9	1064	10	US-09-804-682-29	Sequence 29, Appl
44	53.4	1.9	43058	10	US-09-954-456-292	Sequence 292, App
45	53.4	1.9	43058	10	US-09-954-456-292	Sequence 292, App
46	53.4	1.9	43058	10	US-09-954-456-292	Sequence 292, App
47	52.6	1.9	4176	9	US-09-880-107-9950	Sequence 3950, Ap
48	52.4	1.9	153331	9	US-10-098-841-34	Sequence 34, Appl
49	52.2	1.9	931	9	US-10-093-407-16	Sequence 16, Appl
50	51.8	1.9	998	10	US-10-198-846-8585	Sequence 8585, Ap
51	51.8	1.9	1340	10	US-09-864-761-1804	Sequence 1804, A
52	51.8	1.9	1979	10	US-09-864-761-20550	Sequence 20550, A
53	51.4	1.9	11220	9	US-09-864-761-1784	Sequence 3784, Ap
54	51.4	1.9	11220	9	US-09-860-846-32	Sequence 32, Appl
55	51.4	1.9	11220	9	US-09-860-846-32	Sequence 32, Appl
56	51.4	1.9	11220	9	US-09-860-846-32	Sequence 32, Appl
57	51.4	1.9	36778	9	US-09-861-289-5	Sequence 5, Appl
58	51.4	1.9	36778	9	US-09-861-289-5	Sequence 5, Appl
59	51.4	1.9	36778	10	US-09-861-289-5	Sequence 5, Appl
60	51.4	1.9	37948	9	US-09-988-384B-5	Sequence 384B, Ap
61	51.4	1.9	38506	9	US-09-793-708-19	Sequence 19, Appl
62	51	1.8	1326	10	US-09-749-728B-12	Sequence 12, Appl
63	50.8	1.8	426	10	US-09-960-352-12683	Sequence 12683, A
64	50.2	1.8	1065	10	US-09-804-682-33	Sequence 33, Appl
65	50	1.8	594	9	US-10-123-155-10	Sequence 10, Appl
66	48.6	1.8	249487	9	US-10-026-188-3	Sequence 3, Appl
67	48	1.7	2288	9	US-09-989-920-103	Sequence 103, App
68	47.8	1.7	1918	9	US-10-255-969-5	Sequence 5, Appl
69	47.8	1.7	1918	12	US-10-139-262-5	Sequence 5, Appl
70	47.4	1.7	1614	9	US-09-976-740-45	Sequence 45, Appl
71	47.4	1.7	1614	12	US-10-023-529-45	Sequence 45, Appl
72	47.4	1.7	1614	12	US-10-023-529-45	Sequence 45, Appl
73	47.4	1.7	12425	9	US-09-976-740-50	Sequence 50, Appl
74	47.4	1.7	12425	12	US-10-023-529-50	Sequence 50, Appl
75	47.4	1.7	12425	12	US-10-023-529-50	Sequence 50, Appl
76	46.8	1.7	3372	2	US-10-067-457-2	Sequence 2, Appl
77	46.8	1.7	38186	9	US-09-373-658-38	Sequence 38, Appl
78	46.6	1.7	3454	9	US-10-171-581-312	Sequence 312, App
79	46.6	1.7	3454	10	US-09-969-347-226	Sequence 226, App
80	46.4	1.7	911	9	US-09-989-920-8	Sequence 8, Appl
81	46.2	1.7	42999	9	US-09-799-462A-17	Sequence 17, Appl
82	46.2	1.7	42999	9	US-10-125-767-17	Sequence 17, Appl
83	46.2	1.7	42999	9	US-09-836-911A-17	Sequence 17, Appl
84	46.2	1.7	42999	9	US-10-151-081-17	Sequence 17, Appl
85	46.2	1.7	42999	9	US-10-287-313-17	Sequence 17, Appl
86	46.2	1.7	42999	9	US-10-219-694-17	Sequence 17, Appl
87	46	1.7	7193	9	US-10-071-338-1	Sequence 1, Appl
88	46	1.7	7193	9	US-10-288-985-1	Sequence 1, Appl
89	45.6	1.6	3411	9	US-10-198-846-8872	Sequence 9872, Ap
90	45.6	1.6	9090	9	US-10-000-789-1	Sequence 1, Appl
91	45.6	1.6	9090	9	US-10-171-581-305	Sequence 305, App
92	45.4	1.6	671	9	US-10-184-644-346	Sequence 346, App

QY 781 GCTCAGACAGAGATTAATACAGCTTGTATACATAGCATTTTGGTCTATATTTTTCG 840
 Db 781 GCTCAGACAGAGATTAATACAGCTTGTATACATAGCATTTTGGTCTATATTTTTCG 840
 QY 841 TCTTCTCTGTCTATCTGTGGAAAAAGATGCAATTAAGAGTTTCTCATATGAGAT 900
 Db 841 TCTTCTCTGTCTATCTGTGGAAAAAGATGCAATTAAGAGTTTCTCATATGAGAT 900
 QY 901 GCTCTGTGTGGGACAAATTAATGACAACTATTTGGTATGAGACAAAACCTCCCTA 960
 Db 901 GCTCTGTGTGGGACAAATTAATGACAACTATTTGGTATGAGACAAAACCTCCCTA 960
 QY 961 ACTTGTGCTGGAAATATGCTTTCTGACAGCTTTGACATCTTTGCAATTTCTTTTGA 1020
 Db 961 ACTTGTGCTGGAAATATGCTTTCTGACAGCTTTGACATCTTTGCAATTTCTTTTGA 1020
 QY 1021 CTTCCTCCGGCATTTCTGGCTCAGGTTTGCATTTAAAGTACAAACACCGCCAG 1080
 Db 1021 CTTCCTCCGGCATTTCTGGCTCAGGTTTGCATTTAAAGTACAAACACCGCCAG 1080
 QY 1081 AAACACTTTGAGAAAGAGAGAACCCAGCTCCAACTCATCTGATGTTGGGCTAGT 1140
 Db 1081 AAACACTTTGAGAAAGAGAGAACCCAGCTCCAACTCATCTGATGTTGGGCTAGT 1140
 QY 1141 TACGCACTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCACACTTGAAGCCTTG 1200
 Db 1141 TACGCACTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCACACTTGAAGCCTTG 1200
 QY 1201 CACACCTGCAAGCCTTACCANTCAGAGTATTTAAGAGCCAGTGGCTAGC 1260
 Db 1201 CACACCTGCAAGCCTTACCANTCAGAGTATTTAAGAGCCAGTGGCTAGC 1260
 QY 1261 CCCAGGGGCCAGAGTATTAAGAGCCAGCAACCTCAGTAGTGACAGAGGTCCTCCAGC 1320
 Db 1261 CCCAGGGGCCAGAGTATTAAGAGCCAGCAACCTCAGTAGTGACAGAGGTCCTCCAGC 1320
 QY 1321 ACCGACATCAACAGCCGAGGAGTCCCAACAAAGTGCAAGAGCTGAGCTTCAACGAC 1380
 Db 1321 ACCGACATCAACAGCCGAGGAGTCCCAACAAAGTGCAAGAGCTGAGCTTCAACGAC 1380
 QY 1381 CGAACCCGCTTCGGGCTCGCTGCTCAAAAGTTCTCAGCCCAAAACAGTATAGT 1440
 Db 1381 CGAACCCGCTTCGGGCTCGCTGCTCAAAAGTTCTCAGCCCAAAACAGTATAGT 1440
 QY 1441 GCTGACACAGCCCTTGGCACTGATGATATATGATGAAAAAGATGCGCAGTGTATGA 1500
 Db 1441 GCTGACACAGCCCTTGGCACTGATGATATATGATGAAAAAGATGCGCAGTGTATGA 1500
 QY 1501 TCAGTGAGAGACCTCACCCACCACTTAAACCTGATTCAGCTATCAGATTAATGAAA 1560
 Db 1501 TCAGTGAGAGACCTCACCCACCACTTAAACCTGATTCAGCTATCAGATTAATGAAA 1560
 QY 1561 TTTTCATGTTGCAAAAGAGAGTTTAAAGAAACATTAGCTCCATATGATTAAGATGTC 1620
 Db 1561 TTTTCATGTTGCAAAAGAGAGTTTAAAGAAACATTAGCTCCATATGATTAAGATGTC 1620
 QY 1621 ATTGAACAATATTTCTGCTGCTCATCTGACATGTTGTTAGATTAATTAAGCCTTCAACA 1680
 Db 1621 ATTGAACAATATTTCTGCTGCTCATCTGACATGTTGTTAGATTAATTAAGCCTTCAACA 1680
 QY 1681 CGTGTGATCAAAATTTCTTGGAAAAAGGCAAAATCACATCAGATTAAGAAAGCCGAGAAA 1740
 Db 1681 CGTGTGATCAAAATTTCTTGGAAAAAGGCAAAATCACATCAGATTAAGAAAGCCGAGAAA 1740
 QY 1741 ATAAAGCAGAGATGAGACACAGAGATCTGATGCTGGGTGGGTGCTCAAGTT 1800
 Db 1741 ATAAAGCAGAGATGAGACACAGAGATCTGATGCTGGGTGGGTGCTCAAGTT 1800
 QY 1801 GAAAAACAGTACAGTCCATAGATCAAGAGTGGAGTCCACTAGACATATATCAACAG 1860
 Db 1801 GAAAAACAGTACAGTCCATAGATCAAGAGTGGAGTCCACTAGACATATATCAACAG 1860
 QY 1861 GTCTCTGGAGAAAGGCTCTGCTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTT 1920

Db 1861 GTCTCTGGAGAAAGGCTCTGCTCAGACCCCTGCTTGGCTTCAATTCAGATCCCACTTTT 1920
 QY 1921 GAATGTAAACAGATCTGACTATCAAAAGCCCTGTGGATATAGCAAAAGATCTTGGGTTCC 1980
 Db 1921 GAATGTAAACAGATCTGACTATCAAAAGCCCTGTGGATATAGCAAAAGATCTTGGGTTCC 1980
 QY 1981 GCACAAAACAGTGTGCTGTTATCCAGATCACTAGTGTGCAACATCTGAGAGGCTTGAG 2040
 Db 1981 GCACAAAACAGTGTGCTGTTATCCAGATCACTAGTGTGCAACATCTGAGAGGCTTGAG 2040
 QY 2041 TTCAATCTGAGCCCAATGAGTTGACAGTCCAGACTTTCTAGCGCTTACGCCCTATAG 2100
 Db 2041 TTCAATCTGAGCCCAATGAGTTGACAGTCCAGACTTTCTAGCGCTTACGCCCTATAG 2100
 QY 2101 CACAGTAAACAGACAGAGTCCCAATTAAGTAAAGCATGCTGACAGCTGACAGCCAC 2160
 Db 2101 CACAGTAAACAGACAGAGTCCCAATTAAGTAAAGCATGCTGACAGCTGACAGCCAC 2160
 QY 2161 AACACCAATTCGAAACCAATTAATAGGAGCCAGGAGCCAGGAGCCCAACCACTTACAG 2220
 Db 2161 AACACCAATTCGAAACCAATTAATAGGAGCCAGGAGCCAGGAGCCCAACCACTTACAG 2220
 QY 2221 ATCCACCTCCTCTCCAGCCATCAAGATCTGCCAGGCGGAGAACTCTGACCCCTAAC 2280
 Db 2221 ATCCACCTCCTCTCCAGCCATCAAGATCTGCCAGGCGGAGAACTCTGACCCCTAAC 2280
 QY 2281 CTTGCAAGCTTACAGGAAAGCATTTTGTAGCTCACACCTGCTTGTGCTCCAGGAA 2340
 Db 2281 CTTGCAAGCTTACAGGAAAGCATTTTGTAGCTCACACCTGCTTGTGCTCCAGGAA 2340
 QY 2341 AATGTTGAGTTGACAGTCAAAATCTCACAGGAGCCGTTATAGGAGAAAGCTTTGAC 2400
 Db 2341 AATGTTGAGTTGACAGTCAAAATCTCACAGGAGCCGTTATAGGAGAAAGCTTTGAC 2400
 QY 2401 ATGGAGAGAGAAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
 Db 2401 ATGGAGAGAGAAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
 QY 2461 TTGCTGTGCAAAACCTGATCAGTGTGCAAGGAGCACTGAATATACACTTTCAGGAGT 2520
 Db 2461 TTGCTGTGCAAAACCTGATCAGTGTGCAAGGAGCACTGAATATACACTTTCAGGAGT 2520
 QY 2521 GAGTCAAGTGTGCTGCAAGGAGCACTGAATATACACTTTCAGGAGT 2580
 Db 2521 GAGTCAAGTGTGCTGCAAGGAGCACTGAATATACACTTTCAGGAGT 2580
 QY 2581 TTTATACAGTGAAGAGTGGGTCCGAGAGACAGAGACAGACACTTTTGTATGCCGA 2640
 Db 2581 TTTATACAGTGAAGAGTGGGTCCGAGAGACAGAGACAGACACTTTTGTATGCCGA 2640
 QY 2641 CCGCAGCTGCGCAGGAGAGTGGCTTTGATCAGACTCTCTAAGGACTGGAAGGTACGA 2700
 Db 2641 CCGCAGCTGCGCAGGAGAGTGGCTTTGATCAGACTCTCTAAGGACTGGAAGGTACGA 2700
 QY 2701 TCATCTCAGAGCACTTTGTTAAGGAGAGGAAAGTACAGATGCCCTGAGTGGCTCATGTC 2760
 Db 2701 TCATCTCAGAGCACTTTGTTAAGGAGAGGAAAGTACAGATGCCCTGAGTGGCTCATGTC 2760
 QY 2761 AAACGTAAATAA 2772
 Db 2761 AAACGTAAATAA 2772

RESULT 2
 US-09-825-147-3
 ; Sequence 3, Application US/09825147
 ; Patent No. US20020042505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Y1
 ; APPLICANT: Kieke, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.

QY	186	GTGCTTGGAAAGGCTGTGGCTCGAGCCCTGGCTTTGGCTTATCTCCAGATCCCACTTTT	1920
Db	1920	GTCTCTGGAAAGGCTTGGCTCGAGCCCTGGCTTTGGCTTATCTCCAGATCCCACTTTT	1979
QY	1921	GAATGTGAAACGACATCTGACTATCAAAAGCCCTGTGATAGCAAGAATCTTTCCGCTTCC	1980
Db	1980	GAATGTGAAACGACATCTGACTATCAAAAGCCCTGTGATAGCAAGAATCTTTCCGCTTCC	2039
QY	1981	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTCGAG	2040
Db	2040	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTCGAG	2099
QY	2041	TTGATTTGTGAGCCCAATGAGTTGACAGGCCAGACTTTCTACGGGGCTTAGCCCTACTATG	2100
Db	2100	TTGATTTGTGAGCCCAATGAGTTGACAGGCCAGACTTTCTACGGGGCTTAGCCCTACTATG	2159
QY	2101	CACAGTCAACACACACAGGTGCCAATTAGTCAAAAGCATGGCTCAGAGTGGCAGCCAC	2160
Db	2160	CACAGTCAACACACACAGGTGCCAATTAGTCAAAAGCATGGCTCAGAGTGGCAGCCAC	2219
QY	2161	AACACCAATTGCAAAACCAATTAATATGCGCACCCCAAGCCAGCAGCCGCCAACCACTTTAC	2220
Db	2220	AACACCAATTGCAAAACCAATTAATATGCGCACCCCAAGCCAGCAGCCGCCAACCACTTTAC	2279
QY	2221	ATGCCACCTCTCTCCCGAGGCATCAACATCTGGCCAGGCGCAAGAACTCTGACCCCTAC	2280
Db	2280	ATGCCACCTCTCTCCCGAGGCATCAACATCTGGCCAGGCGCAAGAACTCTGACCCCTAC	2339
QY	2281	CTGCGAGGCTTACAGAAACATTTCTGAGCTGCACCACTGCTTTGGCTCCCAAGGA	2340
Db	2340	CTGCGAGGCTTACAGAAACATTTCTGAGCTGCACCACTGCTTTGGCTCCCAAGGA	2399
QY	2341	AATGTTCAGGTTGCACAGTCAAAATCTGACCAAGGACCGTTCTATGAGAAAAAGCTTGC	2400
Db	2400	AATGTTCAGGTTGCACAGTCAAAATCTGACCAAGGACCGTTCTATGAGAAAAAGCTTGC	2459
QY	2401	ATGGGAGGAGAAACCTGTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	2460
Db	2460	ATGGGAGGAGAAACCTGTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	2519
QY	2461	TTGTCTGTGCAAAACCTGATCAGGTGCAACGAGCAACTGATTAATCAACTTTCAGGAGT	2520
Db	2520	TTGTCTGTGCAAAACCTGATCAGGTGCAACGAGCAACTGATTAATCAACTTTCAGGAGT	2579
QY	2521	GAGTCAAGGTGCTCCAGAGGACGCAAGATTTTACCCTCAANTGAGGGAATCCAAATTG	2580
Db	2580	GAGTCAAGGTGCTCCAGAGGACGCAAGATTTTACCCTCAANTGAGGGAATCCAAATTG	2639
QY	2581	TTTATTAACCTATGAAAGGTGGGTGCCGAGAGACAGACAGACACTTTTGATGCGCA	2640
Db	2640	TTTATTAACCTATGAAAGGTGGGTGCCGAGAGACAGACAGACACTTTTGATGCGCA	2699
QY	2641	CCGAGAGCTCCAGAGGAAGTGCCTTTGACATCAACTCTCTAAGAGCTGGAAGGTACAG	2700
Db	2700	CCGAGAGCTCCAGAGGAAGTGCCTTTGACATCAACTCTCTAAGAGCTGGAAGGTACAG	2759
QY	2701	TCATCTCAGAGCAATTTGTAAAGGACGAGAAAGTACAGATGCCCTCAGCTTCATATGC	2760
Db	2760	TCATCTCAGAGCAATTTGTAAAGGACGAGAAAGTACAGATGCCCTCAGCTTCATATGC	2819
QY	2761	AAACTGAAATTA 2772	
Db	2820	AAACTGAAATTA 2831	

```

? APPLICANT: SEBOHM, Guiscard
? APPLICANT: BUSCH, Andreas E.
? TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF
? TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
? FILE REFERENCE: 38005-119
? CURRENT APPLICATION NUMBER: US/09/813,148
? CURRENT FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: DE 100 13 732.6
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: US 60/194,041
? PRIOR FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1
? LENGTH: 3074
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-813-148-1

```

Query Match	98.3%;	Score 2723.8;	DB 10;	Length 3074;
Best Local Similarity	98.8%;	Pred. No. 0;		
Matches 2765;	Conservative	0;	Mismatches 7;	Indels 27; Gaps 1.
QY	1	ATGCCCGCCACACAGGGGAGAGAGAGGGCGGCCGCCGGGCTCTGGGTGAAGAGC	60	
Db	110	ATGCCCGCCACACAGGGGAGAGAGAGGGCGGCCGCCGGGCTCTGGGTGAAGAGC	169	
QY	61	GGCGCAGCGCGCGCGCGCGCGCGCGCTTGGGACGGCATAGAGATGTGGAG	120	
Db	170	GGCGCAGCGCGCGCGCGCGCGCGCTTGGGACGGCATAGAGATGTGGAG	229	
QY	121	TTCGGGGCGGGGACAGGAGTGTCTCAACCTCGGCAAGCCGCAAGGGGGAAGGGCTGTACTG	180	
Db	230	TTCGGGGCGGGGACAGGAGTGTCTCAACCTCGGCAAGCCGCAAGGGGGAAGGGCTGTACTG	289	
QY	181	CTGGGCAACCCGCGGGCCACGCTCGAGTGGCGGGCGGTGGCTTAGAGGAGAGCCGCCGG	240	
Db	290	CTGGGCAACCCGCGGGCCACGCTCGAGTGGCGGGCGGTGGCTTAGAGGAGAGCCGCCGG	349	
QY	241	GGCAAGCAGGGGGGCCCGGATGAGCCTCTGGGGAAAGCCGCTCTTACACAGTAGCCAG	300	
Db	350	GGCAAGCAGGGGGGCCCGGATGAGCCTCTGGGGAAAGCCCGCTCTTACACAGTAGCCAG	409	
QY	301	AGCTGCCGGGGCAACGTCACGTACCGGGGGGTGCAGAACTACGCTACAAGTGGTGGAG	360	
Db	410	AGCTGCCGGGGCAACGTCACGTACCGGGGGGTGCAGAACTACGCTACAAGTGGTGGAG	469	
QY	361	AGACCCCGGGGCTGGGGGTTTCATACACGCTTTCGTTTTCTGCTGTCTTGGTTGC	420	
Db	470	AGACCCCGGGGCTGGGGGTTTCATACACGCTTTCGTTTTCTGCTGTCTTGGTTGC	529	
QY	421	TTGATTTTGTCAAGTTTCTTACACATCCCTAGACACAAATTTGGCCTCAAGTTGCCTC	480	
Db	530	TTGATTTTGTCAAGTTTCTTACACATCCCTAGACACAAATTTGGCCTCAAGTTGCCTC	589	
QY	481	TTGATCTCGAGTTCGTGATGATTGTCTCTTTGGTTTGGAGTTCATCTCGAATCTGG	540	
Db	590	TTGATCTCGAGTTCGTGATGATTGTCTCTTTGGTTTGGAGTTCATCTCGAATCTGG	649	
QY	541	TCTCGGGGTTCGTGTTCGATATAGAGAGATGGCAAGAAAGCTAGGTTCGTGAAG	600	
Db	650	TCTCGGGGTTCGTGTTCGATATAGAGAGATGGCAAGAAAGCTAGGTTCGTGAAG	709	
QY	601	CCCTTCGTGTTATAGATACCATTTGTTTATACGCTTCAATAGACAGTGTTCGCAAAA	660	
Db	710	CCCTTCGTGTTATAGATACCATTTGTTTATACGCTTCAATAGACAGTGTTCGCAAAA	769	
QY	661	ACTTAGGGTAATATTTTGGCCACGCTTGCACTCAGAAATCTCCGTTTCTCAAGATCCTC	720	
Db	770	ACTTAGGGTAATATTTTGGCCACGCTTGCACTCAGAAATCTCCGTTTCTCAAGATCCTC	829	
QY	721	CGCATGGTGGCATGAGACGGAAGGGAGGACCTTGAATAATCTAGGGTTCAAGTGGTTAT	780	

Db 830 CGATGTCGCGCATGACCGAAGGAGGAGCATTGGAAATTACTGGGTTGAGTGTAT 889
QY 781 GCTCAGACAGGAATTAATCAAGCTTGGTACATGATTTTGGTCTATTTTTCG 840
Db 890 GCTCAGACAGGAATTAATCAAGCTTGGTACATGATTTTGGTCTATTTTTCG 949
QY 841 TCTTTCCTTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTACATATGAGAT 900
Db 950 TCTTTCCTTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTACATATGAGAT 1009
QY 901 GCTCTCTGTGTGTGAGCAATTCATTTGACAACTATTGGCTATGAGACAAAACCTCCCTA 960
Db 1010 GCTCTCTGTGTGTGAGCAATTCATTTGACAACTATTGGCTATGAGACAAAACCTCCCTA 1069
QY 961 ACTTGGCTGGGAAGATGCTTCTGTGAGGCTTGTGACCTCTGGCATTTCTTTTGA 1020
Db 1070 ACTTGGCTGGGAAGATGCTTCTGTGAGGCTTGTGACCTCTGGCATTTCTTTTGA 1129
QY 1021 CTTCCTGCGGCGCATCTTGGCTCAGGTTTTCATTAAGTACAGAAACACCGCGCAG 1080
Db 1130 CTTCCTGCGGCGCATCTTGGCTCAGGTTTTCATTAAGTACAGAAACACCGCGCAG 1189
QY 1081 AAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATTTGAGTGTGCTGAGT 1140
Db 1190 AAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATTTGAGTGTGCTGAGT 1249
QY 1141 TACGACGTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCACACTTGAAGGCTTG 1200
Db 1250 TACGACGTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCACACTTGAAGGCTTG 1309
QY 1201 CACACCTGACAGCCCTTACCA-----TCAGAAAGCTAAGT 1233
Db 1310 CACACCTGACAGCCCTTACCAAGAAACAAAGGGAAGCATCAAGCTAGAAAGCTAAGT 1369
QY 1234 TTTAAGGAGGAGATGTCGATGCTAGGCTAGCCCGAGGAGGAGATTTAAGACCCGAAAGCC 1293
Db 1370 TTTAAGGAGGAGATGTCGATGCTAGGCTAGCCCGAGGAGGAGATTTAAGACCCGAAAGCC 1429
QY 1294 TCAGTAGTGAACAGAGGTCCCAAGACCGACATCAGACGCGAGGAGCTCCCAACAAA 1353
Db 1430 TCAGTAGTGAACAGAGGTCCCAAGACCGACATCAGACGCGAGGAGCTCCCAACAAA 1489
QY 1354 GTGCAGAAAGAGCTGAGGCTTTCAGACGACGAAACCGGCTTCGCTGCGGCTTCAA 1413
Db 1490 GTGCAGAAAGAGCTGAGGCTTTCAGACGACGAAACCGGCTTCGCTGCGGCTTCAA 1549
QY 1414 AGTCTCAGCCAAAACCGATGATGATGCTGACACAGCCCTTGGCACTGATGATAT 1473
Db 1550 AGTCTCAGCCAAAACCGATGATGATGCTGACACAGCCCTTGGCACTGATGATAT 1609
QY 1474 GATGAAAAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
Db 1610 GATGAAAAAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1669
QY 1534 GTCAATTGAGCTATCAGATTAATGAAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAACA 1593
Db 1670 GTCAATTGAGCTATCAGATTAATGAAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAACA 1729
QY 1594 TTAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
Db 1730 TTAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
QY 1654 TTGTGTAGAAATTAAGAGCTTCAACACAGTGTGATCAAAATTTCTTGGAAAAAGGCAATC 1713
Db 1790 TTGTGTAGAAATTAAGAGCTTCAACACAGTGTGATCAAAATTTCTTGGAAAAAGGCAATC 1849
QY 1714 ACATCAGATTAAGAAAGCCGAGAGAAAATTAACAGAGAAATGAGACCAAGACGATCTC 1773
Db 1850 ACATCAGATTAAGAAAGCCGAGAGAAAATTAACAGAGAAATGAGACCAAGACGATCTC 1909
QY 1774 AGTATGCTGGGTGGGTGGGTGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1833
Db 1910 AGTATGCTGGGTGGGTGGGTGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1969

QY 1834 GACTGCTACTAGACATCTAATCAACAGAGTCTCTGGAAAAGGCTCTGCCAGCCCTGCT 1893
Db 1970 GACTGCTACTAGACATCTAATCAACAGAGTCTCTGGAAAAGGCTCTGCCAGCCCTGCT 2029
QY 1894 TTGGCTTCAATTCAGATCCCACTTTTGAATGTAAGACAGATGCTGATATCAAAAGCCCT 1953
Db 2030 TTGGCTTCAATTCAGATCCCACTTTTGAATGTAAGACAGATGCTGATATCAAAAGCCCT 2089
QY 1954 GTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGTATTCAGATCAACT 2013
Db 2090 GTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGTATTCAGATCAACT 2149
QY 2014 AGTGCACAAATCTCGAAGGCTCTGACATTCATCTGACGCCAAATGATTCAGTCCAG 2073
Db 2150 AGTGCACAAATCTCGAAGGCTCTGACATTCATCTGACGCCAAATGATTCAGTCCAG 2209
QY 2074 ACTTCTAGCGCTTATGCTTACTATGACAGTCAAGCAGACAGTCCCAATTAAGTCA 2133
Db 2210 ACTTCTAGCGCTTATGCTTACTATGACAGTCAAGCAGACAGTCCCAATTAAGTCA 2269
QY 2134 AGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTTGCAAAACCAATTAATACGACCC 2193
Db 2270 AGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTTGCAAAACCAATTAATACGACCC 2329
QY 2194 AAGCCAGAGCCCAACCAATTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTG 2253
Db 2330 AAGCCAGAGCCCAACCAATTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTG 2389
QY 2254 CCCAGGCGCAAAACTCTGACCCCTAACCTGACAGCTTACAGAAAGCAATTTGACGTC 2313
Db 2390 CCCAGGCGCAAAACTCTGACCCCTAACCTGACAGCTTACAGAAAGCAATTTGACGTC 2449
QY 2314 ACCACCTGCTTGTGCTCTCAAGAAATGTTAGTTGCAAGTCAAAATCTACCAAG 2373
Db 2450 ACCACCTGCTTGTGCTCTCAAGAAATGTTAGTTGCAAGTCAAAATCTACCAAG 2509
QY 2374 GACCGTTCTATGAGAAAACCTTTGACATGGAAGGAAATCTGTTGCTGTCTGCC 2433
Db 2510 GACCGTTCTATGAGAAAACCTTTGACATGGAAGGAAATCTGTTGCTGTCTGCC 2569
QY 2434 ATGGTGCCGAAGACTTTGGGCAAAATCTTGTGTGCAAAACCTGATCAGTCCAGCAG 2493
Db 2570 ATGGTGCCGAAGACTTTGGGCAAAATCTTGTGTGCAAAACCTGATCAGTCCAGCAG 2629
QY 2494 GAACCTGAATATACAACTTTTCAAGGAGTGAATGCAAGTGGCTCCAGAGCAGCAAGATTTT 2553
Db 2630 GAACCTGAATATACAACTTTTCAAGGAGTGAATGCAAGTGGCTCCAGAGCAGCAAGATTTT 2689
QY 2554 TACCCCAATGAGAGGAATCCAAATTTGTTATTAAGTGAAGAGTGGTCCGAAAGAG 2613
Db 2690 TACCCCAATGAGAGGAATCCAAATTTGTTATTAAGTGAAGAGTGGTCCGAAAGAG 2749
QY 2614 ACAGAGACAGACATTTTGAATGCGGACCGCAGCCTCCAGGGAAGCTGCTTTCATCA 2673
Db 2750 ACAGAGACAGACATTTTGAATGCGGACCGCAGCCTCCAGGGAAGCTGCTTTCATCA 2809
QY 2674 GACTCTCTAAGAGCTGGAAGTACAGATCATCTCAGAGCAATTTTGAAGGCAAGGAAGT 2733
Db 2810 GACTCTCTAAGAGCTGGAAGTACAGATCATCTCAGAGCAATTTTGAAGGCAAGGAAGT 2869
QY 2734 ACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2772
Db 2870 ACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2908

RESULT 4
US-09-810-796-3
: Sequence 3, Application US/09810796
: Patent No. US20020102677A1
: GENERAL INFORMATION:
: APPLICANT: Jega, Timothy James
: APPLICANT: ICAGEN, Inc.


```

Db      1801 CAGATCCACCTTTTGAATGTGAACAGACATCTGATCAATCAAAAGCCCTGTGATGCAAA 1860
      1966 GATCTTTGGGTTCCGCACAAAACAGTGGCTGTATTCAGATCACTAGTSCCAACATC 2025
      1861 GATCTTTGGGTTCCGCACAAAACAGTGGCTGTATTCAGATCACTAGTSCCAACATC 1920
      2026 TCGAGAGGCTTCAGATTCATTTGACGCCCAATGATTCAGTCCCACTTTCTACGG 2085
      1921 TCGAGAGGCTTCAGATTCATTTGACGCCCAATGATTCAGTCCCACTTTCTACGG 1980
      2086 CTATGACCTCTATGACAGTCAAGCAACACAGGTGCCAATGATCAAGGATGAGCTCA 2145
      1981 CTATGACCTCTATGACAGTCAAGCAACACAGGTGCCAATGATTCAGTCCCACTTTCTAC 2040
      2146 GCAGTGGCAGCCACCAACACCATTCGCAACCAATTAATACGCGACCCCAAGCCAGAGCC 2205
      2041 GCAGTGGCAGCCACCAACACCATTCGCAACCAATTAATACGCGACCCCAAGCCAGAGCC 2100
      2206 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCCAGAG 2265
      2101 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCCAGAG 2160
      2266 ACCTGACACCTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCCAGAG 2325
      2161 ACCTGACACCTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCGCCAGAG 2220
      2326 GTTGCCCTCAAGAAATGTTTCAAGTTGCACAGTCAATCTCAACAGAGACGCTTATG 2385
      2221 GTTGCCCTCAAGAAATGTTTCAAGTTGCACAGTCAATCTCAACAGAGACGCTTATG 2280
      2386 AGGAAAAGCTTTGACATGGGAGGAAACTGTTGTCGTGTCCTCAATGATGCGGAG 2445
      2281 AGGAAAAGCTTTGACATGGGAGGAAACTGTTGTCGTGTCCTCAATGATGCGGAG 2340
      2446 GACTTGGGCAATTTTGTCTGTGCAAAAACCTGATCAGTGCACGAGAACTGAATATA 2505
      2341 GACTTGGGCAATTTTGTCTGTGCAAAAACCTGATCAGTGCACGAGAACTGAATATA 2400
      2506 CAACTTTCAGGAGTGAATCAAGTGGCTCCAGAGGCAAGCAATTTTCCCAATG 2565
      2401 CAACTTTCAGGAGTGAATCAAGTGGCTCCAGAGGCAAGCAATTTTCCCAATG 2460
      2566 AGGAAATCCAATTTGTTTATACTGATGAAGAGTGGTCCCGAAGAGACAGAGAC 2625
      2461 AGGAAATCCAATTTTATACTGATGAAGAGTGGTCCCGAAGAGACAGAGAC 2520
      2626 ACTTTTATGCGGCAACCGAGCCTGCGAGGAAAGTGCCTTTCATCAGACTCTAAG 2685
      2521 ACTTTTATGCGGCAACCGAGCCTGCGAGGAAAGTGCCTTTCATCAGACTCTAAG 2580
      2686 ACTGGAAGTCAAGTCAATCTCAAGAGCAATTTGTAAGGCAAGAAATACAGATGCCCTC 2745
      2581 ACTGGAAGTCAAGTCAATCTCAAGAGCAATTTGTAAGGCAAGAAATACAGATGCCCTC 2640
      2746 AGCTTGCCTCATGTCAAACTGAATATA 2772
      2641 AGCTTGCCTCATGTCAAACTGAATATA 2667

```

```

RESULT 5
US-09-810-796-1
: Sequence 1, Application US/09810796
: Patent No. US20020102677A1
: GENERAL INFORMATION:
: APPLICANT: Jega, Timothy James
: TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
: FILE REFERENCE: 018512-005010US
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 60/190,954
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 17

```

```

: SOFTWARE: Patentl Ver. 2.1
: SEQ ID NO 1
: LENGTH: 3071
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human outwardly rectifying, voltage-gated
: NAME/KEY: CDS
: LOCATION: (10)..(2703)
: OTHER INFORMATION: KCNQ5-1
: US-09-810-796-1

```

```

Query Match          95.1% Score 2635.4; DB 10; Length 3071;
Best Local Similarity 98.9% Pred. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

```

```

      97 GGCACGGCATGAAGAGATGAGTGGGCGCGGCGCAAGGAGTGTCTGAACTCGGCGAGCC 156
      1 GGCACGGCATGAAGAGATGAGTGGGCGCGGCGCAAGGAGTGTCTGAACTCGGCGAGCC 60
      157 GCCAGGGCGAGAGGCTGTCTGAGTGGGCGCGGCGCAAGGAGTGTCTGAACTCGGCGAGCC 216
      61 GCCAGGGCGAGAGGCTGTCTGAGTGGGCGCGGCGCAAGGAGTGTCTGAACTCGGCGAGCC 120
      217 GGTGCGCTGAGGAGAGCGCGGCGGCAAGCAGAGGCGCGGCGATGAGCTGCTGGGGAAG 276
      121 GGTGCGCTGAGGAGAGCGCGGCGGCAAGCAGAGGCGCGGCGATGAGCTGCTGGGGAAG 180
      277 CCGCTCTTACACGATGAGCAGAGTCCGCGCGCAAGTCAATGACCTGCTGGGGAAG 336
      181 CCGCTCTTACACGATGAGCAGAGTCCGCGCGCAAGTCAATGACCTGCTGGGGAAG 240
      337 AACTACCTTACACGATGAGCAGAGTCCGCGCGCAAGTCAATGACCTGCTGGGGAAG 396
      241 AACTACCTTACACGATGAGCAGAGTCCGCGCGCAAGTCAATGACCTGCTGGGGAAG 300
      397 GTTTTCTCTCTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 456
      301 GTTTTCTCTCTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
      457 ACAAATTTGGGCTCAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 516
      361 ACAAATTTGGGCTCAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 420
      517 TTGAGATCATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
      421 TTGAGATCATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
      577 GGAAGACTGAGTGTGCTGCAAAAGCCCTTCTGTTATGATGATGATGATGATGATGATGAT 636
      481 GGAAGACTGAGTGTGCTGCAAAAGCCCTTCTGTTATGATGATGATGATGATGATGATGAT 540
      637 TCAATGACAGTGTGTTTTCGCAAAAGTCAAGGATGATGATGATGATGATGATGATGATGAT 696
      541 TCAATGACAGTGTGTTTTCGCAAAAGTCAAGGATGATGATGATGATGATGATGATGATGAT 600
      697 AGTCTCCGTTTCTTACAGATCTCCGATGATGATGATGATGATGATGATGATGATGATGATG 756
      601 AGTCTCCGTTTCTTACAGATCTCCGATGATGATGATGATGATGATGATGATGATGATGATG 660
      757 AATTTACTGGGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 816
      661 AATTTACTGGGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
      817 GGAATTTGGGTTTCTTATTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG 876
      721 GGAATTTGGGTTTCTTATTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG 780
      877 AAGAGTTTCTTACATATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 936
      781 AAGAGTTTCTTACATATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

```



```

: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human outwardly-rectifying, voltage-gated
: OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
: NAME/KEY: CDS
: LOCATION: (1)..(2694)
: OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

```

```

Query Match      94.7%; Score 2625.2; DB 10; Length 2694;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

```

```

QY 106 ATGAAGATGTGAGTTCGGGCGGCGGAGGAGGCTGCTGTAAGTCCGAGCCGCGGAGGC 165
Db 1 ATGAAGATGTGAGTTCGGGCGGCGGAGGAGGCTGCTGTAAGTCCGAGCCGCGGAGGC 60
QY 166 GACGGCTGTACTGCTGCGGCAACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 225
Db 61 GACGGCTGTACTGCTGCGGCAACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 120
QY 226 AGGAGAGACCGCGGCGGCGGAGGAGGCGGCGGAGTGAAGCTGCTGCGGAGAGCCGCTCT 285
Db 121 AGGAGAGACCGCGGCGGCGGAGGAGGCGGCGGAGTGAAGCTGCTGCGGAGAGCCGCTCT 180
QY 286 TACACGATAGCAGAGCTGCGGCGGCGGCAAGTCAAGTACCGGCGGCGGCGGAGTACCTG 345
Db 181 TACACGATAGCAGAGCTGCGGCGGCGGCGGCAAGTCAAGTACCGGCGGCGGAGTACCTG 240
QY 346 TACACGATGTGAGAGAGACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 405
Db 241 TACACGATGTGAGAGAGACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
QY 406 CTGTGCTTGGTGTGATTTTGTAGTGTTCATCCATCCCTGAGCACACAAATTTG 465
Db 301 CTGTGCTTGGTGTGATTTTGTAGTGTTCATCCATCCCTGAGCACACAAATTTG 360
QY 466 GCGTCAAGTGGCTGTGATTCCTGAGTTCGATGATGATGCTGCTTGTGTTGGAGTTC 525
Db 361 GCGTCAAGTGGCTGTGATTCCTGAGTTCGATGATGATGCTGCTTGTGTTGGAGTTC 420
QY 526 ATCATTCGATGTGCTGCGGCGGCTGCTGCTGATATAGAGATGCGAAGAACTG 585
Db 421 ATCATTCGATGTGCTGCGGCGGCTGCTGCTGATATAGAGATGCGAAGAACTG 480
QY 586 AGGTTCGTCGAAAGCCCTTGTGTATAGATACCATGTTCTTATCGCTCAATAGCA 645
Db 481 AGGTTCGTCGAAAGCCCTTGTGTATAGATACCATGTTCTTATCGCTCAATAGCA 540
QY 646 GTTGTTCGCAAAAACACTAGGATATATTTTGGCAGCTGTGACACAGAACTCTCGT 705
Db 541 GTTGTTCGCAAAAACACTAGGATATATTTTGGCAGCTGTGACACAGAACTCTCGT 600
QY 706 TTCTTACGATCTCCGCAATGCTGCGCATGAGACCGAAGGAGGAGCACTTGGAAATTTCTG 765
Db 601 TTCTTACGATCTCCGCAATGCTGCGCATGAGACCGAAGGAGGAGCACTTGGAAATTTCTG 660
QY 766 GGTTCAGAGGTTTATGCTACAGCAAGGAATTAATACAGCTGTGATCATAGATTTTGG 825
Db 661 GGTTCAGAGGTTTATGCTACAGCAAGGAATTAATACAGCTGTGATCATAGATTTTGG 720
QY 826 GTTCTTATTTTTCCTTCTCTTGTCTATCTGCTGGAAGAAAGATGCAATTAAGAGTTT 885
Db 721 GTTCTTATTTTTCCTTCTCTTGTCTATCTGCTGGAAGAAAGATGCAATTAAGAGTTT 780
QY 886 TCTCATATGCAAGATGCTCTGCTGCTGCGACAAATTAATCATTTGAGTATGGA 945
Db 781 TCTCATATGCAAGATGCTCTGCTGCTGCGACAAATTAATCATTTGAGTATGGA 840
QY 946 GACAAACCTCCCTTAATGCTGCGGAGAGATGCTTCTGACAGCTTGCACCTCTGGC 1005
Db 841 GACAAACCTCCCTTAATGCTGCGGAGAGATGCTTCTGACAGCTTGCACCTCTGGC 900

```

```

QY 1006 ATTCTTTCTTTGCACTTCCGCGGATCTTGCTCAGGTTTGCATTAAAGTACAA 1065
Db 901 ATTCTTTCTTTGCACTTCCGCGGATCTTGCTCAGGTTTGCATTAAAGTACAA 960
QY 1066 GAACAACCCGCGCAAGAACTTTGAGAAAAAGAAAGAACCAAGCTGCCAATTCAG 1125
Db 961 GAACAACCCGCGCAAGAACTTTGAGAAAAAGAAAGAACCAAGCTGCCAATTCAG 1020
QY 1126 TGTGTTGGGCTGTTGCGAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCA 1185
Db 1021 TGTGTTGGGCTGTTGCGAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCA 1080
QY 1186 CACTTGAAGGCTTTCGACACCTGCGAGCTTACCA----- 1220
Db 1081 CACTTGAAGGCTTTCGACACCTGCGAGCTTACCAAGAAAGAAAGAAAGCAAGCATCAAGC 1140
QY 1221 --TCAAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCCGAGGCGCAGATTT 1278
Db 1141 AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCCGAGGCGCAGATTT 1200
QY 1279 AAGAGCGAGACGCTGAGTGAAGTGAAGAGGATCCCAAGCAGCAGATCAGACCGAG 1338
Db 1201 AAGAGCGAGACGCTGAGTGAAGTGAAGAGGATCCCAAGCAGCAGATCAGACCGAG 1260
QY 1339 GGCAGTCCACCAAGTGCAGAAAGCTGAGCTTCAACGACGACCGGCTTCCGCGCC 1398
Db 1261 GGCAGTCCACCAAGTGCAGAAAGCTGAGCTTCAACGACGACCGGCTTCCGCGCC 1320
QY 1399 TCGCTGCGCTCAAAAATTTCTAGCGCAAAACCAAGTATGATGCTGACACAGCCTTGGC 1458
Db 1321 TCGCTGCGCTCAAAAATTTCTAGCGCAAAACCAAGTATGATGCTGACACAGCCTTGGC 1380
QY 1459 ACTGATGATATATATGATGAAAAAGATGCCAGTGTATGATGCTGGAAGACCTCAC 1518
Db 1381 ACTGATGATATATATGATGAAAAAGATGCCAGTGTATGATGCTGGAAGACCTCAC 1440
QY 1519 CCACCACTTAAACGTGATTCGAGCTATCAGAAATTAATGAATTTGATGCAAAACGG 1578
Db 1441 CCACCACTTAAACGTGATTCGAGCTATCAGAAATTAATGAATTTGATGCAAAACGG 1500
QY 1579 AAGTTTAAAGAAATTTACCTCCATATGATGATTAAGATGTCATTGAAATATCTGCT 1638
Db 1501 AAGTTTAAAGAAATTTACCTCCATATGATGATTAAGATGTCATTGAAATATCTGCT 1560
QY 1639 GGTATCTGAGCAATGTTGTGTAGAAATTAAGACCTTCAAAACGCTGATCAAAATCTT 1698
Db 1561 GGTATCTGAGCAATGTTGTGTAGAAATTAAGACCTTCAAAACGCTGATCAAAATCTT 1620
QY 1699 GGAAGAGGCGCAATTCATCAGATTAAGAAAGCGAGAGAAATTAACAGCAGACATGAG 1758
Db 1621 GGAAGAGGCGCAATTCATCAGATTAAGAAAGCGAGAGAAATTAACAGCAGACATGAG 1680
QY 1759 ACCACAGAGATCTCAATATGCTGCGGTGGGTGCTCAAGGTGGAAGAAACAGTACAGTCC 1818
Db 1681 ACCACAGAGATCTCAATATGCTGCGGTGGGTGCTCAAGGTGGAAGAAACAGTACAGTCC 1740
QY 1819 ATGAATTCGAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT 1878
Db 1741 ATGAATTCGAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT 1800
QY 1879 GCGTCAGCCCTGCTTGGCTTATTCAGATTCGACCTTTTGAATGTGAACAGACATCT 1938
Db 1801 GCGTCAGCCCTGCTTGGCTTATTCAGATTCGACCTTTTGAATGTGAACAGACATCT 1860
QY 1939 GACTATCAAAAGCCCTGCTGATAGCAAAAGATTTTGGGTTCCGCAAAACAGTGGCTGC 1998
Db 1861 GACTATCAAAAGCCCTGCTGATAGCAAAAGATTTTGGGTTCCGCAAAACAGTGGCTGC 1920
QY 1999 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTGCGAGTTCTATCTGAGGCAAT 2058
Db 1921 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTGCGAGTTCTATCTGAGGCAAT 1980

```


OY		1069	CAACACCGCCAGAAACACTTTGGAAAAAAGAAGAACACCACCTGCGCAACCTCATTCATGTG	1128
Dd		967	CAGCATTGGCAAAAACACTTTGGAAAAAGCGCGGAACCCCTTGCAGGTCTGATCCAGTCT	1026
OY		1129	GTTTGGCGTGATTACGCAGCTGATGAGAAATCTGTTTCCATTGCCAACCCTGGAAACCCACAC	1188
Dd		1027	GCGTGGAGATTCTATGCTACTTAACCTCTCACGCCAGCACTGCACCTCAGCTGGCAGTAGAC	1086
OY		1189	T-----	1189
Dd		1087	TACGAGCGGACAGTCACTGTCGCCCATGATACAGACTCCCACTTGAACCAAGCTGGAG	1146
OY		1190	-----TGAAGGCGCTTGACACCTGC	1209
Dd		1147	CTGCTGAGGAATCTCAAGAGCAATCTGCACTCACTTCAGGAAGAAGGCCACACCCAGAG	1206
OY		1210	AGCCCTACAATCAGAAAGCTPAAGTTTTAAGAGCGAG---TGCGCATGCGCTAGCCCCAGG	1266
Dd		1207	CCATCACCAAGTCAAGAAAGTCAAGTTTAAAGATCGTCTCTTCACACCCCCTGGAGGATG	1266
OY		1267	GGCCAGAGTATTAAAGACCCGACAAGCCTCAAGTAGTACAGSAGSGTCCCCAAGCACCGAC	1326
Dd		1267	GCTGCCAAGSAAAGGSGTCTCCCCAGGCCACAGAGGTCCGGCGGTCCCCCATGCGGAT	1326
OY		1327	ATCACAGCCGAGGGCAGTCCCAACCAAAGTCGAGAAGCTGAGCTTTCAACGACCGAAC	1386
Dd		1327	CAGAGTCTTGATGATACACCCGAGCAAGGTGCGCCAAAGAGCTGAGACCTTGGTGAACGCGAGC	1386
OY		1387	CGCTCCGGCCCTCGCGCGCCCTCAAAAAGTTCACAGCCAACCAAGATATGATGCTCGAC	1446
Dd		1387	CGCACAGCCCAAGGCTTTCCGCATPAAGGGGTCTGCATCCCGCGAATTCGAAGCAACAG	1446
OY		1447	ACACCCCTTGCGACATGATGATGTATGATGAAAAAAGAGATCCAGTGTGATGATCAAGT	1506
Dd		1447	C---TCCTGGGAGGAGACATGATGAGAGACAACAAAGAGCTTAACTGGGATTTGTGACT	1503
OY		1507	GAAACACTCAACCCCAACACTTAAACATGTCTATTGGAGCTATCAGAAATTATGAATTTTCAT	1566
Dd		1504	GAAATATTTACCCCTGGCGCTCAAAAGTAAAGATCAAGAGCTGTGTGTTATCGGTTCTTG	1563
OY		1567	GTTCCAAAACGGAATTTAAAGAAACATATTAGCTCAATGATGTTAAAGATCATTTGAA	1626
Dd		1564	GTAATCAAGCAAAAGTTCAAAAGAGAGTGTGGCCCATATGATGTGATGAGAGCTCATCGAA	1623
OY		1627	CAATATTTCTGCTGCTCATCTGGACATGTTGTGTGAATTTAAAGCCTTCAAAACAGTGT	1686
Dd		1624	CAGTACTCTGCTGACACTTGATATGTTGTCCGCAATCAAGAGCTGCGACATCCAGAGTGT	1683
OY		1687	GATCAAAATCTTGGAAAAAGGSCAAATCCATCAGATTAGAAGAGCGGAGAAAAATAATACA	1748
Dd		1684	GACCAAGATTGTGGGGCGGGGCCCAACATTAACGATTAAGGA---TCGCACCAAGAGCCCA	1744
OY		1747	GCAGAAATGAGACACAGACGATCTCGATGCTCGGTGGGTGCTCAAGGTTGAAAAA	1806
Dd		1741	GGCGAAAGGAGAGCTGCCCCGAAGACCCAGCATGATGAGGACGGCTTGGGAAAGGTGGAGAAA	1800
OY		1807	CAGGTAACGTCATAGATTCACAGCTGAGCGCCATACAGCATATATCAACAG	1860
Dd		1801	CAGGCTTGTCCATGGAAGAAGCTGCACTTCTGTGTGAGCATTTATACACAG	1854

```

? TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
? FILE REFERENCE: PC58adiv
? CURRENT APPLICATION NUMBER: US/10/128,870
? PRIOR APPLICATION NUMBER: 09/105,058
? PRIOR FILING DATE: June 26, 1998
? PRIOR APPLICATION NUMBER: 60/055,599
? PRIOR FILING DATE: August 12, 1997
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 896
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Consensus
? OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
? FEATURE:
? OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
? OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
? US-10-128-870-1

```

Query Match	16.8%; Score 465.4; DB 9; Length 896;
-------------	---------------------------------------

OY	295	AGCCAGACCTCCGGCGCAACGTACAGTACCGGGGGGTCAGAACTACTACTGTACAAAGT	354
Db	13	RGSMSCMSYSAAGMGMMAAGCCWMTSTACCGSMKMSMSCAAMTTTTMTCTACRACGS	72
OY	355	CTGAGAGACCCCGCGCGCTGGCGCTTCACTACACAGCTGCTTTCTCCCTGCTTT	414
Db	73	CTRAGACRCCSCGSGGCTGGGCGTTSMTYTAACCAACGGSWSGTTCTCCTBHTDYYTS	132
OY	415	GCTTGCTGATTTTGTCAAGTGTTTTCTACCATCCTGAGCACACAAAATGGCCCTCAGT	474
Db	133	KSSTGCYBRTKCTKCTGTS - YKCCACAMTCAAGGAGTAAAGAGAMRKYYCBRRGGS	191
OY	475	TGCCCTTGATCCCTGAGCTTCGTGATGATGTCGCTTTGGTTGGAGTTCAATCATCGA	534
Db	192	KSSCTYMSWMTYDGAABAYMKTKRCYATYKRSPTVTHYGGHGBAGAGWYKYRTGMOR	251
OY	535	ATCTGCTCTCGGGGTGCTGTTGTTCGATATAGAGATGGCAAGAAAGTACGATTTGCT	594
Db	252	ATCTGGGGYCGWGMGTGYSTYCGCGRACMFMGGCTGAGGGGGMRGTSAAAGTTGGC	311
OY	595	CGAAAGCCCTCTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCAATGTTTCT	654
Db	312	MGAARCCVCHSTGYRTGWTBAYATCMTKGTGCTSATYGCCTCYRKSCTDGTSPKGY	371
OY	655	GCAAAAGCTCAGGGTAATATTTTGGCCACAGCTGCACATCAGAAAGTCTCCGTTTCTACAG	714
Db	372	GYBGHMMWMCANGGCAAGYTYTTCYACVUTY - -CTBGRNAGCYTGGGSTTYCYTRAR	428
OY	715	ATCCCGCAGATGTCGCGATGAGCCGAAGGGAGGACACTGGAAATATTCAGGGTACAGG	774
Db	429	ATYTRCGSATMTSCBATHGACCGGMRGSHGGCACTGGAAAGTBYTGGGMMCDGY	488
OY	775	GTTTATGCTCACAGCAAGAAATTAATCACAGCTGGTACATAGATTTTGGTCTTAAT	834
Db	489	RCTRYGCGYCAACGCAARBARCTSRFSACKGGSTGTACATGAGYTTCTCTBMSHCATAC	548
OY	835	TTTTGCTCTTCCTGTCTATCTGGGGAAGAAGATGCCAATAAAGATTTCTTACATAT	894
Db	549	CTKCTYCTCTTCTGTSTACTTGGYWGKRAARSSDGAARMBGAYSMNTTYGASACCTAY	608
OY	895	CGAGATGCTCTGTGTGGGGCAACAATTACATTGACATATTGGCTATTTGGAGACAAACT	954
Db	609	GCGRATGCMCTSTGGTGGGGCTGTGATCAACVCTGRVACCATTTGGCTAYGGRGCAAGWMM	668
OY	955	CCCCCACTTGGCTGGGAAGTGGCTTCTGAGAGTTGGTTCACCTCTTGCAATTTCTTC	1011
Db	669	CCYMAAAGCTGGRAMGSMGKCTSHDGCVCYACSTTMYCCYTAATYGGTGTCTVTTY	728

```

QY 1015 TTGGATCTCCGCGGCGATTCCTGCTCAGGTTTGCATTAAAGTACAGAACAC 1074
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 TTYGCBCTKCCGCGGCGATTTGGGRTCYGSGTCCCTSARCTBCARGACARAY 788
QY 1075 CCGCAGAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGG 1134
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 789 MGKARARACACTTTGAGAAARMGAGABCCDGCDCGWRBCTSATYACAGKCGCTGG 848
QY 1135 CGTAGTACGAGCTGA 1151
    | : ||| | : |
Db 849 AGRTWYATYGCYACTAA 865

RESULT 10
US-10-131-685-1
; Sequence 1, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauser, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; FEATURE:
; OTHER INFORMATION: y-wc or t; r-a or g; m-a or c; k-g or t; s-g or c;
; OTHER INFORMATION: w-a or t; h-a, c, or t; b-g, t, or c; v-g, c, or a
US-10-131-685-1

Query Match
Best Local Similarity 53.7%; Pred. No. 1.4e-134; Length 896;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;

QY 295 AGCCAGAGCTCCGCGGCGCAAGTACCGGCGGTCGAGAACTACCTGTACACGTG 354
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 13 RGSMSCCMSYSAAGMAGAGCCWMSYACCGSMRSMSCARAMTTMTCTACACGYS 72
QY 355 CTGAGAGAGACCCCGCGGCTGGCGCTCATCTACCAAGCTTTCCTCTCTCTCTT 414
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 73 CTGAGAGAGACCCCGCGGCTGGCGCTCATCTACCAAGCTTTCCTCTCTCTCTT 132
QY 415 GATTGCTGATTTTTCAGTGTTCCTACCATCCCTGAGACACAAATTTGGCCCAAGT 474
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 133 KSTGTCTBTCTKCTGCTGTS-YKWCACAMTCAAGAGATYAGAGAMRKTYCBRRGRS 191
QY 475 TGCCTCTTGATCTCGAGTTCGATGATGTCGCTCTTGTGTTGAGCTTCATTCGA 534
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 192 KSCCTYWSWTMTGARAAMTKRCYATKTSRTVTYGGHGBAGTWTYKXTGMR 251
QY 535 ATCTGCTGCTGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 ATTGGGCTGCGMGAGTGTGTGCGGCTACMRMGCGTGGMGSGMGRCTSAAGTTTGGC 311
QY 595 CGAAGACCCCTTCTGCTTATATACCATTTCTTATGCTTCTTATAGAGCTGTTTCT 654
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 312 MGGAARCCVCTSTGYRIRGWTBGAATGWTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371

```

```

QY 655 GCAAAACCTCAGGTAATATTTTCCACAGCTCTGACACTCAGAAAGTCTCGCTTCTACAG 714
    | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : |||
Db 372 GYBGGHMMCCARGGCAAGTGTTCYGCYACTY---CTBCGAAAGTCTCGCTTCTACAR 428
QY 715 ATCTCCGCATGATGCGGCGATGACCGAAGGAGGACCTTGGAAATTAAGTGGTTCAGTG 774
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 429 ATYTRGSATGMSICGBATGACCGGMRGHRGACCTGGAAGCTBTYTGGMTCGIV 488
QY 775 GTTATGCTCAGCAAGAAATTAATCAGACCTTGTATACATAGATTTTGGTCTTAT 834
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 489 RTCTRYGCYCACAGCAARGARTSACKGCTGTGATATYGGYTCCTBMSHCATAC 548
QY 835 TTTGCTCTTCTCTGCTATCTGTTGGAAGAAGTGGCAATTAAGATTTTCTCATAT 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 549 CTKCTYCTRTTYCTKGTSTACTGTGWRARARSSDGRMBGASMTTGGASACGTAY 608
QY 895 GCAGATGCTCTCTGCTGGGCGACAAATTACATTTGCAACTATTTGGCTATGAGACAAACT 954
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 GCRGATGCMCTSTGTGGGCTGATCATCACTGRCVACATTTGCTATGAGACAGMM 668
QY 955 CCCCCTAATGCTGGGAGATTTGCTTCTGACAGGCTTTGCACTCTTGGATTTCTTTC 1014
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 669 CCYMARACSTGGRAMGSMGKCTSHTDGCVACASTTYMCCYMATYGGYCTCTVTTY 728
QY 1015 TTGGACTTCTCGCGGCGATTTCTGCGTCCAGTTTGCATTAAAGTACAGAACACAC 1074
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 TTYGCBCTKCCGCGGCGATTTGGGRTCYGSGTCCCTSARCTBCARGACARAY 788
QY 1075 CCGCAGAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGG 1134
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 789 MGKARARACACTTTGAGAAARMGAGABCCDGCDCGWRBCTSATYACAGKCGCTGG 848
QY 1135 CGTAGTACGAGCTGA 1151
    | : ||| | : |
Db 849 AGRTWYATYGCYACTAA 865

RESULT 11
US-10-128-870-26
; Sequence 26, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Neubauser, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aD1Y
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-870-26

Query Match
Best Local Similarity 56.8%; Pred. No. 9.2e-123; Length 2565;
Matches 924; Conservative 0; Mismatches 647; Indels 57; Gaps 5;

QY 118 GAGTGGGCGGCGGCGGAGGATGCTGCTGCACTGCGCAGCGCCAGGCGGCGCTGCTA 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 GCGGCGGCGGCGGCGGAGAGAGGAAAGTGGGCGCTGCGCCGCGGCGACGTGAGCAA 102

```

QY 178 CTGCTGGGACCCCGCGCCACGCTCGGTGGCGGCGGTGGCTGAGGAGAGCGG 237
 Db 103 GTACACTGGGCGCTCGGGGCGGAGCCGACAAAGAGGAGACCTGCTGGAGGCGG 162
 QY 238 CGGGGCAAGAGAGGCGGCGGATGAGCTGCTGGGAGCGCTCTTACAGAGTAC 297
 Db 163 GGGCGGAGAGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGG 222
 QY 298 CAGAGCTGCG-----GGCGCAAGCTGAGTACCGGCGGCGGCGGCGGCGGCGG 348
 Db 223 CTGAGCG 282
 QY 349 AACGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
 Db 283 GAGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 342
 QY 409 GTCTTTGGTTCGATTTTGTGAGTGTTCCTACCATCCGAGACACAAATGGCC 468
 Db 343 GTCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 402
 QY 469 TCAAGTTCCTCTGATCTGAGTTCGATGATGCTGCTGCTGCTGCTGCTGCTG 528
 Db 403 GGAAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 462
 QY 529 ATTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
 Db 463 TTGAGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
 QY 589 TTTGCTGGAAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
 Db 523 TTGCGCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 582
 QY 649 GTTTCGCAAAAGCTGAGGTAATATTTTGCACGCTGCTGCTGCTGCTGCTG 708
 Db 583 GTGCTGTGGGAAACCAAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639
 QY 709 CTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 Db 640 CTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
 QY 769 TCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 Db 700 TCAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
 QY 829 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
 Db 760 CTGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
 QY 874 -----AATTAAGATTCTTCAATATGAGATGCTGCTGCTGCTGCTG 918
 Db 820 CAAGAGAGAGATGAAGAGAGAGATGAGAGCTGAGAGCTGCTGCTGCTGCTG 879
 QY 919 ATTACATGACACTATTTGCTATGAGAGCAAACTCCCACTTGGCTGGAGATG 978
 Db 880 ATACACATGCGCACATTTGCTATGAGAGCAACCAAGAGAGAGAGAGAGAG 939
 QY 979 CTCTTTCAGAGCTTTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
 Db 940 ATTGCGGCGCGCTTTCCTTAATGAGGCTCTCTTTTTCCTTCCAGCGGCT 999
 QY 1039 GGTCTAGGTTTTCATTAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
 Db 1000 GGGTTCGGGCTGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
 QY 1099 AGGAGACAGCTGCAACTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1158
 Db 1060 AGGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
 QY 1159 TCTGTTTCATTTG-----CAACTGAGAGAGAGAGAGAGAGAGAGAGAG 1209
 Db 1120 AGGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179

QY 1210 AGCCCTACCAATTCAGAGCTAGTTTAAAGAGAGCGAGCGCATGGCTAGCCAGGCG 1269
 Db 1180 AGGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
 QY 1270 CAGAGTATTAAG 1329
 Db 1240 CTCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
 QY 1330 ACAGCGAG 1389
 Db 1300 GCGATTAAG 1359
 QY 1390 TTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1449
 Db 1360 TTCCGCGAG 1419
 QY 1450 GCGCTGCGAG 1509
 Db 1420 ACAGGTGAG 1473
 QY 1510 GAGCTACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569
 Db 1474 GAGATGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
 QY 1570 GCAAAAG 1629
 Db 1534 TATTAAG 1593
 QY 1630 TATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1689
 Db 1594 TATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1653
 QY 1690 CAATTCCT 1697
 Db 1654 ATGATTTT 1661

RESULT 12
 US-10-131-685-26
 ; Sequence 26, Application US/10131685
 ; Publication No. US20030044912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blane, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ACON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; PRIORITY FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 26
 ; LENGTH: 2565
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-131-685-26

Query Match 15.5%; Score 428.8; DB 9; Length 2565;
 Best Local Similarity 56.8%; Pred. No. 9.2e-123;
 Matches 924; Conservative 0; Mismatches 647; Indels 57; Gaps 5;

QY 118 GAGTCGGGCGGCGGAGAGGCTGCTGCACTGCGAGAGAGAGAGAGAGAGAGAG 177
 Db 43 GCGGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 102
 QY 178 CTGCTGGGAG 237

QY 289 ACGAGTACCGAGCTGCCGGCGCAACGTCAAGTACCGGGGTGAGAACTACTGTAC 348
 Db 247 GGGCCGGGGAAGCCCCCAAGGCAACGCTTCTACCGGAGGTGAGAACTTCTCTAC 306
 QY 349 AAGCTGCGGAGAGACCCCGGGGCTGGGCTGATCTACACGCTTCTCTCTCT 408
 Db 307 AAGCTGCGGAGAGACCCCGGGGCTGGGCTGATCTACACGCTTCTCTCTCT 366
 QY 409 GTCTTTGGTCTGATTTTGTCTGATTTTCTACCATCTGAGCACAATAATGGCC 468
 Db 367 GTTTTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 426
 QY 469 TCAAGTGGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 528
 Db 427 GAGGGGGGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 486
 QY 529 ATTGGAATCTGCTGCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 Db 487 GTGGGATCTGGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 QY 589 TTTGCTGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 Db 547 TTTGCTGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 QY 649 GTTCTGCAAAACTGAGGTAATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTG 708
 Db 607 CTGGCGCGGCTCCAGGCGCAACGCTTTGGCAGCTGCTGCTGCTGCTGCTGCTG 666
 QY 709 CTACAGATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 Db 667 CTGAGATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 QY 769 TCAAGTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 Db 727 TCTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
 QY 829 CTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 Db 787 CTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
 QY 889 ACATATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 Db 847 ACCTATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 QY 949 AAAACTCCCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
 Db 907 AAGTACCCCGAGCTGAGAGGCGAGGCTCTTGGGCACTTCACTTCACTGCTGCT 966
 QY 1009 TCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
 Db 967 TCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
 QY 1069 CAACACCGGCGAGAACTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1128
 Db 1027 CAGACGAGGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1086
 QY 1129 GTTGGGCTAGTTACGC 1145
 Db 1087 GCCTGGAGATTTTACGC 1103
 RESULT 14
 ; Sequence 19, Application US/10131685
 ; Publication NO. US2003004912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blamir, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neuhauer, Michael G.
 ; APPLICANT: Yang, Wen-Pl
 ; TITLE OF INVENTION: KONO PORASSIUM CHANNELS AND METHODS OF MODULATING SAME

; FILE REFERENCE: DC58aCON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; PRIOR FILING DATE: 1997-08-12
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 3287
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-131-685-19
 Query Match 15.5%; Score 428.4; DB 9; Length 3287;
 Best Local Similarity 64.8%; Freq. No. 1.5e-122;
 Matches 633; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
 QY 169 GAGCTGCTAGCTGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
 Db 127 GAGCTGCTAGCTGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
 QY 229 GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 288
 Db 187 GCGGCGCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 246
 QY 289 ACGAGTACCGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 Db 247 GCGGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 306
 QY 349 AAGTGTGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 Db 307 AAGTGTGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 366
 QY 409 GTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
 Db 367 GTTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
 QY 469 TCAAGTGGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 528
 Db 427 GAGGGGCGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 486
 QY 529 ATTGGAATCTGCTGCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 Db 487 GTGGGATCTGGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 QY 589 TTTGCTGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 Db 547 TTTGCTGGAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 QY 649 GTTCTGCAAAACTGAGGTAATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTG 708
 Db 607 CTGGCGCGGCTCCAGGCGCAACGCTTTGGCAGCTGCTGCTGCTGCTGCTGCTG 666
 QY 709 CTACAGATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 Db 667 CTGAGATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 QY 769 TCAAGTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 Db 727 TCTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
 QY 829 CTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 Db 787 CTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
 QY 889 ACATATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 Db 847 ACCTATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 QY 949 AAAACTCCCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008

Db 907 AAGTACCCCAAGACCTGGAAGGAGGAGCTCTTGGGCAACCTTACCCCTCATCGGTGTC 966
QY 1009 TCTTTCTTTCGACCTTCCTGCGGCACTTCTGCTCAGGTTTGTGATTAAGTACAGAA 1068
Db 967 TCTTCTTTCGCGCTCTGCGGCACTTCTGCTGAGGCTTGGGTTTGGCCGAAGGTTGAGAG 1026
QY 1069 CACACCCCGGCAAGCACTTTGAGAAAGAGAGACCCAGCTGCGCAACCTCATTCAGTGT 1128
Db 1027 CAGCAGAGGAG 1086
QY 1129 GTTGGCGGTAGTACGC 1145
Db 1087 GCTGGAGATTTTACGC 1103

RESULT 15

US-10-128-870-3
; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridboff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiv
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNO2
US-10-128-870-3

Query Match 15.2%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 8.4e-121;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 299 AGAGTGGCGGCGCAAGTCAAGTACCGGCGGTGAGAACTACTGTACAGTGTG 358
Db 17 AGCCCCCAAGGCAAGCGCTTCTACCGCAAGCTGCAAGTTCCTCTACAGAGCGCTG 76
QY 359 AGAGACCCCGGCGGTGAGTATCTACACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 418
Db 77 AGCGGCGCGGCGGTGAGTATCTACACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 136
QY 419 GCTTATTTTGTAGTCTTCTTCTACCATCTGAGCAGACAAATTTGGCCCAAGTTGCC 478
Db 137 GCTGCTGCTGTGTGTTTCCACATCAAGAGATGAGAAAGCTGAGAGGGGCGCC 196
QY 479 TCTTATCTCTGAGTTCGTATGATGATGCTGCTTGTGAGTTCATTCATTCGAATCT 538
Db 197 TCTACATCTCTGAGAAATCGTACATGCTGTGTGTTGGCGTGTGAGTACTGCTGCGGATCT 256
QY 539 GGTCTGCGGCTGCTGTGTGATATAGAGAGATGAGCAAGAACTGAGTTGCTGAA 598
Db 257 GGGCGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 316
QY 599 AGCCCTCTGTGTATAGATACCATGTTCTTATGCTTCAATAGCAAGTTGTTCTGAA 658
Db 317 AACGCTCTGTGTATAGATATCATGTGTCTATCGCTCATTCGCTGCTGCTGCTGCTGCTGCTG 376

QY 659 AACTCAGGATATATTTTGGCCAGCTGCTGCTCAGAGATCTCCGTTTCTACAGATTC 718
Db 377 GCTCCAGGCAAGCTCTTTCGCAATCTGCGCTCCGAGAGCTGCGCTTCTGCAAGTTC 436
QY 719 TCCGATGCTGCGCATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 778
Db 437 TGGGATGATGCCATGAGACCGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 496
QY 779 ATGCTACAGCAAGGATATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
Db 497 ATGCCACAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 556
QY 839 CGCTTCTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
Db 557 CCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
QY 899 ATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958
Db 617 ATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
QY 959 TAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
Db 677 AGACCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 736
QY 1019 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078
Db 737 CGCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 796
QY 1079 AGAAGCACTTTGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1138
Db 797 AGAAGCACTTTGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 856
QY 1139 GTTACGC 1145
Db 857 TTTACGC 863

RESULT 16

US-10-131-685-3
; Sequence 3, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58acon
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNO2
US-10-131-685-3

Query Match 15.2%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 8.4e-121;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 299 AGAGTGGCGGCGCAAGTCAAGTACCGGCGGTGAGAACTACTGTACAGTGTG 358
Db 17 AGCCCCCAAGGCAAGCGCTTCTACCGCAAGCTGCAAGTTCCTCTACAGAGCGCTG 76

OY 1149 TGA 1151
Db 867 TAA 869

RESULT 18

US-10-131-685-5
; Sequence 5, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blauar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aCON
; CURRENT FILING DATE: 2002-07-23
; PRIOR FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-131-685-5

Query Match 15.2%; Score 420.6; DB 9; Length 900;
Best Local Similarity 68.7%; Pred. No. 1.5e-120;
Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

OY 309 GCGCAGCTCAAGTACCGGGGTGAGAACTACTGTACAGCTGCTGGAGAGACCCG 368
Db 27 GCGCAACCCCTTCTACCGCACTCGCAATTCCTCTACAGCTGCTAGAGCGGCCG 86
OY 369 GCGGTGGCGTCACTACCAAGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 428
Db 87 GCGGTGGCGTCACTACCAAGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 146
OY 429 GTCAAGTCTTCTACCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db 147 TTCTGTCTTCTACCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
OY 489 GCGGTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
Db 207 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
OY 549 TTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db 267 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
OY 609 TGTAT 668
Db 327 TGTAT 386
OY 669 TAAAT 728
Db 387 CAAT 446
OY 729 GCGCATGAGACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 788
Db 447 CCGAT 506
OY 789 CAAGAT 848
Db 507 CAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566

OY 849 TGTCTATCTGTGAGAAAGATGCCAATAAGAGTTTCTACATATGACAGTCTCTG 908
Db 567 GGTGTACTGTGCAAAAAGGTGAGATGACACTTTTACACCTTACGAGATGACTCTG 626
OY 909 GTGGGGCACAATTAT 968
Db 627 GTGGGGCTAT 686
OY 969 GGGAGATTTGCTTCTGACAGCTTGTGACCTTCTGACCTTCTGACCTTCTGACCT 1028
Db 687 GGGAGGCTCTGACAGCTTGTGACCTTCTGACCTTCTGACCTTCTGACCTTCTGAC 746
OY 1029 GCGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
Db 747 TGGCATTTTGGATTCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 806
OY 1089 TGAGAAAAGAGACCGACCTGCGCACTTATTCAGTGTGTTGGCTAGTTAGCAGC 1148
Db 807 TGAGAAAAGAGACCGACCTGCGCACTTATTCAGTGTGTTGGCTAGTTAGCAGC 866
OY 1149 TGA 1151
Db 867 TAA 869

RESULT 19

US-10-128-870-17
; Sequence 17, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blauar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribokoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aDIV
; CURRENT FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2002-07-23
; PRIOR FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 930 nucleotides of human KCNQ3
US-10-128-870-17

Query Match 13.1%; Score 363.8; DB 9; Length 930;
Best Local Similarity 65.5%; Pred. No. 9.6e-103;
Matches 580; Conservative 0; Mismatches 272; Indels 33; Gaps 2;

OY 291 GAGTACCAAGAGCTGCCGCGCAAGCTCAAGTACCGGCGGTGAGAGAACTACTGACAA 350
Db 12 GAGCCGCCCAAGTCAAGAAAGAAAGCAAGTACCGGCGGCACTTATGATCTACGA 71
OY 351 CGGTGAG 410
Db 72 CGGCTGAG 131
OY 411 CTGTGCTGCTGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
Db 132 CCGTGGGCTGCTGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
OY 471 AAGTGGCTTCTGATTCCTGAGTTCGATGATGATGATGATGATGATGATGATGATGAT 530

```

Db      192 AGACTGCTCTGTTACTGAGACATTTGCTATTTTCATCTTGGAGCCGAGTTGCTT 251
Qy      531 TCGAATCTGCTGCGGGTGTCTGTTGCGATATAGAGATGCAAGAACTGAGGT 590
Db      252 GAGATCTGGGCTGTGATGTTGCTGCGATACAAAGGCTGGCGGCGGCTGATG 311
Qy      591 TGTCTGAAAGCCCTTCTGTATATGATACCATTTGCTTATCGCTCAATAGCACTT 650
Db      312 TGCAGGAAGCCCTTGTGATGTTGACATCTTTGTGCTGATTTGCTTGTGCTG 371
Qy      651 TTCTGCAAAAACCTGAGGTAATATTTTTCGACGCTGACATCAGAGTCTCCGTTCT 710
Db      372 TGTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCAAGCCTGGGCTTCC 428
Qy      711 ACAATCTCGGCAATGTTGCGCATGAGCGAAGGAGGAGCACTTGAATTTACTGGTTC 770
Db      429 GCAATCTCGGCAATGTTGCGCATGAGCGAAGGAGGAGGAGGAGGAGGAGGAGG 488
Qy      771 AGTGTATATGCTGACAGCAAGAAATTAATACAGCTTGTGATAGATTTTGTGCT 830
Db      489 AGCATCTGTGCGCCACAGCAAGAAATTAATACAGCTTGTGATAGATTTTGTGCT 548
Qy      831 TATTTTTCGTTCTTCTGTTCTATCTGTTGAGAAAGATGCC-----873
Db      549 CATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 608
Qy      874 -----AATAAAGATTTTCTACATATGCAATGCTCTCTGTTGGGCGCAAT 920
Db      609 AGGAGAGGATGAAGAAAGAGATTTGAGACATGATGCTGTTGGTGGGCTGTAT 668
Qy      921 TACATGACAACTATTTGCTATGAGACAAACTCCCTTAATGCTTGGAGATTTGCT 980
Db      669 CACATCTGCGCCACATTTGCTATGAGACAAACTCCCTTAATGCTTGGAGATTTGCT 728
Qy      981 TTCTGCAAGCTTGTGACTTCTTGGCATTTCTTTTGTGACATCTTCCGCGCATTTG 1040
Db      729 TGCGGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 788
Qy      1041 CTCAGTTTTCATTAAGTACAGAACACACCGCGGAAACCTTTGAGAAAAGAG 1100
Db      789 GTCCGGGCTGCGCCTCAAGGTGAGAGACACACCGCTTGAAGAAAGAG 848
Qy      1101 GAACCCAGCTGCGCAACTCATTCAGTGTGTTGGCGGTATTAACG 1145
Db      849 GAAGCCAGCTGCTGAGCTCATTCAGGCTGCCCTGGAGGATTAATGCG 893

RESULT 20
US-10-131-685-17
; Sequence 17, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCON PORASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIOR APPLICATION NUMBER: 2002-07-23
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 17
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; OTHER INFORMATION: 930 nucleotides of human KCNQ3
US-10-131-685-17
Query Match      13.1%, Score 363.8, DB 9, Length 930;
Best Local Similarity 65.5%, Pred. No. 9,6e-103;
Matches 580; Conservative 0; Mismatches 272; Indels 33; Gaps 2;

Qy      291 GAGTAGCAGAGCTGCGCGCCCAACGATACAGCGGGGGGAGAGACTACTGTACAA 350
Db      12 GAGCGGCCCACTCAAGAAACAAACGCGCAAGTACCGGCGCATCAAACTTGATCTACGA 71
Qy      351 CGTCTGAGAGAGACCCGCGGCGCTTATCTACACAGCTTGTGTTTCTCTCTGT 410
Db      72 CGCCCTGAGAGAGACCGGGGCGCTGCGCTGTTTACACAGCGGTTGTTCTGATGT 131
Qy      411 CTTTGTTGCTGTGATTTTGTGAGTTTGTACATCCCTGAGACACAAATTTGCGCTC 470
Db      132 CTTGGGGTCTGTGATTTTGTGCTGCTTACACATCAAGGATGATGAGACTGTCTCGG 191
Qy      471 AAGTTGCTCTGTATCTGAGTTCGAGTTCGATGATTTGCTTGTGTTGGAGTTGATCAT 530
Db      192 AGACTGCTTGTGTTACTGAGACATTTGCTATTTTCACTTTTGAAGCCGAGTTGCTTT 251
Qy      531 TCGAATCTGCTCGGGTGTCTGTTGATATGAGAGATGCAAGAAAGTGAAGTT 590
Db      252 GAGATCTGGGCTGCTGATGTTGCTGCGATACAAAGCTGGCGGCGCATGAAGTT 311
Qy      591 TGTCTGAAAGCCCTTCTGTTGTTATAGATACATTTGTTTATCGCTTCAATAGCATGTT 650
Db      312 TGCCAGAGAGCCCTGCTGATGTTGAGACATTTTGTGATGCTTGTGCTGCTGTTGCTG 371
Qy      651 TTCTGCAAAAACCTGAGGTAATATTTTGGCACGCTGCTACACAGCTTGCCTGTTCT 710
Db      372 TGTGTGGGAAACCAAGGCAATGTTTGTGCGCACT---CCCTGCAAGCCTGCGCTTCT 428
Qy      711 ACAATCTCGGCAATGTTGCTGATGAGACCAAGGAGGAGGAGGAGGAGGAGGAGGAG 770
Db      429 GCAATCTGCGCATGCTGCGATGAGACCGGAGAGGTGGACCTGGAAGCTTCTGCGCTC 488
Qy      771 AGTGTATATGCTGACAGCAAGAAATTAATACAGCTTGTGATAGATTTTGTGCTT 830
Db      489 AGCATCTGTGCGCCACAGCAAGAAATTAATACAGCTTGTGATAGATTTTGTGCTT 548
Qy      831 TATTTTTCGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 873
Db      549 CATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 608
Qy      874 -----AATAAAGATTTTCTACATATGCAATGCTCTCTGTTGGGCGCAAT 920
Db      609 AGGAGAGGATGAAGAAAGAGATTTGAGACCTATGACAGATGCCCTGTTGGGCGCTGAT 668
Qy      921 TACATGACAACTATTTGCTATGAGACAAACTCCCTTAATGCTTGGAGATTTGCT 980
Db      669 CACATCTGCGCCACATTTGCTATGAGACAAACTCCCTTAATGCTTGGAGATTTGCT 728
Qy      981 TTCTGCAAGCTTGTGACTTCTTGGCATTTCTTTTGTGACATCTTCCGCGCATTTG 1040
Db      729 TGCGGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 788
Qy      1041 CTCAGTTTTCATTAAGTACAGAACACACCGCGGAAACCTTTGAGAAAAGAG 1100
Db      789 GTCCGGGCTGCGCCTCAAGGTGAGAGACACACCGCTTGAAGAAAGAG 848
Qy      1101 GAACCCAGCTGCGCAACTCATTCAGTGTGTTGGCGGTATTAACG 1145
Db      849 GAAGCCAGCTGCTGAGCTCATTCAGGCTGCCCTGGAGGATTAATGCG 893

RESULT 21
US-10-128-870-7
; Sequence 7, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:

```


448 CTTGAGCAGACAAAATTTGGCTCAAGATTGCTTGTGATCTGGATGCTGATGATGTC 507
598 GAGACAGATATGCGCCCTGGCCACGGGAGCTCTTCTGATGAGATGCGTGGTG 657
508 GTCTTTGGTTTGAATTCATATTCGATGCTGCTGCGGTTGCTGTTGCTGATATAGA 567
658 TTTCTGGGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
568 GGATGGCAGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
718 GGGCTTGGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
628 CTATTCCTTCAATAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
778 GTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
688 GCACTGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
838 GGCATCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
748 GGCATGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
898 GGCATGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
808 TGATACATAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
958 CTGATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
868 GATGCCAATAA-----GAGTTTCTACATATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 912
1018 GACCCGATGAAAGAGTCAAGGCGCGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 1077
913 GGCACATTTACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
1078 GGGGTGGTCAAGTACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
973 AGATTGCTTGTGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
1138 AAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
1033 ATTCTG 1092
1198 ATTCTG 1257
1093 AAAAGAGAAAGAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1151
1258 CGGAGATCCCGGGGCGAGCTCAGCTCATTGAGACGAGGAGTGTCTATGCTGCGGA 1316

RESULT 25
US-09-880-107-3358
; Sequence 3358, Application us/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Iwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3358
; LENGTH: 2821
; ORGANISM: Homo sapiens
; FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 U40990
US-09-880-107-3358

Query Match
Best Local Similarity 59.3%; P-Value 6.5e-72;
Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

329 GGGTGCAGAACTACCTGATACAGCTGCTGAGAGACCCCGGCTGG---GCTTCACT 385
116 GGGGCGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 175
386 ACCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
176 ACCACTTCCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
446 TCCCTGAGCAGCAAAAATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
236 TCGAGCAGTATGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295
506 TCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
296 TGTCTTGGGAGAGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
566 GAGATGCAAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
356 TGGGCTCTGGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
626 TTTTATGCTTCAATAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685
416 TGTCTG 475
686 CTGACATCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
476 CGGCGCATGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
746 GAGGCACTTGAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 805
536 GAGGCACTTGAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 595
806 CTGATACATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
596 CCTGATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
866 AGAGTCCCAATAA-----GAGTTTCTACATATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 910
656 AGAGTCCCAATAA-----GAGTTTCTACATATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 975
911 GGGGCGACATTAATGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
716 GGGGCGTGTGCTACAGTACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
971 GAGATGCTTGTGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
776 GGAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
1031 GCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
836 GATTTCTG 895
1091 AGAAAGAGAAAGAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
896 ACCGCGAGATCCCGGGGCGAGCTCAGCTCATTGAGACGAGTGTCTATGCTGCTGCTGCTGCTG 955
1151 A 1151
956 A 956

RESULT 26
US-09-960-352-13343
; Sequence 13343, Application us/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

```

: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT APPLICATION NUMBER: US/09/960.352
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 13343
: LENGTH: 416
: TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 57-LIB3058-010-Q1-K1-G2
US-09-960-352-13343

```

```

Query Match          4.7%; Score 130.4; DB 10; Length 416;
Best Local Similarity 62.4%; Pred. No. 6.7e-30;
Matches 256; Conservative 0; Mismatches 121; Indels 33; Gaps 2;

```

```

QY 616 GATACATGTTCTTATGCTTACATAGCATGTTCTTGCAGAAAACATCAGGTAATATT 675
   || || || || || || || || || || || || || || || || || || || || || ||
Db 2 GACATCTTTGTGCTGATGCGCTCGCTGCTGTTGCCGGAGAACAGGCGACGCTC 61
QY 676 TTTCACAGCTGTCAGACAGAGTCTCCGTTTCTACAGATCCCGCATGTGCGCATG 735
   || || || || || || || || || || || || || || || || || || || || || ||
Db 62 CGGGCCACGT---CCCTCGGAGTGTGCGCTTCCGACAGATCTTGAGATGCTGCGAATG 118
QY 736 GACCGAAGGAGGACGACTTGGAAATTAAGTGTGAGTGTGTTTANGCTCAGACAGAA 795
   || || || || || || || || || || || || || || || || || || || || || ||
Db 119 GACCGAGGGGCGGACCTGGAAGCTCCTGGCTCGGCGCATGTGCGCCACAGCAAGAG 178
QY 796 TTAATCAGCTGTGGTATAGATTTTGTCTTATTTTTCGTCCTTCTGCTAT 855
   || || || || || || || || || || || || || || || || || || || || || ||
Db 179 CTCATCACCGCTGCTGATGCGCTCGCTGCTGTTGCCGGAGAACAGGCGACGCTC 238
QY 856 CTGCTGGAAGAGATG-----CCATTAAGAGATT 885
   || || || || || || || || || || || || || || || || || || || || || ||
Db 239 CTGCTGGAAGAGATGTCGCGAGGTGATGCCAAGAGAGATGAAGAGAGATTT 298
QY 886 TCTACATATGCAATGCTCTCTGCTGCGGACACATTAATTAACAATATGCTATGGA 945
   || || || || || || || || || || || || || || || || || || || || || ||
Db 299 GAGACCTACGACATGCTGCTGTGCGGCGCTGATCACATGGCCACCATTTGGCTACGA 358
QY 946 GACAAAACCTCCCTAATCTGTGCTGGAGATGCTTTTGCAGGCTTTC 995
   || || || || || || || || || || || || || || || || || || || || || ||
Db 359 GACAAAGCGCCCAAAAGCTGGAGAGCCGCTGTGATGAGCCACCTTTTC 408

```

RESULT 27

```

US-09-783-590-4509
: Sequence 4509, Application US/09783590
: Patent No. US20020110850A1
: GENERAL INFORMATION:
: APPLICANT: Dillon, Patrick J.
: APPLICANT: Haselaine, William A.
: APPLICANT: Li, Haodong
: APPLICANT: Rosen, Craig A.
: APPLICANT: Ruben, Steven M.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
: FILE REFERENCE: PO-16.2C1
: CURRENT APPLICATION NUMBER: US/09/783.590
: CURRENT FILING DATE: 2000-07-15
: PRIOR APPLICATION NUMBER: 08/420,856
: PRIOR FILING DATE: 1995-04-12
: PRIOR APPLICATION NUMBER: 08/346,731
: PRIOR FILING DATE: 1994-11-21
: NUMBER OF SEQ ID NOS: 12485
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4509
: LENGTH: 429
: TYPE: DNA

```

```

: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (25)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (31)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (54)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (130)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (181)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (214)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (253)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (287)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (313)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (314)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (346)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (355)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (358)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (366)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (392)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (400)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (407)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (422)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-4509

```

```

Query Match          3.8%; Score 104.2; DB 10; Length 429;
Best Local Similarity 58.6%; Pred. No. 1.1e-21;
Matches 197; Conservative 0; Mismatches 124; Indels 15; Gaps 1;

```

```

QY 665 AGGTAATATTTTGGCCAGCTCTGACATGCAAGTCCGTTTCTACAGATCTCCGCA 724
   || || || || || || || || || || || || || || || || || || || || || ||
Db 15 AGGGGAGGTTTTCNACGTCGACAGGCGCATCCNCTCTGCAATCCCAAGGA 74
QY 725 TGGTGCCATGAGCCAGAGGAGGAGCACTTGGAATTAATGAGTTTCACTGTTATGCTC 784
   || || || || || || || || || || || || || || || || || || || || || ||
Db 75 TGCTACACGTCGACCCGACAGAGGACCTGAGGCTCTGCGCTCCGTCTTNAATCC 134
QY 785 ACAGCAAGGAATTAATCAGAGCTTGTACATAGATTTTGTCTTATTTTTCGCTT 844
   || || || || || || || || || || || || || || || || || || || || || ||
Db 135 ACCGCGAGAGCTGATTAACACACCTGTACATCGGCTTCTGCGCTTNAATCTTCCCTCGT 194

```



```

; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Eneidck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Masserman, Wyleth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)...(1437)
; US-09-963-285-3

```

```

Query Match      2.0%; Score 56.4; DB 10; Length 4158;
Best Local Similarity 53.4%; Pred. No. 6.2e-06;
Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

```

```

QY 23 GAGAGGAGGCGGCGCGCGCGCTGCTGCTGTAAGAGCGCGGCGCGCGCGCGCGCG 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1048 GAGCGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 GCGGGGCGCGCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 988 GCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 143 TGAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 928 TGCACCT-GGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 203 TCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 869 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 809 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 40
US-09-963-285-1/c
; Sequence 1, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
; APPLICANT: Eneidck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyleth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/09/963,285
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 1
; LENGTH: 6458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2235)...(3737)
; US-09-963-285-1

```

```

Query Match      2.0%; Score 56.4; DB 10; Length 6458;
Best Local Similarity 53.4%; Pred. No. 8.8e-06;
Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

```

```

QY 23 GAGAGGAGGCGGCGCGCGCGCGCTGCGTGAAGAGCGCGCGCGCGCGCGCGCG 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3348 GAGCGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 GCGGCGCGCGCGCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3288 GCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 143 TGAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3228 TGCACCT-GGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 203 TCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3169 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3109 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3088
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 41
US-10-184-644-202
; Sequence 202, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-184-644-202

```

```

Query Match      2.0%; Score 56.2; DB 9; Length 440;
Best Local Similarity 21.7%; Pred. No. 1.2e-06;
Matches 60; Conservative 75; Mismatches 142; Indels 0; Gaps 0;

```

```

QY 10 CACACGCGCGGAGAGAGAGCGCGCGCGCGCGCTGCGTGAAGAGCGCGCGCG 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 128 VRSGWGVPGHSGAMETSGHGIRFGSGGLGCGGNGGLGTPMWHGYPGNSAGSFGNN 187
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 188 PGAPWGGGNGNPPNFTNTGAVNAQPGYGSYRASNONEGCTNPPPSGGSSNSGGG 247
QY 130 GCGAGGGGCTGCTGAACCTGCGACGCGCGGAGGGGCTGTACTGCTGGGACG 189
Db 248 SGGSGSSSSGSGNDNNSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 307
QY 190 GCGCGGGCCACGCTGCTGCGCGCGGCTGCGCTTGAAGGAGACCGCGGCGCAAGCAG 249
Db 308 SSMGSSSTGSSSSGNGHSGSGGNGHKPCCEKPGNENRSGESGIGGFRGGVSSNMREISKE 367
QY 250 GGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTT 286
Db 368 GNRLLGSGDNYRGOGSSSWGSGGDAVGAVNTVNSSET 404

```

```

RESULT 42
US-10-184-634-202
; Sequence 202, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William J.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184, 634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-202

```

```

Query Match 2.0%; Score 56.2; DB 9; Length 440;
Best Local Similarity 21.7%; Pred. No. 1.2e-06;
Matches 60; Conservative 75; Mismatches 142; Indels 0; Gaps 0;

QY 10 CACACGCGGAGAGAGAGAGGCGCGCGCGGCTGTGCTGAAGCGCGGACG 69
Db 128 VHSQMGVPGHSGAMETSGGNGIFGSGGIGGOGGCGNPGGIGTPWVHGYPNSAGSFGMN 187
QY 70 GGGGCGCGCGCGCGCGCGCGCTTGGCGACGCGCATGAAGATGTGAGTGGGCGG 129
Db 188 PGAPWGGGNGNPPNFTNTGAVNAQPGYGSYRASNONEGCTNPPPSGGSSNSGGG 247
QY 130 GCGAGGGGCTGCTGAACCTGCGACGCGCGGAGGGGCTGTACTGCTGGGACG 189
Db 248 SGGSGSSSSGSGNDNNSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 307
QY 190 GCGCGGGCCACGCTGCTGCGCGCGGCTGCGCTTGAAGGAGACCGCGGCGCAAGCAG 249
Db 308 SSMGSSSTGSSSSGNGHSGSGGNGHKPCCEKPGNENRSGESGIGGFRGGVSSNMREISKE 367
QY 250 GGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTT 286
Db 368 GNRLLGSGDNYRGOGSSSWGSGGDAVGAVNTVNSSET 404

```

```

RESULT 43
US-09-804-682-29/C
; Sequence 29, Application US/09804682
; Patent No. US20020106765A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Kinders, Robert
; APPLICANT: Corey, Michael J.
; TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR
; FILE OF INVENTION: MODULATING THE SAME
; FILE REFERENCE: 130001.406
; CURRENT APPLICATION NUMBER: US/09/804, 682
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, 72, 110, 209, 214, 231, 232,
; LOCATION: 235, 237, 238, 244, 245, 246, 256, 282, 292, 297, 306, 319,
; LOCATION: 321, 323, 330, 334, 340, 349, 354, 355, 363, 372, 376, 378,
; LOCATION: 397, 405, 432, 437, 454, 455, 457, 458, 459, 468, 470
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562,
; LOCATION: 583, 600, 611, 613, 623, 624, 632, 654, 674, 681, 687, 691,
; LOCATION: 694, 701, 713, 716, 720, 721, 725, 731, 734, 735, 739, 743,
; LOCATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,
; LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,
; LOCATION: 1043, 1047, 1049, 1051, 1054, 1056
; OTHER INFORMATION: n = A,T,C or G
US-09-804-682-29

```

```

Query Match 2.0%; Score 54.6; DB 10; Length 1064;
Best Local Similarity 46.5%; Pred. No. 7.8e-06;
Matches 120; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 16 GCGGAGAGAGAGAGAGGCGCGCGCGGCTGTGCTGAAGCGCGGAGCGGCGG 75
Db 645 GGGGGGGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 586
QY 76 GCGGCGCGCGCGCGGCGCTTGGGCGACGCGCATGAAGATGTGAATCGGCGGCGCAG 135
Db 585 GANAGAGGGGCGGCGGCGTGTGGGNGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 526
QY 136 GTGCTGTGAACCTGCGACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 195
Db 525 GNGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 466
QY 196 GCCAGGCTGCTGCGCGCGCGGCTGTGCTGAAGGAGAGCGCGGCGCAAGGAGGCC 255
Db 465 GGGGGGNNNGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 406
QY 256 CGGATGAGGCTGCTGGGG 273
Db 405 NGAGGAGGAGGAGGAGGAGG 388

```

```

RESULT 44
US-09-954-456-292
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954, 456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233, 617
; PRIOR FILING DATE: 2000-09-18

```

```

RESULT 45
US-09-954-456-529
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638

```

```

RESULT 46
US-09-880-107-3950
Sequence 3950, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880.107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3950
LENGTH: 43058
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 284721
US-09-880-107-3950

```

Query Match	1.9%;	Score 53.4;	DB 10;	Length 43058;
Best Local Similarity	50.6%;	Pred. No. 0.00034;		
Matches 129; Conservative	0;	Mismatches 126;	Indels 0;	Gaps 0

QY 28 GAGGCGCGCGCGCGCGCGCTCTGTGGTGAAGACGCGCGCGCGCGCGCGCGCG 87
 Db 25554 GCGGGGCG 25613
 QY 88 GGGCGCTGTGGGCG 147
 Db 25614 GGTTCG 25673
 QY 148 TCGGCAAGCG 207
 Db 25674 GCGGGGCG 25733
 QY 208 GCGGCG 267
 Db 25734 TGGGCG 25793
 QY 268 CTGGGAGCGCGCGCTC 282
 Db 25794 CCGGCGCGCGCGCGCG 25808

RESULT 47

US-10-098-841-34/c
 ; Sequence 34, Application US/10098841
 ; Publication No. US20020197679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Xu, Chongjun
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhao, Qing-A.
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Drmanac, Radote T.
 ; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
 ; FILE REFERENCE: 784CIP2
 ; CURRENT APPLICATION NUMBER: US/10/098,841
 ; PRIOR APPLICATION NUMBER: 2002-03-13
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 331
 ; SOFTWARE: PL_genes Version 1.0
 ; SEQ ID NO 34
 ; LENGTH: 4176
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1508)..(3430)
 ; US-10-098-841-34

Query Match 1.9%; Score 52.6; DB 9; Length 4176;
 Best Local Similarity 52.0%; Pred. No. 9.7e-05;
 Matches 141; Conservative 0; Mismatches 129; Indels 1; Gaps 1;

QY 27 GAGGCGCGCGCGCGCGCGCTCTGTGGTGAAGACGCGCGCGCGCGCGCGCGCG 86
 Db 1798 GAAGTTGGCGCGCGCGCGCGCGCTCTGTGGTGAAGACGCGCGCGCGCGCGCG 1739
 QY 87 GGGGCGCTGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 146

Db 1738 GGCCTCGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1679
 QY 147 CTGGGAGCG 206
 Db 1678 GCGGCG 1619
 QY 207 TGGCGCGCGCGCGT-GGCTTGAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 265
 Db 1618 GCTACAGCGCGCTGTGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1559
 QY 266 TGCTGGGGAAGCGCGCTCTTACACAGTAG 296
 Db 1558 GTCCGGGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1528

RESULT 48

US-10-095-407-16/c
 ; Sequence 16, Application US/10095407
 ; Patent No. US20020164330A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 09404/052001
 ; CURRENT APPLICATION NUMBER: US/10/095,407
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/091,650
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: US 60/054,646
 ; PRIOR FILING DATE: 1997-08-04
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 152331
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1)..(152331)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-095-407-16

Query Match 1.9%; Score 52.4; DB 9; Length 152331;
 Best Local Similarity 49.6%; Pred. No. 0.0019;
 Matches 119; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 16 GCGGAGAGAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 75
 Db 22102 GGGGCGGGGCGGTGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 22043
 QY 76 GCGGCG 135
 Db 22042 GGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 21983
 QY 136 GTCTGTGAACCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
 Db 21982 GGGGCGGGGCGGTGTGGGGCGCGCGGGGCGCGCGGGGCGCGGGGCGCGCG 21923
 QY 196 GCCAGCGCTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 255
 Db 21922 GCNCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCG 21863

RESULT 49

US-10-198-846-8585
 ; Sequence 8585, Application US/10198846
 ; Publication No. US20030099974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steimann, Kathleen

APPLICANT: Hank, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OR INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1804
LENGTH: 998
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035685.13 SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
US-09-864-761-1804

Query Match 1.9%; Score 51.8; DB 10; Length 998;
Best Local Similarity 52.6%; Pred. No. 5,6e-05;
Matches 113; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 827 TTTCTATTATTTTCGCTTCCCTTGCTACTGTGGGAAGATGCCAATAAAGATTTT 886
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 TTATGATCTTCTCCACGCTTGCTTCTTCTGTGTAAGAAGATGAGACACCAAGTTCA 390
887 CTACATATGCAGATCCTCTGTGTTGGGACAATTACATTTGACCACTATTTGGCTATGGAG 946


```

Db      389  AAAGCATCCAGCCTTTCTGTGGGCGCCACATCACCATGACTACTGTGGGTATGAG 330
OY      947  ACAAACTCCCTACTTGGCTGGGAGATTGCTTTGCAAGCTTTGCACCTCCTTGGA 1006
Db      329  ACATCTACCCCAAGAGCTCTCCTGGGAAATGTTGGGGACTCTGTCATTCAGAGAG 270
OY      1007 TTTCTTTCTTGGCACTTCCTGCGGCAATTCCTGGC 1041
Db      269  TCCTGGTATGCTCTTCCCATCCCATCATGTC 235

```

Search completed: June 19, 2003, 13:32:23
 Job time : 391 secs


```

Db 669 CCWVARACSTGGRAMGSGMKTSHDGCVCACSTYMCCTYMATYGYGTCCTVY 728
QY 1015 TTTCACATCTCTCCGCGCATCTTGCTCAGTTTGATTAAGTACAAACACAC 1074
Db 729 TTYGCBCTKCCMGDGGCATYTTGGGRTYGGSTYKGGCCCTSAAGTBCARGACARAY 788
QY 1075 CGCCAGAACACTTTGAGAAAGAACACCCAGCTGCCACCTCATTCAGTGTGTTGG 1134
Db 789 MGKARARACACTTTGAGAAAGMGABCCDGDGCMGRBCTATYACGKCGCTGG 848
QY 1135 CGTAGTACGACGCTGA 1151
Db 849 AGRTMYATGACYACVAA 865

RESULT 4
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KONO2 AND KONO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177, 650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

```

```

QY 39 CGCGGGGCTCTGGGTGAAGACGGCGACGGCGGCGGGCGGCGGCTTGG 98
Db 34 CGCAGGGCGGGCGGGCGGGCTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 93
QY 99 CAGCGGATGATGATGTGGATGGGGCGGG--GGCAGGGTGTGTGATCACTCGGCACGC 156
Db 94 GCTAACCCACCGGAGGGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 153
QY 157 GCGAGGGGCGAGCGGCTCTGTACTGTGGGACCGCGGGCGGGCGGGCGGGCGGG 216
Db 154 GCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 213
QY 217 GGTGGCTGAGGAGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 276
Db 214 ACCCTGCTGCTGAGGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 273
QY 277 CCGCTCTCTTACAGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAG 327
Db 274 GGGCTCTGCGGCAAGACCGCGGTGAGCGGGCGGGCGGGCGGGCGGGCGGG 333
QY 328 CGGGTGCAGAACTACCTGTACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 387
Db 334 CGCATCCAACTTTGATCTAGACGCCCTGGAGAGAGAGAGAGAGAGAGAGAGAG 393
QY 388 CAGCGCTTCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
Db 394 CAGCGCTTCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453
QY 448 CCTAGCACACAAATTTGGCTCAAGTGGCTCTGTATCTGTAGATGTGTGTATG 507
Db 454 AAGAGATATGAGACTGTCTGGAGACAGTGTCTGTATCTGTAGATGTGTGTATG 513
QY 508 GTCTTGTGTTGAGATTCATCATTCATTCATTCATTCATTCATTCATTCATTCAT 567
Db 514 ATCTTGGAGCGGAGCTTGTCTGTGAGATTCATTCATTCATTCATTCATTCATTCAT 573
QY 568 GGATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
Db 574 GGGTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 633
QY 628 CTATATCGCTCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
Db 634 CTGATGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 691
QY 688 GCACATCAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747
Db 692 -CCCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
QY 748 GGCACCTTGGAAATTTAGTGGGTCTAGTGGGTCTAGTGGGTCTAGTGGGTCTAG 807
Db 751 GGCACCTTGGAAATTTAGTGGGTCTAGTGGGTCTAGTGGGTCTAGTGGGTCTAG 810
QY 808 TGTATCATAGATTTTGGTCTTATTTTGGTCTTATTTTGGTCTTATTTTGGTCTT 867
Db 811 TGTATCATAGATTTTGGTCTTATTTTGGTCTTATTTTGGTCTTATTTTGGTCTT 870
QY 868 GATGCC-----AATTAAGAGTTTCTATCATATGA 897
Db 871 GACGTCCAGAGGTGGATGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 898 GATGCTCTGTGGTGGGCAATTTACATTTGACATTTGATTTGATTTGATTTGATTT 957
Db 931 GATGCTCTGTGGTGGGCAATTTACATTTGACATTTGATTTGATTTGATTTGATTT 990
QY 958 CTAACTTGGCTGGGAGAGATTTGCTTCTGAGGCTTTGACATTTGATTTGATTTGATTT 1017
Db 991 AAACGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
QY 1018 GCACCTTCTGCGGCAATTTCTGCTCAGCTTTTGATTTAAAGTACAAACACCGC 1077
Db 1051 GCGCTTCCAGCGGCGATCTGGGGTCCGGGCTGCGGCTCAAGGTGACAGAGCAACCGT 1110
QY 1078 CAGAAACACTTTTGAAGAAAGAGAACCCAGCTGCCAACCCTATTAAGTGTGTTGGCGT 1137

```

Query Match 15.8%; Score 438.2; DB 4; Length 2914;
 Best Local Similarity 56.6%; Pred. No. 1.2e-105;
 Matches 967; Conservative 0; Mismatches 683; Indels 59; Gaps 6;

QY 1091 AGAAAAGAAACCCGCGTCCCAACTCATTGCTGTGGCGTAATGTTACCAGCTG 1150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1301 AGAAGAAAGAAGAACAGCTGCAGGAAGCTCATCCAGGCTGCTGGAGATATATGCTACCA 1360
QY 1151 A---TGAGAAATCTGTGTTCATTGCCAACTCGGA-----AGCCACACTTGAAGGCTTGC 1201
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1361 ACCCCAAACAGGTTGGATCTGTGGCAACCTGGAGATCTTATGATACATGTTGCTCTTCC 1420
QY 1202 ACACCTCAGCCCTTACCATAAGAGCTAAAGTTTAAAGAGCGAGTCCGCTGAGCC 1261
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1421 CATCTCTCAGAGAAAGAAACAACCTGGAMCAGCACAGCCACCAAAGCTGTGCTCTTGGATC 1480
QY 1262 CCAGGGGCCGAGAGATTAAAGGCGGACAGGCTCAGTAGGGGACAGGAGGTCCCCACAGA 1321
Db 1481 GGGTTCGCCCTTCTTAATCTCTGCTGTAAGCAATTAAGGAAAGCTATTACCTCTCGA 1540
QY 1322 CCGACATCACAGCCGAGGCGAGTCCACCAAAAGTCAGAAAGAGCTGGAGCTTCAAGACC 1381
Db 1541 ATGTAGATGGCATATGAAGAAAGCCCTTCCAAGAGCCAAAGCCTGTGGCTTAATACATA 1600
QY 1382 GAACCCGCTTCGGGCGCTCGCTGCGCTCAAAAGTTCTCAGCCAAAACCACTGATAGATG 1441
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1601 AAGAGCCTTTCCGACCGCCCTTCGCGATGAAGGCTTCGCTTTCGACAGMTCTGAAG 1660
QY 1442 CTGCACACAGCCCTTGGACATGATGATATATGATGAAAAAGATGACAGTGTATGAT 1501
Db 1661 ATGCTGGGACAGCGAGCCACCTATGCA-----GAAGCAGGGGCTATGGGATACWTCC 1714
QY 1502 CAGTGAAGACCTCACCCACACACTTAANAAGTGTATCGATTCGAGCTATCAGAAATTAAGAA 1561
Db 1715 TCATTGMAAGCATGATGCTCCCTKCCCTTMAAGGCTGCGCATCCGAGTGTGAGAAATTTACAGT 1774
QY 1562 TTCAATGTTGCAAAACGGAAGTTTAAGAAACATTACGTCATATGATGTTAAAGATGCA 1621
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1775 TCCGCTCATATATAAAAAAGTTCAAGGAGAGGTTGAGGCTTATGATGTGAAAAATGGA 1834
QY 1622 TTGAACAATATTCGTGCTGTCATCTGGACATGTTGTAGAAATTAAGAGCCCTTCAACAC 1681
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1835 TTGAGCAGATTTGGCCGCGACATCTTGACATGCTTTCAGAGATAAAGTACTACAGACAA 1894
QY 1682 GTGTTGATCAAAATTCCT 1697
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1895 GAATGATATGATTTTT 1910

RESULT 6
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Lepert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation

```

? LOCATION: (975)..(976)
? OTHER INFORMATION: There is an insertion of a GT between nucleotides
? OTHER INFORMATION: 975 and 976 in kindred K1504.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (978)
? OTHER INFORMATION: The mutation A to G occurs at this base in kindred
? OTHER INFORMATION: K3904.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (1043)
? OTHER INFORMATION: The mutation G to A occurs at this base in kindred
? OTHER INFORMATION: K1705.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (1691)..(1703)
? OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
? OTHER INFORMATION: deleted in kindred K3369.
? FEATURE:
? NAME/KEY: allele
? LOCATION: (1039)
? OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
? OTHER INFORMATION: the control population.
? FEATURE:
? NAME/KEY: allele
? LOCATION: (1846)
? OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
? OTHER INFORMATION: the control population.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (1469)
? OTHER INFORMATION: The mutation C to T occurs at this base in kindred
? OTHER INFORMATION: K1525.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (1094)
? OTHER INFORMATION: The mutation C to T occurs at this base in kindred
? OTHER INFORMATION: K443.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (1155)
? OTHER INFORMATION: The mutation G to A occurs at this base in kindred
? OTHER INFORMATION: K4516.
? FEATURE:
? NAME/KEY: mutation
? LOCATION: (2736)..(2737)
? OTHER INFORMATION: There is an insertion of GGGCC between these two
? OTHER INFORMATION: nucleotides in K3963.
US-09-177-650-1

Query Match      15.5%; Score 429.4; DB 4; Length 3232;
Best Local Similarity 61.5%; Pred. No. 2.6e-103;
Matches 707; Conservative 0; Mismatches 436; Indels 6; Gaps 1

QY      3  GCCCGGCCACACGCGGGGAGGAGAGAGGGGGCGCGCCCGGCGCTGTGGGTGAAGAGCG 62
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      22  GCCATGCGGCTCCGGCGGGGGGCGCTGAGCTGGGGGCCCGCCCGCCCGCGCTCGC 81
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      63  CGCAGCGCGGCGGCGGCGGGGCGGCGGCGCTTGGGCAACGCGCATGAAGATGGAAGTC 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      82  CCGCGCTAGCGCTGAGCCGACCGCGGGCGGCTCCCGCAGGACACATGTGTCAGAAATC 141
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      123  GGGCGGGGCAAGGCTGTCTGTGAACCTGGCGACGCCCA-----GGGCGAGCGCTGCT 176
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      142  GCGCAACGCGGCGCTATACCCCGCGCCGACGCGGGGAGAAAGACTGAAGGTGGGCTTGT 201
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      177  ACTGCTGGGCAACCGCGGCGGCGACGCTGGGTGGGCGGCGGCTGGCTGAGGAGAGACCG 236
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      202  GGGGCTGACCCCGCGCGCGCCGACTCCACCCGGGACGGGGCGCTGTGATGCGGCTC 261
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      237  CCGGGGCAAGCAGGGGCGCCGGATGAGCTTGCTGGGAAAGCCGCTCTTACACGATAG 296
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      262  CGAGGCGCCCAAGCGCGGCGAGATCTTACGAACACTGGCGGGGCGGGGCGGCGCGG 321
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db	802	CTATGGCCACAGCAAGGAGCTGGTCACTGCCTGGTAACTGGCTTCCATTCTCATCT	861
QY	837	TTGCTCTTTCTCTTCTATCTGGTGGAAAGGATGCCAATTAAGATTCTTACATATGC	896
Db	862	GGCCTCCTCTCCCTGGTGTACTTGGGAGAGAAAGGGGAGAAACACCACCTTTCACACTACGC	921
QY	897	AGATGCTCTCGTGGGGGACAACTTAATACATATTTGGCTATGGAGACAACATCC	956
Db	922	GGATGCACTCTGGTGGGGCCGTGATCAGCGTACACCACTTTGGCTACGGGGACAAGTACC	981
QY	957	CTTAACTTGGCTGGGAAGATTGCTTTTCGACGCTTTGCACTCTTGGCAATTTCTCTT	1016
Db	982	CCAAACCTGGGAACGGCAGGCTCTTTGGGGCCAACTTCAACCTCATCGGTGACTCCTTCTT	1041
QY	1017	TGCACCTCTGCGCCGCAATTTTGGCTCAGTTTGGCAATTAAGATACAAGAACACACCG	1076
Db	1042	CGCGCTGCTGTCAGGCACTTTGGGGGTCTGGGTTTGCCCTGAAGGTTTCAGGAGCAGACACAG	1101
QY	1077	CCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCACCACTCAATCAGTGTGTTGGCG	1138
Db	1102	GCAAAACACACTTTGAGAAAGAGGGCGGAACCCGCGACAGAGGCTGATCCAGTGGCCTGGAG	1161
QY	1137	TAGTTACGC	1145
Db	1162	ATTCTACGC	1170

```

RESULT 8
US-09-105-058C-26
: Sequence 26, Application US/09105058C
: Patent No. 6403360
: GENERAL INFORMATION:
: APPLICANT: Blanar, Michael A.
: APPLICANT: Dworetzky, Steven
: APPLICANT: Gribkoff, Valentin K.
: APPLICANT: Levesque, Paul C.
: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauer, Michael G.
: APPLICANT: Yang, Wen-Pin
: TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: 3053-4052
: CURRENT APPLICATION NUMBER: US/09/105,058C
: PRIOR FILING DATE: 1998-08-26
: PRIOR FILING DATE: 1997-08-12
: NUMBER OF SEQ. ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 26
: LENGTH: 2565
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-105-058C-26

```

[illegible]

Qy	34.9	TACGTCGAGAGACACCCCGGGCGTTCATCTACACACGCTTCGTTTCCTT	408
Db	283	GACGCGCTGGAGAGACCGCGGGGCGTGGCGCTTTCACACGCGCTTGCTGATT	342
Qy	409	GCTCTTGGTGGCTGATATTTTGTCACTGTTTCTACATCCCTGACACAAATTTGCC	468
Db	343	GCTCCGGGGGTGCTGATTCTGGCGTCTGACACCATTCACAGGATATGAGACTGTG	402
Qy	469	TCACGTCGCTTCGTGATCCTGGAGTTGCGTATGATGTGCTTTGGATTTCATC	528
Db	403	GGAGACTGGCTCTGCTACTGAGACATTTGCTATTTTCATCTTTGGAGCCGAGTTTCT	462
Qy	529	ATTGCAATCTGGTCTGGGGTTGGCTGTGCGATATPACAGAGTGGCAAGAACTGAG	588
Db	463	TTGAGGATCTGGGCTGTGATGATTGCTCCGATACAAAGGCTGGCGGGCCGACTGAG	522
Qy	589	TTTGGCTCAAAAGCCCTTCTGTGTTATAGATACATTTGTTATTCGTTCAATAGCACTT	648
Db	523	TTTGGCAAGAAAGCCCTGTGCGATGTGGACATCTTTGTGTGATTTGCCCTGTGGCAG	582
Qy	649	GTTTTCGCAAAAACCTCAGGGTAAATTTTGGCACGCTGCACCTAGAAATCTCCGTTTC	708
Db	583	GTTGCTGTGGGAAACCAAGGCAATGTTTGGCGCACCCT--CCCTCCGAAGCCTGGCGTTC	639
Qy	709	CTACAGATCTCCGATGGTGGCGCATGAGACCGAAGGGGAGCGACTTGGAAATPACGAGT	768
Db	640	CTGCAGATCTCGCATGCTGCGGATGGACCGAAGGTTGGACCTGGAAAGCTTCTGGCG	699
Qy	769	TCAGTGTATTATGTCACAGCAAGAAATTAACAGCGTTGGTACATAGATTTTGGTT	828
Db	700	TCAGGCATCTGTGCCACAGCAAAACATCAACAGGCGCTGGTACATGGTTTCTGTACA	759
Qy	829	CTTATTTTGTGCTTTCCTCTGTCTATCTGCTGTAAGAAAGATGCC-----	873
Db	760	CTCATCTTCTTCTCAATTTCTTGTCTACCTGCTGTGAAAGAGCTCCAGAGGTGATGCA	819
Qy	874	-----AATTAAGATTTTCTACATATGAGATGCTCTGGTGGGGGACACA	918
Db	820	CAGAGAGAGAGATGAAAGAGATTTGAGACTATGACGATGAGCCCTGTGGTGGGGCCGTG	879
Qy	919	ATTACATTGACAACATAATTGGCTATGAGAGACAACATCCCTCACTTGGCTGGAGAAATVG	978
Db	880	ATCACACATGGCCACCATTTGGCTATGTGAAGACAAGACCAACCAAGCTGGGAAAGCGCGTGTG	939
Qy	979	CTTCTGCAAGGCTTTGCACTCCCTGGCAATTTCTTTTGTGCACTTCTGCGGCAATTCCTT	1033
Db	940	ATTGCGCGCACCTTTTCCCTTAATTTGGCGCTCTCTTTTGGCCCTTCCACGCGGGCACTCTG	999
Qy	1033	GGCTCAGGTTTGGCATTAANAATACAAAGAAACAACCGCCAAACAACTTTGAGAAAGA	1099
Db	1000	GGGTCCGGGCTGGCCCTCAAGGTGAGAGAGACAACCGTCACAAACACTTTGAGAAAGG	1055
Qy	1099	AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTAGCAGCTGATAGAAA	1158
Db	1060	AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCGTGAAGTATTTATGCTACCAACCCCAAC	1111
Qy	1159	TCGTGTTTCCATTG-----CAACCTGGAAGCCACACTTGAAGGCTTGCACACTGCG	1205
Db	1120	AGGATTTGACCTGGTGGCGCATGTGAGATTTTATGATCATGTCGTCTTTTCTTTCTTCTTC	1175
Qy	1210	AGCCTTACCAATCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCAAGGGCG	1267
Db	1180	AGGAAGAACAACCTGGAGGACACATTCACCCCAAAAAGTGGGCTCTTGGATGGGTTGCG	1233
Qy	1270	CAGAGATTAAAGCGCGACAACCTCAGTAGGTGACAGAGGTTCCCAAGCACACATCAT	1323
Db	1240	CTTTCTAATCTCTGTGTGTAGCAATTAAGAAAGCTAATTAACCCCTCTGATTTAGAT	1297
Qy	1330	ACAGCGAGGCGAGTCCACCAAGTGCAGAAAGAGCTGGAGCTTCAACGACCGAAACCGCG	1388
Db	1300	GCCATTAAGAAAGATGCTTCTTAAGAACCAACCAAGCCTGTGGCTTAAACAATTAAGAGGCT	1355

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: 900 nucleotides of human KCNQ2
 US-09-105-058C-3

Query Match 15.2%; Score 421.4; DB 4; Length 900;
 Best Local Similarity 68.7%; Pred. No. 1.7e-101;
 Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

299 AGAGTCCGCGGCAAGTCAAGTACGCGGCGGCGAGCACTACTGACACGCTGCG 358
 17 AGCCCCCAAGCCCAAGCCCTTACCGCAAGCTGCAAAATTCCTTACACGCTGCG 76
 359 AGAGACCCCGCGGCGGCGCTTACATACACGCTTCTTCTCTCTCTCTCTCTCT 418
 77 AGCGGCGCGGCGGCGCTTACATACACGCTTCTCTCTCTCTCTCTCTCTCTCT 136
 419 GCTTGAATTTGTAGTCTTTTACACATCCCTGACACACAAATTTGGCTCAAGTTGCC 478
 137 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196
 479 TCTTGAATCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
 197 TCTACATCTCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
 539 GGTCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
 257 GGGCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
 599 AGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
 317 AACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
 659 AAACCTGAGGATATATTTTTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
 377 GCTCCAGGCGCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
 719 TCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 778
 437 TCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
 779 ATGCTCAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 838
 497 ATGCTCAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 556
 839 CGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
 557 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
 899 ATGCTCAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 958
 617 ATGCTCAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 676
 959 TAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
 677 AGACCTGAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 736
 1019 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
 737 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
 1079 AGAACAATTTGAGAAAG 1138
 797 AGAACAATTTGAGAAAG 856
 1139 GTTACGC 1145
 857 TTACGC 863

Sequence 5, Application US/09105058C
 Patent No. 6403360
 GENERAL INFORMATION:
 APPLICANT: Blannar, Michael A.
 APPLICANT: Dworetzky, Steven
 APPLICANT: Gribkoff, Valentin K.
 APPLICANT: Levesque, Paul C.
 APPLICANT: Little, Wayne A.
 APPLICANT: Neubauer, Michael G.
 APPLICANT: Yang, Wen-Pin
 TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 FILE REFERENCE: 3053-4052
 CURRENT APPLICATION NUMBER: US/09/105,058C
 PRIOR FILING DATE: 1998-06-26
 PRIOR FILING DATE: 1997-08-12
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
 LENGTH: 900
 TYPE: DNA
 ORGANISM: mouse
 FEATURE:
 OTHER INFORMATION: 900 nucleotides of murine KCNQ2
 US-09-105-058C-5

Query Match 15.2%; Score 420.6; DB 4; Length 900;
 Best Local Similarity 68.7%; Pred. No. 2.0e-101;
 Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

309 GCGCAAGCTCAAGTACCGGCGGCTGAGAGTACCTACAGCTGCTGAGAGACCCG 368
 27 GCGCAAGCTTCTACCGGAGCTGAGAGTACCTACAGCTGCTGAGAGACCCG 86
 369 CGGCTGCGGCTTACATACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
 87 CGGCTGCGGCTTACATACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146
 429 GTGAGTCTTACATACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
 147 TCTGCTGCTTACATACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
 489 GGAGTCTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
 207 GGAATTCGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
 549 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
 267 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 609 TGTATGATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
 327 TGTATGATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
 669 TAAATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
 387 CAATGCTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
 729 GCGCATGAGCAAGGAGGAGCACTTGAATTAATTAATTAATTAATTAATTAATTAATTA 788
 447 CCGTATGAGCAAGGAGGAGGAGCACTTGAATTAATTAATTAATTAATTAATTAATTAAT 506
 789 CAAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 848
 507 CAAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 566
 849 TGTATCTGCTGAGAAAG 908
 567 GGTATCTTGGAGAAAG 626
 909 GTGGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 968
 627 GTGGGCTGATCACTTACAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 686

QY 969 GGAAGATTCCTTCTGACGCTTTCACCTCCTTGGCATTTCTTCTTGGCATTCTCTGC 1028
 DB 687 CGGGGGGCTGCTGGGACGACCTTACCTCCTGATGCTGCTCTTCTGCTCTGCTGC 746
 QY 1029 CGGCATCTTGGCTGAGTTTGGCATTTAAAGTACAAACACACCGGAGAAACACTT 1088
 DB 747 TGGCATTTTGGGATTCGGCTTTTCCCTGAAGTCCAGACACATCGGCAAAACACTT 806
 QY 1089 TGAGAAAAGAAAGAACCCAGCTGCGCACTCATTCAGTGTGTTGGCGTAAAGCAGC 1148
 DB 807 TGAGAAAAGGCGGACACCTGCGGACGATCTGATCAGTCTGCTGGAGATTCATGCTAC 866
 QY 1149 TGA 1151
 DB 867 TAA 869
 RESULT 12
 US-09-105-058C-17
 ; Sequence 17, Application US/09105058C
 ; Patent No. 6403360
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: 3053-4052
 ; CURRENT APPLICATION NUMBER: US/09/105,058C
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: 930 nucleotides of human KCNQ3
 US-09-105-058C-17
 Query Match 13.1%; Score 363.8; DB 4; Length 930;
 Best Local Similarity 65.5%; Pred. No. 2.8e-86;
 Matches 580; Conservative 0; Mismatches 272; Indels 33; Gaps 2;
 QY 291 GAGTACGACGAGCTGCGGCGGCAAGTACAGTACCGGCGGCGGAGAGAACTACCTACAA 350
 DB 12 GAGCGCGCCAGTCAAGAAACAAACGCAAGTACCGGCGGCGGCAAACTTGAATACGA 71
 QY 351 CGTCTGAGAGACCCCGGCGGCTGAGCTTCACTACACGCTTCTGTTCTCTCTGT 410
 DB 72 CGCCCTGAGAGACCGCGGCGGCTGAGCTTCACTACACGCTTCTGTTCTCTCTGT 131
 QY 411 CTTTGGTCTGATTTTGTGCACTGTTTCTACCATCCCTGAGACACAAATTTGGCTC 470
 DB 132 CCGGGGCTGCTGATTTGCTGCTCTGACCACTTAAAGATATGAGACTGTCGCGG 191
 QY 471 AAGTACCTCTGATCTGAGTTCGATGATGCTGCTGTTGGATTCATCAT 530
 DB 192 AGACTGCTCTGATCTGATGAGATTTGCTATTTTATCTTGGAGCCGATTTGCTT 251
 QY 531 TCGAATCTGCTGCTGCGGCTGCTGTTGCTGATATAGATGAGAGAGAGACTGAGTT 590
 DB 252 GAGGATCTGCGGCTGAGATGCTGCTGCTGATACAAAGGCTGCGGCGGCGGCTGAGTT 311
 QY 591 TCGTGAAGACCTCTGCTGCTTATAGTACATTTGTTCTTCTGCTTCAATAGCAGTTGT 650
 DB 312 TCCAGGAAAGCCCTGCTGATGTTGACATCTTGTGCTGATGCTCTGTCGAGTGT 371

QY 651 TTCTGAAAACCTCAGGTAATATTTTGGCAGCTGCTGACCTGAGAGTCTCTCTCT 710
 DB 372 TGTCTGGGGAACCAAGGCAATGTTTGGCCACTCTCTGAGAGCTCTGCTCTCT 428
 QY 711 ACAGATCTCTCCGATGCTGCGATGACCGAAGGGAAGGCACTTGAATTAATCTGCTG 770
 DB 429 GCGATCTCTGCGATGCTGCGATGAGCGGAGAGGATGAGCTGCTGCTGCTGCTG 488
 QY 771 AGTGTATTTGCTCAGCAGCAAGGAATTAATACAGCTTGTGATATAGATTTTGGTCT 830
 DB 489 AGCATCTCTGCTGCGCAGCAAGGAATTAATACAGCTTGTGATATAGATTTTGGTCT 548
 QY 831 TATTTTGTCT 873
 DB 549 CATCT 608
 QY 874 -----AATAAGATTTTCTATATGACAGTCTCTCTGAGGAGCAANT 920
 DB 609 AGGAGAGAGATGAAAGAGAGTTTGAACCTATGACAGATCCCTGCTGAGGCTGAT 668
 QY 921 TACATGACACATATGCTATGAGACAAACCTCCCTAATCTGCTGAGGAGATGCT 980
 DB 669 CACATGCGCCACATTTGCTATGAGACAAACCTCCCTAATCTGCTGAGGAGATGCT 728
 QY 981 TCTGAGGCTTGCATCT 1040
 DB 729 TGGCGCACCTTTTCT 788
 QY 1041 CTCAGTTTTCATTAAGTACAGAAACACCCGCAAGAACTTTGAGAAAGAAAG 1100
 DB 789 GTCGGGCTGCGCTCAAGGAGGAGCAACCGCTGAGAGCACTTGAAGAAAGAG 848
 QY 1101 GAAGCCAGTGCACCACTCATCTAGTGTGTTGGGTAGTTACGC 1145
 DB 849 GAAGCCAGTGCAGCTCATCTAGGCTGCTGAGGATTAATATGC 893
 RESULT 13
 US-09-105-058C-17
 ; Sequence 7, Application US/09105058C
 ; Patent No. 6403360
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: 3053-4052
 ; CURRENT APPLICATION NUMBER: US/09/105,058C
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: rat
 ; ORGANISM: rat
 US-09-105-058C-17
 Query Match 12.1%; Score 334.2; DB 4; Length 735;
 Best Local Similarity 68.4%; Pred. No. 1.6e-78;
 Matches 462; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
 QY 477 CCTCTGATCTCTGAGTTCGATGATGCTCTTGTGTTGGATTCATTCGAAT 536
 DB 30 CCTCTACATCTTGAATCGTACCATGCTGATGCTGTTGATCTTGTGAGAAAT 89
 QY 537 CTGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596


```

Db      1018 GAGCGGTGAACAGTCAAGGCGCGGTGGAGTTGGCAGCTACGACAGATGCCGTGAGTGG 1077
QY      913 GGCACATTTACATTTGACACTATTGGCTATGAGACAAACTCCCTACTTTGGCTGGGA 972
Db      1078 GGGGTGTGACATGACACCATCGCTATGGGACAAAGTGCCTCCACAGCTGGGTGGG 1137
QY      973 AGATTGCTTCTGAGGCTTTGACCTGCTGGCATTTCTTCTTGGCATTTCTGCTGCGGC 1032
Db      1138 AAGACCATCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
QY      1033 ATTCTTGGCTCAGATTTTGGATTAAAGTACAGACACACCGCCAGAAACACTTTGAG 1092
Db      1198 ATTCTTGGCTCGGGGTTTGGCCTGAGGTGACAGACAGAGGACAAAGACTTCAAC 1257
QY      1093 AAAAGAAGAACCCAGCTGCCAACCTTATTCAGTGTGTTGGCTAGTTAGCAGCTGA 1151
Db      1258 CGCAGATCCCGGCGGACGCTCCTCATTCAGACCCGATGAGGTGCTATGCTGCCGA 1316

```

RESULT 20

```

US-09-444-295-1
; Sequence 1, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MIRK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
US-09-444-295-1

```

```

Query Match      9.7%; Score 267.8; DB 4; Length 3181;
Best Local Similarity 59.5%; Pred. No. 1.1e-60;
Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

```

```

QY      331 GTGCAGAACTACCTGTACAGTGTGAGAGACCCCGGCTG---CGCTTATCTAC 387
Db      478 GTCCAGGCGCCGCTCTACACCTCTCGAGCGTCCACCGCTGGAAATGCTTGGTTAC 537
QY      388 CAGCTTTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
Db      538 CACTTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 597
QY      448 CCTGAGCACAATAATGGCTCAAGTTGCTTGTATCTGATCTGAGTTGCTGATGATTGTC 507
Db      598 GAGCAGTATGCGCGCTGCGCAGCGGAGACTCTCTCTGATGATGAGATGCTGCGTGGG 657
QY      508 GTCTTTGGTTGAGTTCATTCATTCGAATCTGCTGCGGTTGCTGTTGCTGATATAGA 567

```

```

Db      658 TTCTTGGGACGAGTACGTGTGTCGCCCTCTGTCGCCCGCTGCCAGCAACTACGTG 717
QY      568 GATGACGAAGAGACTGAGGTTTGGCTGGAAGCCCTTCTGTGTTATAGATACATTGTT 627
Db      718 GGGCTGTGGGGCGGCTGCGCTTTGGCCGGAAGCCATTTCATCATCTGACTATGCTG 777
QY      628 CTATTCGCTTCAATACAGTGTGTTTTCGCAAAAACCTCAGGGTAATATTTTGGCAGCT 687
Db      778 GTGTGGCTCCCATGAGTGTCTGTGCTGGGCTCCCAAGGGGCGAGTGTGGCCACGCG 837
QY      688 GCACCTAGAAAGTCTCGCTTCTCTACAGATCTCCGCTGATGTGGCTGACGACCGAGGGA 747
Db      838 GGCATCAGGGGCAATCCGCTTCTGCAAGATCTGAGATGCTTACACGTCGACCGACAGGA 897
QY      748 GGCATGGAATTAATACGGGTCTGAGTGTGTTATGCTCAGACAGCAAGATTAATACAGCT 807
Db      898 GGCACCTGAGGCTCTGCGGCTCGTGTCTTCAATCCACCGCCAGGAGCTGATTAACACC 957
QY      808 TGCTACATAGATTTTGTCTTCTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 867
Db      958 CTGTACATCGGCTTCCCTGCGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
QY      868 GATGCCAATATA-----GAGTTTCTACATATGAGATGCTCTGTGGG 912
Db      1018 GACGCGGTGAACAGTCAAGGCGCGGTGAGTTCGGAGTTCGAGATGCGAGATGCGCTGGTGG 1077
QY      913 GGCACATTTACATTTGACACTATTGGCTATGAGACAAACTCCCTACTTTGGCTGGGA 972
Db      1078 GGGGTGTGACACTGACACCATCTGCTATGAGGACAAAGTGGCCGACAGCTGGGTGGG 1137
QY      973 AGATTGCTTCTGAGGCTTTGACCTCTGTCATCTTGGCATTTCTTCTTGGCACTTCTGCGGC 1032
Db      1138 AAGACCATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
QY      1033 ATTCTTGGCTCAGATTTTGGATTAAAGTCAAAACAAACACCGCCAGAAACACTTTGAG 1092
Db      1198 ATTCTTGGCTCGGGGTTTGGCTGAGGTGAGGACGAGGACAAAGCAACACTTCAAC 1257
QY      1093 AAAAGAAGAACCCAGCTGCCAACCTTATTCAGTGTGTTGGCTAGTTAGCAGCTGA 1151
Db      1258 CGCAGATCCCGGCGGACGCTCCTCATTCAGACCCGATGAGGTGCTATGCTGCCGA 1316

```

RESULT 21

```

US-09-597-732-1
; Sequence 1, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Connors, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181

```

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (163)..(2190)
 US-09-597-732-1

Query Match 9.7%; Score 267.8; DB 4; Length 3181;
 Best Local Similarity 59.5%; Pred. No. 1.1e-60;
 Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

331 GTGCAAGACTACTGTACACGCTGGAGAGACCCCGGCTG---GCCTTACATAC 387
 478 GTCCAGGGCCGGCTACAACTTCGAGAGCCGACGCGCGGAGAAATGCTTGTTAC 537
 388 CACGCTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 447
 538 CACTTCGGCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 597
 448 CCGAGCACAACAAATGGCTTCAGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 507
 598 GAGCAGTATGCCCGCTTCGACAGGGGAGCTCTCTTCGATGGAGATCGTCTGTGTG 657
 508 GTCCTTGGTTGGAGTTCAATCAATCTGCTTCGGGGTCTGTTTGTGATATAGA 567
 658 TTCTTCGGAGGAGATACGTGGTCCGCTTCGTGCTGCGCGCGCGCCAGCAAGTACGTG 717
 568 GGATGGCAGAGAAAGACTGAGTTGCTCGAAAGCCCTTCGTATATAGATACATGTT 627
 718 GGCTCTGGGGGGGGCTGGCTTCGCGGAGAGCCATTTCATCAGCTCATCTGCTG 777
 628 CTATTCGCTTCAATAGCAGTTCTTCGCAAAAATCAGGGTAATATTTTCCACGCT 687
 778 GTGCGGCTCCATGCTGCTTCCTTCCTTCGAGGCTCCAAAGGGGAGGTGTGCCACGTG 837
 688 GCACACAGAGCTCGCTTCCTTCAGATCCCTTCGATGGTGGCATGAGACCGAAGGGA 747
 838 GCATCAGAGGGGATCCGCTTCCTTCGATCAGATCTGAGATGCTACACGTCGACCGG 897
 748 GGCACCTGGAAATTAATGAGTTCAGTTCCTTCATGCTACAGCAAGAAATTAATCA 807
 898 GGCACCTGGAGGCTCTGGGGCTCCGCTTCCTTCATCAGCAGGAGCTGATACCAAC 957
 808 TGTGACATAGATTTTGGTTCCTTCATTTTGGTCTTCCTTCCTTCCTTCCTTCCT 867
 958 CTGACATAGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 1017
 868 GATCCCAATATAA-----GAGTTTCTACATATGACAGATGCTCTGTGGTGG 912
 1018 GAGCGGTGGAAGAGTACAGGCGCGCTGGAGTTCGAGCTACGCAAGTGGCTGTGGTGG 1077
 913 GGCACATTAATTAATGACATTAATGAGTTCGCTTCCTTCCTTCCTTCCTTCCTTC 972
 1078 GGGGTGGTACAGTACCAACATCGGCTATGGGAGCAAGTGGCCCAAGAGTGGTGGG 1137
 973 AGATTGCTTTCGAGGCTTCGATCCTTCGATTCCTTCCTTCCTTCCTTCCTTCCT 1032
 1138 AAGACCATGCT 1197
 1033 ATTCTTGGCTCAGGTTTTCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1092
 1198 ATTCTTGGCTCAGGTTTTCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1257
 1093 AAAAGAAAGAACCCAGCTGCAACCTCAATCAATGTTGGGCTGATACGAGCTGA 1151
 1258 CGGAGATCCCGGGGAGCTCACTCATTCAGACCGCATGGAAGTGAATGCTGCGGA 1316

RESULT 22
 US-09-135-021-79
 Sequence 79, Application US/09135021A
 Patent No. 6150104
 GENERAL INFORMATION:

APPLICANT: Splawski, Igor
 APPLICANT: Keating, Mark T.
 TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVL01 WHICH CAUSES JERVELL
 TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
 FILE REFERENCE: 2323-128
 CURRENT APPLICATION NUMBER: US/09/135.021A
 CURRENT FILING DATE: 1998-08-17
 EARLIER APPLICATION NUMBER: 08/874,655
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/094,477
 EARLIER FILING DATE: 1998-07-29
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 79
 LENGTH: 2734
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1743)
 US-09-135-021-79

Query Match 9.6%; Score 266.6; DB 3; Length 2734;
 Best Local Similarity 59.3%; Pred. No. 2.1e-60;
 Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

329 GGGTGAGACTACCTGCTACAGCTGCTGGAGAGACCCCGGCTG---GCCTCATCT 385
 29 GCGGCGAGGGCCGCTGTACAACTTCCTCGAGCGCTCCACGCGGCGGAAATGCTTCGTT 88
 386 ACCAGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 445
 89 ACCACTTCGCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 148
 446 TCCCTAGACACACAAATTTGGCTCAAGTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 505
 149 TCGAGCAGTATGCGCGCCCTTCGACAGGAGCTTCCTTCCTTCCTTCCTTCCTTCCT 208
 506 TCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 565
 209 TGTCTTCGAGAGAGTACGTGCTCCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 268
 566 GAGAGTGCAGAGAGAGTACGTGCTTCGAAAGCCCTTCCTTCCTTCCTTCCTTCCTTC 625
 269 TGGGCTTCGAGGCGGCTTCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 328
 626 TTTTATGCTTCATATAGAGTGTGTTCTGCAAAAATCAGAGGTAATTTTGGCAGCT 685
 329 TGTCTGCTTCATGATGATGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 388
 686 CTGCACTCAGAAAGTCTCCGTTCTTCATAGATCCCTCCGATGCTGCGATGAGACCAAGG 745
 389 GGGCATCAGGGGATCCGCTTCCTTCGATATCCGATGATGCTACAGCTCAACCCCGCAG 448
 746 GAGGCACTTGAATTAATGAGTTCAGTTCCTTCATGCTACAGCAAGAAATTAATCAAG 805
 449 GAGGCACTTGAAGGCTTCGAGGCTTCGCTTCCTTCATCCACCGCAGAGAGCTGATACCA 508
 806 CTGATACATAGATTTTGGTTCCTTCATTTTTCGTTTCCTTCCTTCCTTCCTTCCTTC 865
 509 CCTGTACATGAGCTTCGAGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 568
 866 AGGATGCCAATAA-----GAGTTTCTACATATGACAGATGCTCTGTGGT 910
 569 AGGAGCGGTGGAAGAGTACAGGCGCGGTGGAATTCGCGACGCTACGAGATGCTGTGCT 628
 911 GGGCACAATTAATTAATGACATTAATGAGTTCGATGAGACAAATCTCCCTAATCTGCTGG 970
 629 GGGGCTGTGTACAGTACACACATCGGCTATGGGAGCAAGTGGCCCAAGAGTGGGTGG 688
 971 GAAAGTGTGTTCTTCGAGGCTTCGATCCTTCGATTTCTTCCTTCCTTCCTTCCTTCCT 1030
 689 GGAAGACCATGCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 748

QY 866 AGGATGCCATATA-----GAGTTTCTACATATGACAGATGCTCTCTGT 910
 DB 656 AGGACGGGGTACAGACTAGCCGGCTGGAGTTGGCAGCTACGACATGGCTGTGT 715
 QY 911 GGGGCAATATACATATGACACTATGCTATGAGACAAATCCCTTAATCTGGCTGG 970
 DB 716 GGGGGGGTGTACAGTACCACTGGCTATGGGGAAAGAGTGGCCCAAGAGTGGGTCG 775
 QY 971 GAAGATTGCTTTTGCAGGCTTTGCACTCTTGGCAATTTCTTTTCACTTCTGCGC 1030
 DB 776 GGAAGACATATGCT 835
 QY 1031 GCATTTCTGGCTACGTTTTCATTAAGATACAAAGAACACACCCGAGAAAGCTTTG 1090
 DB 836 GGAATTTGGCTGGGGTGGCTTGGCTGAGACAGCAAGAGAGAGAGCACTTCA 895
 QY 1091 AGAAGAGAGAGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCGTAGTTACGAGCTG 1150
 DB 896 ACCGGGAGATCCCGGGCGGAGCCCTCATTCTACAGACCGCATGGAGTGTATGCTGCGG 955
 QY 1151 A 1151
 DB 956 A 956

RESULT 26
 US-09-135-021-5
 ; Sequence 5, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVL011 WHICH CAUSES JERVELL
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135,021A
 ; CURRENT FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 08/874,655
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 3182
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (163)..(1011)
 ; FEATURE:
 ; NAME/KEY: mutation
 ; LOCATION: (730)
 ; OTHER INFORMATION: This base is an insertion as compared to the
 ; OTHER INFORMATION: wild-type.
 US-09-135-021-5

Query Match 9.3%; Score 258.4; DB 3; Length 3182;
 Best Local Similarity 59.5%; Pred. No. 3.3e-58;
 Matches 500; Conservative 0; Mismatches 321; Indels 19; Gaps 3;
 QY 331 GTGCGAGACTACCTGTACAGTGTGAGAGACCCCGGGGCTG---GGGTCACTTAC 387
 DB 478 GTCCAGGGCCGCTTACACTTCTCGAGCTCCACCGGCTGGAAAGCTTCGTTTAC 537
 QY 388 CACGCTTTCGTTTCT 447
 DB 538 CACTTCGGCGTCT 597
 QY 448 CCTGAGCACACAAATTTGGCTCCTCAAGTTCCTTATCTCTGAGTTCGAGATGTC 507
 DB 598 GAGCAGTATGCGCCCTGGCCAGCGGAGCTCTCTCTGATGAGATGCTGTGTGTG 657

QY 508 GTCTTTGGTTTGGAGTTTATCATTCGAAATCGTCTGCGGGTTGCTTTGTCATA-TAG 566
 DB 658 TTCTTTGGGAGGAGTACGATGCTGCTGCTCTGCTGCGCCGCGGCTGCGAGAAATAGCTG 717
 QY 567 AGGATGGCAAGAGAGACTGAGTTTGTCTGCAAAACCTCTTGTCTTATAGTACCATTGT 626
 DB 718 GGCCTATGGGGGGGCGGCTGCGCTTGGCCGGAAGCCATTTTCATTCATGCACTATGCT 777
 QY 627 TCTTATGCTTCAATATGCAATTTGTTTCTGCAAAATCAGGAGTATATTTTGGCAGCTG 686
 DB 778 GGTGCGGCTTCATATGTTGTTCTCTGCTGCGGCTCAGAGGAGGAGGTTGTCACGCTC 837
 QY 687 TGCATCAGAGAGTCTCGTTTCTTACAGATCTTCCGATGCTGCGCATGAGACCGAAGGG 746
 DB 838 GGCATATCAGGAGGATCTCGCTTCTCGAGATCTTATGATGCTATACAGTGCAGCCGACAGG 897
 QY 747 AGGCATTTGAAATTTACTGGGTTCAAGTTTATGCTCAGACAGCAAGATTAATCAGAC 806
 DB 898 AGGCACCTGAGAGGCTCTGCGCTTCTGCTGCTTCTATCACCAGGAGGCTGATTAACGAC 957
 QY 807 TTGTTACATAGATTTTGTCTTATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 866
 DB 958 CCTGTACATCGGCTTCTCTGCGCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
 QY 867 GATGACCAATATA-----GAGTTTCTACATATGAGATGCTCTCTGCTG 911
 DB 1018 GAGACGGGTGAGACAGTACAGCCCGGCTGAGATTTGGCAGTACGAGATGGCTGTGGTG 1077
 QY 912 GGGCACAATTTACATTTGACAACTATTTGCTATGAGACAAATCCCTTAATCTGGCTGG 971
 DB 1078 GGGGCTGTGACAGTACACCACTTCTGCTATGAGGAGCAAGGTGCGCAGAGTGGGTGG 1137
 QY 972 AAGATTCTTCTGACAGCTTTGCACTTCTGCAATTTCTTCTTCTTCTTCTGCTGCTGG 1031
 DB 1138 GAAGACCATGCTCTGCT 1197
 QY 1032 CATCTTGGCTCAGATTGCTTAAAGTACAAAGAACACCCGAGAAACCTTTGA 1091
 DB 1198 GATTCCTTGGCTCGGGGTTTGGCCTGAAGTGCAGAGAGAGAGAGAGACACTTCA 1257
 QY 1092 GAAAAGAGAGAACCCAGCTGCCAACTTATTCAGTGTGTTGGCTAGTTACGAGCTGA 1151
 DB 1258 CCGCAGATCCCGCGGAGCCTCATCTATTCAGACCCGATGAGAGTGTATGTCGCA 1317

RESULT 27
 US-09-177-650-102
 ; Sequence 102, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MCDON2 AND KCNQ3 IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177,650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 102
 ; LENGTH: 171
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-177-650-102

Query Match 3.5%; Score 95.8; DB 4; Length 171;
 Best Local Similarity 72.5%; Pred. No. 5.7e-16;
 Matches 124; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```

RESULT 31
US-09-177-650-101
; Sequence 101, Application US/091776500
; Patent No. 6413719
; GENERAL INFORMATION:

```



```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-177-650-117

```

Query Match	2.2%	Score 60.8	DB 4	Length 85;
Best Local Similarity	62.5%	Pred. No. 2.2e-06;		
Matches 95; Conservative	0;	Mismatches 57;	Indels 0;	Gaps 0

QY 468 CTTCAAGTGTCTCTTGATCTGAGATCTGATGATCTGCTCTTGGTTGGAGTTCAT 527
 Db 441 CTCATATATGCTCTTCATATGACAGAGACATTTTCCTATTTCATCTTTGGACCGAGTTTGC 500
 QY 528 CATTCGAAATCTGCTCTGCGGGTTCCTGTTGTCGATATAGAGATGGCAAGAAAGCTGAG 587
 Db 501 TTTTAGGATCTGGGGCTGCTGATATGTTGCTGCCGATACAAAGGCTGGCGGGCCGACTGAA 560
 QY 588 GTTTTGCTCGAAAGCCCTTCTGTGTTATAGATA 619
 Db 561 GTTTGCCAGGAAGCCCTCTGTGATCTTGAGTA 592

```

RESULT 35
US-09-165-264-8
; Sequence 8, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuralayah
; TITLE OF INVENTION: Multi-loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
; US-09-165-264-8

```

[illegible]

RESULT 36
 US-09-165-264-7
 : Sequence No, Application US/09165264
 : Patent No, 6197510
 : GENERAL INFORMATION:
 : APPLICANT: Vinayagamoorthy, Thuralayah
 : TITLE OF INVENTION: Multi-Loct Genomic Analysis

```

: FILE REFERENCE: 44747
: CURRENT APPLICATION NUMBER: US/09/165,264
: CURRENT FILING DATE: 1998-10-01
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 320
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-7

```

	Query Match	2.1%;	Score 59.2;	DB 4;	length 320;
	Best Local Similarity	51.1%;	Pred. No. 3,6e-06;		
	Matches 139;	Conservative 0;	Mismatches 133;	Indels 0;	Gaps 0
QY	16	GCGGGAGAGAGAGAGCGCGCGCGCGCGCTGTGGTGAAGAGCGCGCGACGCGCGCG	75		
Db	47	GG	106		
QY	76	GCGCGCGGGCGGGGGCGCTTGAGCGACGCGCATGAAGGATGTGTGATCGGCGCGGACAG	135		
Db	107	GG	166		
QY	136	GTGCTGCTGAACTGGGCGACCGCCGAGGGGGCGAGGGCTGTCTACTGTGGGACCCGCGCG	195		
Db	167	GG	226		
QY	196	GCCACGCTTGGTGGCGGCGGGCGGTGTGGCTGTGAAGGAGACCCCGCGGCAAGCAGGAGGCC	255		
Db	227	GG	286		
QY	256	CGGATGAGCCCTGCTGGGAGACCCGCTCTCTTA	287		
Db	287	GGGGGGGGGGGGGAGGCTACGCCTTAA	318		

```

RESULT 37
US-09-165-264-13
; Sequence 13: Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuratayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
; US-09-165-264-13

```

[illegible]

RESULT 49

Query Match	1.9%;	Score 552.4;	DB 4;	Length 4411529;
Best Local Similarity	54.2%;	Pred. Nc. 0.03;		
Matches 129;	Conservative	0;	Mismatches 106;	Indels 3;
				Gaps 1;

```

QY      6  CCGCCACACGCGGAGAGAGAGGCGCGCCCGCGGCTGTGGTGAAGCGGCGC  65
Db      3054633  CGGCGCCACAGGCGCGCGTGGCAACGGCGGTCGGGCGGGCTGTTCGGCGC  3054692
QY      66  AGCGCGCGCGCGCGCGCGCGGCGCGCTTGGGCAAGCGGCAWGAAGATGTGAGTCGGG  125
Db      3054693  CGGCGGTGCGCGCGCGCGCGCGCTTCAGCGACACCGGTGGACCGCGGCGG---CTGG  3054749
QY      126  CCGGGGCGAGGCTGTCTGAACCTCGGCAAGCGCGCAAGGCGGCGGCTGTACTGTGGG  185
Db      3054750  CGGCGCGCGCGCGGCTGTTCGGCCCGGCGGCGGCTCGGGCGGCTTCGGCGA  3054809
QY      186  CAGCCGCGCGCGCACAGCTCGGTGGCGGCGGCGGCTGAGGAGAGCGCGCGGCGG  243
Db      3054810  CACCGGTGGGACCGCGCGGCGGCGGCGGCTGTTCGGCTGTGGCGGCGGCGC  3054867

```

Search completed: June 19, 2003, 11:25:11
 Job time : 192 secs


```

80 129.8 4.7 461 9 A1347525
C 81 129.2 4.7 411 12 BF414224
82 128.8 4.6 267 12 BG185740
C 83 128.2 4.6 226 9 A1705051
84 128.2 4.6 330 10 AM533367
C 85 128 4.6 239 10 AM122800
86 124.6 4.5 650 13 B1228823
87 124.6 4.5 493 9 A1439544
88 124.2 4.5 1068 12 BF311176
89 124 4.5 335 12 BG218030
90 123.8 4.5 545 12 BE753839
C 91 123.4 4.5 344 13 B1049443
C 92 119 4.3 631 10 BE159001
93 114 4.1 334 9 AA091374
94 113.6 4.1 425 10 BE648243
95 113.2 4.1 311 14 H23702
C 96 112.8 4.1 443 9 A1871417
97 112.4 4.1 530 12 BE721570
98 110 4.0 539 12 AM135705
99 109.6 4.0 160 12 BE959223
C 100 108.4 3.9 899 17 A1769029
C 101 107.2 3.9 442 9 A1769029
C 102 107.2 3.9 1087 17 CANS05CVN
C 103 106.8 3.9 442 12 BG979542
C 104 106.8 3.9 812 12 BG328061
C 105 105.8 3.8 742 17 CANS020XL
C 106 102.6 3.7 372 14 H51419
107 101.4 3.7 668 13 BM616365
108 96 3.5 451 12 BF109081
109 95.2 3.4 653 17 A1343821
110 94.6 3.4 418 9 A1344361
111 94.4 3.4 482 14 R36327
C 112 94.2 3.4 515 14 H08544
C 113 94.2 3.4 410 16 A1638340
C 114 93.8 3.4 595 17 DR78N8T
115 93 3.4 228 14 T03719
C 116 93 3.4 984 14 CANS0462C
117 93 3.4 1019 17 CANS02909
118 92.2 3.3 269 14 H86059
119 90.6 3.3 449 14 T78692
120 89 3.2 979 17 CANS02PU9
121 89 3.2 1024 17 CANS02XIT
C 122 88 3.2 523 12 AM183543
C 123 87.6 3.2 244 10 BE755715
124 86.4 3.1 360 14 C63600
125 85 3.1 662 12 BB657491
C 126 83.8 3.0 475 12 BF412048
C 127 83 3.0 805 17 CANS03E1A
128 81.8 3.0 121 12 BF549164
C 129 81.2 2.9 442 9 A1637723
130 81.2 2.9 682 13 BM627759
131 81.2 2.9 696 13 BM613188
132 81 2.9 260 9 AL732172
133 81 2.9 312 12 BF798699
C 134 80.8 2.9 841 17 CANS0236E
C 135 80 2.9 955 17 CANS02XIT
C 136 80 2.9 994 17 CANS028EF
C 137 80 2.9 1009 17 CANS036DE
C 138 79.6 2.9 776 17 CANS010RY
C 139 77.6 2.8 903 17 CANS022P4
C 140 77.4 2.8 271 12 BF415113
C 141 75.6 2.7 729 13 B1891823
C 142 75.2 2.7 467 9 A1177094
143 74.2 2.7 327 12 BF809118
144 73.2 2.6 685 12 BG7866336
145 73 2.6 468 14 B0608819
146 71.8 2.6 461 17 A0754702
147 71.6 2.6 429 13 BM609600
C 148 71.4 2.6 1101 17 CANS05406
C 149 71.4 2.6 925 9 AL581447
C 150 71 2.6 1153 14 BM804596

```

ALIGNMENTS

```

RESULT 1
LOCUS BE158938
DEFINITION M60-HT0404-210200-001-c04 HT0404 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE158938
VERSION BE158938.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 658)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=st2-MR0-HT0404-210
200-001-c04&lc=2000-02-21&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 657.
location/Qualifiers
source 1..658
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HT0404"
/deov_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 181 a 175 c 153 g 149 t
ORIGIN
Query Match 23.0%; Score 637.2; DB 10; Length 658;
Best local Similarity 99.5%; Pred. No. 3,6e-138;
Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 936 TGGCTATGAGACAAACCTCCCTAACTGGCTGGAGAGATGCTTCTGACAGGCTTGC 995
|||||
DB 17 TGGCTATGAGACAAACCTCCCTAACTGGCTGGAGAGATGCTTCTGACAGGCTTGC 76
|||||
QY 996 ACTCCCTGTCATCTTCTTCTTCTGACACTTCCGCGGCACTTGTGGCTAGGTTTGCAAT 1055
|||||
DB 77 ACTCCCTGTCATCTTCTTCTTCTGACACTTCCGCGGCACTTGTGGCTAGGTTTGCAAT 136
|||||
QY 1056 AAAAGTACAAAGACACACCGCAGAAACCTTGGAGAAAGAGAACCCAGCTGCCAA 1115
|||||
DB 137 AAAAGTACAAAGACACACCGCAGAAACCTTGGAGAAAGAGAACCCAGCTGCCAA 196
|||||
QY 1116 CCTCATTCAGTGTGTTGGCGGTAGTACGACGATGAGAAATCTGTTCCATTCGACAC 1175
|||||

```

Db	197	CGCATTCAGTGTGTTGGCGTAGTTCAGCAGAGCTGATGAGAAATCTGTTCCATTGCAAC	256
Qy	1176	CTGGAAAGCCACTTGTGAAGGCGCTTGACACACTGTAGGCCCTTACCAATCAGAAAGCTAAAGTTT	1235
Db	257	CTGGAAAGCCACTTGTGAAGGCGCTTGACACACTGTAGGCCCTTACCAATCAGAAAGCTAAAGTTT	316
Qy	1236	TAAGGAGCGAGTGGCGCATGGCTAGGCCAGGAGGCGCAAGTATTTAAAGCCGACAAAGCTC	1295
Db	317	TAAGGAGCGAGTGGCGCATGGCTAGGCCAGGAGGCGCAAGTATTTAAAGCCGACAAAGCTC	376
Qy	1296	AGTAGGTGACAGAGAGGTGCCCAAGCAGACATCAGACGCGAGGGCAGTCCCAAAAGT	1355
Db	377	AGTAGGTGACAGAGAGGTGCCCAAGCAGACATCAGACGCGAGGGCAGTCCCAAAAGT	436
Qy	1356	GCAGAAAGCGTGGAGGCTTTCAAACGACGACCCGTCGCCGGCCCTCGGTGGCGCTCAAAAG	1415
Db	437	GCAGAAAGCGTGGAGGCTTTCAAACGACGACCCGTCGCCGGCCCTCGGTGGCGCTCAAAAG	496
Qy	1416	TTCTCAGCCCAAAACCAAGTATGATGCTGTGACACAGCCCTTGCGACTGATGATATGA	1475
Db	497	TTCTCAGCCCAAAACCAAGTATGATGCTGTGACACAGCCCTTGCGACTGATGATATGA	556
Qy	1476	TGAAAAAGATGCCAGTGTGATGTATCATGTGAGGAGAGCTCACCCCAACACTTAATAACGT	1535
Db	557	TGAAAAAGATGCCAGTGTGATGTATCATGTGAGGAGAGCTCACCCCAACACTTAATAACGT	616
Qy	1536	CATTCGAGCTATCAGAAATTATGAATTTCATGTTGCAAAAG	1577
Db	617	CATTCGAGCTATCAGAAATTATGAATTTCATGTTGCAAAAG	658
RESULT 2	BG532543	734 bp	EST 03-APR-2001
LOCUS	602562103P1 NIH_MGC_61	Homo sapiens	cdna IMAGE:4699776 5',
DEFINITION	mRNA sequence.		
ACCESSION	BG532543		
VERSION	BG532543.1	GI:13524082	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 734)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgshps-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: CLONETECH Laboratories, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LITCM1512 row: f column: 01		
	High quality sequence stop: 699.		
FEATURES	Location/Qualifiers		

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:469976"
/clone_1lb="NH_MCC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pMR-11B (Clontech); Site_1:
Site1 (ggcgccgttcggc); Site_2: Site1 (ggccatcatggc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCGCATATGAGCC-3' and 3' adaptor
sequence: 5'-ATTCTGATGAGCGGAGCGGCCACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average

```

[illegible]

TAG_TISSUE=corpus-striatum
 TAG_SRO=ACGC"
 BASE COUNT 107 a 151 c 174 g 152 t
 ORIGIN
 Query Match 18.7%; Score 518.4; DB 10; Length 584;
 Best Local Similarity 93.0%; Pred. No. 2,1e-110;
 Matches 543; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 152 CAGCCCGCAGGCGAGCGCCCTGCTACTGCTGGCACCAGCGCGCCAGCGCTCGTGGCG 211
 1 CGGCCCGCAGGCGAGCGCCCTGCTACTGCTGGCACCAGCGCGCCAGCGCTCGTGGCG 60
 QY 212 GCGCGCGCTGCTGAGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 271
 61 GCGCGCGCGCTGAGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 272 GGAAGCGCTCTCTTACAGCAGTACAGCAGCTGCGCGCGCGCGCGCGCGCGCGCGCG 331
 121 GGAAGCGCTCTCTTACAGCAGTACAGCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 QY 332 TGCAGAACTACCTGTACAGCTGCTGAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 391
 181 TGCAGAACTACCTGTACAGCTGCTGAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 392 CTTTCGCTTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
 241 CTTTCGCTTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 452 AGCAGCAAAATGCGCTCAAGTTCCTTGAATCCTGAGATTCGATGATGATGCTGCT 511
 301 AGCAGCAAAATGCGCTCAAGTTCCTTGAATCCTGAGATTCGATGATGATGCTGCT 360
 QY 512 TTGGTTGGAGTTATCATTCGAAATCTGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTG 571
 361 TTGGTTGGAGTTATCATTCGAAATCTGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTG 420
 DB 572 GGCAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
 421 GGCAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 632 TCGCTCAATAGCAGTTGTTCTGCAAAACCTGAGGTAATTTTGGCAGCTGTCAC 691
 481 TCGCTCAATAGCAGTTGTTCTGCAAAACCTGAGGTAATTTTGGCAGCTGTCAC 540
 DB 692 TCAGAACTCTCGCTTCTACAGATCCCGCATGCTGCGCATG 735
 541 TCAGAACTCTCGCTTCTACAGATCCCGCATGCTGCGCATG 584

RESULT 8
 BF959996/c 506 bp mRNA linear EST 22-JAN-2001
 LOCUS BF959996
 DEFINITION QV2-NN0045-051200-526-909 NN0045 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF959996
 VERSION BF959996.1 GI:12377271
 KEYWORDS EST.
 SOURCE human.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 506)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2st2-QV2-NN0045-
 051200-526-909&tl=2000-12-03&tl=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 506.
 Location/Qualifiers
 1..506
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous system; Vector: puc18; Site: 1; Smal;
 site: 2; Smal: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 125 a 108 c 104 g 168 t 1 others
 ORIGIN
 Query Match 17.7%; Score 490.6; DB 12; Length 506;
 Best Local Similarity 98.0%; Pred. No. 6.5e-104;
 Matches 496; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1458 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1517
 506 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 447
 DB 1518 CCCACCTTTAAACCTGCTCAGCTATCAGATTAATGAAATTTTCATGTTGCAAAAG 1577
 446 CCCACCTTTAAACCTGCTCAGCTATCAGATTAATGAAATTTTCATGTTGCAAAAG 387
 QY 1578 GAAGTTTAAGAAACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1637
 386 GAAGTTTAAGAAACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 327
 DB 1638 TGGTCATCTGACATGTTGTTGATGATTAAGCCTTAAACAGCTGTTGATCAATTC 1697
 326 TGGTCATCTGACATGTTGTTGATGATTAAGCCTTAAACAGCTGTTGATCAATTC 267
 QY 1698 TGGAAAGGGCAATCAGATCAGATTAAGAGAGCCGAGAGAAATTAAGAGCAACATGA 1757
 266 TGGAAAGGGCAATCAGATCAGATTAAGAGAGCCGAGAGAAATTAAGAGCAACATGA 207
 DB 1758 GACCACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1817
 206 GACCACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 147
 QY 1818 CATGAAATCCAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1877
 146 CATGAAATCCAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 87
 DB 1878 TGCCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1937
 86 TGCCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 27
 QY 1938 TGACTATCAAGCCCTGAGATAGA 1963
 26 TGACTATCAAGCCCTGAGATAGA 1
 DB

RESULT 9
 BB624101 632 bp mRNA linear EST 26-OCT-2001
 LOCUS BB624101

Db 315 GTTGTCTAGATTAAAGCCTTCAACACGCTGTTGATCAATTTCTTGGAAGGCAAT 256

QY 1713 CACATTCAGTAAAGAGCCGAGAGAAATACAGCAGAACATGAGACACAGATCT 1772

Db 255 CACATTCAGTAAAGAGCCGAGAGAAATACAGCAGAACATGAGACACAGATCT 196

QY 1773 CAGTATGCTCGGCTGGTGTCAAGTTGAAAAACAGTACATCTAGATTCAGACT 1832

Db 195 CAGTATGCTCGGCTGGTGTCAAGTTGAAAAACAGTACATCTAGATTCAGACT 136

QY 1833 GGAATCTCTACTAGATCTATCAACAGTCTCTGGAAGAGCTCTGCTCAGCCCTGC 1892

Db 135 GGAATCTCTACTAGATCTATCAACAGTCTCTGGAAGAGCTCTGCTCAGCCCTGC 76

QY 1893 TTTGGCTTCATTCAGATCCACCTTTTGAATGGAACAGATCTGATCAAGCC 1951

Db 75 TTTGGCTTCATTCAGATCCACCTTTTGAATGGAACAGATCTGATCAAGCC 17

RESULT 13
BE103175 469 bp mRNA linear EST 13-JUN-2000
LOCUS UI-R-BT1-axq-h-11-0-UI.s1 UI-R-BT1 Rattus norvegicus CDNA clone
DEFINITION UI-R-BT1-axq-h-11-0-UI 3', mRNA sequence.
ACCESSION BE103175
VERSION BE103175.1 GI:8495314
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 469)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found. Not a site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this CDNA sequence: 1-71,
>C_richlow_complexity
Seq primer: M13 Forward
POLYA-No.

FEATURES
source

Location/Qualifiers
1. 469
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1-axq-h-11-0-UI"
/clone_lib="UI-R-BT1"
/dev_stage="adult"
/lab_host="DHI0B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The library
UI-R-BT1 is a subtracted library derived from a mixture of
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
rategen.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_SEQ=None found"

BASE COUNT 79 a 120 c 152 g 118 t

ORIGIN

Query Match 15.0%; Score 416.2; DB 10; Length 469;
Best Local Similarity 93.0%; Pred. No. 1,6e-86;
Matches 436; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 152 CAGCCGCCAGGGGCGAGCGGCTCTACTGCTGGGCAACCCGCGGCGACGCTGGTGGC 211

Db 1 CGGCCGCCAGGGGCGAGCGGCTCTACTGCTGGGCAACCCGCGGCGACGCTGGTGGC 60

QY 212 GCGGCGGCTGCTGAGGAGAGCCGCGGCGCAAGCAGGGGCGCCGATGAGCCCTGCTG 271

Db 61 GCGGCGGCGCTGAGGAGAGCCGCGGCGCAAGCAGGGGCGCCGATGAGCCCTGCTG 120

QY 272 GGAAGCCGCTCTCTTACAGAGTAGCCAGCAGCTGCGGCGCCAGCTAAGTACCGGGG 331

Db 121 GGAAGCCGCTCTCTTACAGAGTAGCCAGCAGCTGCGGCGCCAGCTAAGTACCGGGG 180

QY 332 TGAGAACTACCTGTACCAACGCTGTGAGAGACCCGCGGCTGGCGCTTACACAG 391

Db 181 TGAGAACTACCTGTACCAACGCTGTGAGAGACCCGCGGCTGGCGCTTACACAG 240

QY 392 CTTTCCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451

Db 241 CTTTCCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 452 AGCACAACAATGCGCTCAGTTCCTCTGATTCCTGAGTTCGATGATGCTGCTGCT 511

Db 301 AGCACAACAATGCGCTCAGTTCCTCTGATTCCTGAGTTCGATGATGCTGCTGCTGCT 360

QY 512 TTGGTTGGAGTTCATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 571

Db 361 TTGGTTGGAGTTCATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 420

QY 572 GGCAGGAGAGCTGAGCTTCTCGAAGCCCTTCTGTATAGATAC 620

Db 421 GGCAGGAGAGCTGAGCTTCTCGAAGCCCTTCTGTATAGATAC 469

RESULT 14
BF954375 517 bp mRNA linear EST 22-JAN-2001
LOCUS QV2-NN0045-131100-414-f08 NN0045 Homo sapiens CDNA, mRNA sequence.
DEFINITION BF954375
ACCESSION BF954375
VERSION BF954375.1 GI:12371650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 517)
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL Contact: Simpson A.J.G.
MEDLINE Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=QV2-825-147-1-NN0045-1)

Qy	1896	GGCTCATTCAGATCCAC	1915
Db	549	GGCTCATTCAGATCCAC	568

RESULT 16

LOCUS	AZ443350	477 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	IM0323811R	Mouse 10kb	plasmid	library	Mus musculus genomic
DESCRIPTION	clone UNGC1M0238118 R,	DNA sequence.			
KEYWORDS	U03500				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 477)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Hartmann, J., Kozlov, P., Lachlan, R., Macdonald, S., Madsen, O.,

FEATURES

Source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="tUUGC1M238H18"
 /clone_lib="Mouse 10kb plasmid tUUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-gold, T1-resistant, F-"
 note="Vector: PWD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (q11473211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT	100 a	98 c	150 g	129 t
ORIGIN				

Query Match	13.7%;	Score 378.4;	DB 17;	Length 477;
Best Local Similarity	87.2%;	Pred. No. 1.1e-77;		
Matches 415;	Conservative	0;	Mismatches 61;	Indels 0;
				Gaps 0;

QY	1981	GCACAAAACAGTGGCTCTTATCCAGATTCACATCTGTGTCCAAATCTCTGAAGAGCGCTGAC	2040
Db	476	GCACAAAACAGCGGCTCTTTAACGAGGTACAGCCAGTGCACAACTCTCAAGAGCGCTGAC	417
QY	2041	TTTCATTCGAGCGCAAAATGAGTTGACGTGCCAGACTTTCACGCGCTTAGCCCTACTATG	2100
Db	416	TTTCATTCCTAACACCAAAATGAGTTGAGTCTGACGCTTCTATGCGCTTAGGCCCTACTATG	357
QY	2101	CACAGTCACGAAACACAGAGTGGCAATTAATGTCAAAGCATGGCTGACGAGAGTGGCGCCAC	2160
Db	356	CACAGCCAAAGTATACCCAGGTACCCATGATGTAAAAATGACGGCTCTCTCGTGTGACCAAC	297
QY	2161	AACACCAATTCGAAACCAAAATTAATATGAGGCAACCCACAGCCAGCAGCCCAACAACATTTAC	2220
Db	296	AATAAACATGTGAAACCAAAATTAATGAGGCGCGACCCAAAGCCAGCAGCCCAACAACATTTAC	237
QY	2221	ATCCCACTCTCTCTCCACAGCCATCAAGCATGTGCCACAGGCCAAGAAACTCTGACCCCTAAC	2280
Db	236	ATCCCTCTCTCTCTCGGCATCAAGCACTGTGTCAGGCCCAAGAACTCTCTCTCTCAAC	177
QY	2281	CCTGAGGCTTACAGGAAGCATTTCTGACGTCAACACACTGCTGTTGTCCCTCCAAAGAA	2340
Db	176	CCCAACGGCTTACAAAGAAAGATTTCTGATGTCAACACACTGCTGTTGTCCCTCCAAAGAA	117
QY	2341	AATGTTCAAGTTGCACAGTCAAAATCTCAACCAAGAACGTTCTATGAGGAAAAAGCTTTGAC	2400
Db	116	AGTGTTCAGTTTGCACAGTCAAACTGTACCAAGAACGTTCTCTGAGGAAAAAGTTTGAC	57
QY	2401	ATGGAGAGAGAAACGTGTGTCTCTGTGCCATGTGCGGAAGAGATTTGGGCA	2456
Db	56	ATGGAGAGAGAAACGTGTGTCTCTGTGCCCATGTGCGCGCCCAAGTGTGCCAAGATTTGGGCA	1

RESULT 17

LOCUS	434 bp	RNA	linear	EST 19-JUL-2001
DEFINITION	B2290441	UT-R-DKO-clw-g-12-0-UT.s1	UT-R-DKO Rattus norvegicus	CDNA clone
		UT-R-DKO-clw-g-12-0-UT 3',	mRNA sequence.	

REFERENCE	1 (bases 1 to 434)
AUTHORS	Bonaldo, M. F., Lennon, G. and Soares, M. B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
JOURNAL	discovery
MEDLINE	Genome Res. 6 (9), 791-806 (1996)
COMMENT	97044477
	Contact: Soares, MB

Email: msources@blue.weeg.nyu.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat brain pool library cDNA library Preparation: M.B. Soares Lab Clone distribution: (www.resgen.com)
Research Genetics
Seq primer: M13 Forward
POLYA=yes.

FEATURES

Source

```
Location/Qualifiers
1. . 434
/organism="Rattus norvegicus"
```

```

/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DKO-clf-c-12-0-UI"
/clone.lib="UI-R-DKO"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pTR73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-DKO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
brain-nRAP (20%), heart-nRAP (20%), kidney-nRAP (20%),
aorta-nRAP (20%), and placenta-nRAP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldi, Lennon & Soares (Genome Research 6:
791-806, 1996). For construction of the DKO subtracted
library, plasmid DNA from each of the five individually
tagged normalized libraries was mixed in the proportions
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized libraries
was then used as a tracer in a subtractive hybridization
template preparation (PCR amplified inserts from a plasmid DNA
arrayed clones from each of the five non-normalized
libraries of brain (C10s), heart (C50s), kidney (C100s),
aorta (C100s), and placenta (C100s). The resulting pool of
approximately 5,000 clones represented about 33.3% of the
final driver population. A set of about 2,000 arrayed
clones from each of the five normalized libraries of brain
(C100), heart (C50), kidney (C100), aorta (C100), and
placenta (C100). The resulting pool of about 10,000 clones
represented about 66.6% of the final driver population.
TAG_LIB=UI-R-DKO
TAG_TISSUE=rat brain pool
TAG_SEQ=ACTTC"
BASE COUNT      82 a      109 g      145 t      1 others
ORIGIN
Query Match      12.8%; Score 356.2; DB 13; Length 434;
Best Local Similarity 88.7%; Pred. No. 1.7e-72;
Matches 385; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
1307 GGAGGTCGCCAAGCAGCAGATCATCAGCCGAGGCGATCCCAAGAGAGAGCT 1366
|||||
434 GGAGATCCCAACACACGATCATCTGAGGCGAGCCCAAGAGAGAGCT 375
1367 GGAGCTTCAAGCAGCAGCAGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCT 1426
|||||
374 GGAGCTTCAAGCAGCAGCAGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCT 315
1427 AACCACTGATGATGCTGACACAGCCTTGGCAGTATGATGATGATGATGATGAT 1486
|||||
314 AGACGCTGATGATGCTGACACAGCCTTGGCAGTATGATGATGATGATGATGAT 255
1487 GCGAGTATGATGCTGACACAGCCTTGGCAGTATGATGATGATGATGATGATGAT 1546
|||||
254 GCGAGTATGATGCTGACACAGCCTTGGCAGTATGATGATGATGATGATGATGAT 195
1547 TCAGATTTGAATTTGATGTCAGCAAGAGAGTTAAGAAACATTAAGTCCATATG 1606
|||||
194 TCAGATTTGAATTTGATGTCAGCAAGAGAGTTAAGAAACATTAAGTCCATATG 135
1607 ATGTAAGATGCTGATGCAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1666
|||||
134 ATGTAAGATGCTGATGCAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 75

```

```

OY 1667 AAGCCTTCAACACGCTGTCATCAATTTCTTGGAAAAAGGCGAATCATCATGATGACA 1726
|||||
DB 74 AAGCCTTCAACACGCTGTCATCAATTTCTTGGAAAAAGGCGAATCATCATGATGACA 15
OY 1727 AGAGCGAGAGGAAA 1740
|||||
DB 14 AAAAAAAAAAAAAA 1
RESULT 18
LOCUS BG732557 528 bp mRNA linear EST 11-MAY-2001
DEFINITION BG732557
ACCESSION BG732557
VERSION BG732557.1 GI:14018840
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE 1 (bases 1 to 528)
AUTHORS Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.,
and Keefe, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@meat.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGCAGCAGC
Plate: 106 row: D column: 19
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..528
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone.lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      112 a      197 c      135 g      84 t
ORIGIN
Query Match      12.3%; Score 339.8; DB 12; Length 528;
Best Local Similarity 79.4%; Pred. No. 1.2e-68;
Matches 436; Conservative 0; Mismatches 92; Indels 21; Gaps 2;
1961 GCAAGATCTTTCGGGTTCCGACAAAGAGTGGCTGTTATCCAGATCACTAGTGCCA 2020
|||||
DB 1 GCAAGATCTTTCGGGTTCCGACAAAGAGTGGCTGTTATCCAGATCACTAGTGCCA 60
2021 ACATCTGAGAGGCGCTGAGTTCATTCGAGCGCAATAGATGATGATGATGATGATGAT 2080
|||||
DB 61 ACATCTGAGAGGCGCTGAGTTCATTCGAGCGCAATAGATGATGATGATGATGATGAT 120
2081 ACGGCTTAGGCGCTGATGACAGTCAAGCAAGCAGGTGCGCAATTAAGTCAAGGATG 2140
|||||
DB 121 ACGGCTTAGGCGCTGATGACAGTCAAGCAAGCAGGTGCGCAATTAAGTCAAGGATG 177
OY 2141 GCTGAGAGTGGGCGGCGCAACACATTTGCAACCAATTAATACGCGACCCAGCCAG 2200
|||||

```

D _b	178	GCCCAAGGGGGGATACCCACAGCATGCACACCAAAATAAACGGCGGTCCAAAGCGCC	237
O _y	2201	CAGCCCCAACACTTTACAGATGCCACCTCTCTCCAGGCATCAAAGACTTGCACAGGC	2260
D _b	238	CGGCCCAGCAGCACTTGTCAGATCCCGCTCTCTCCCGCCCTCAAGCACCTCTCC-----	292
O _y	2261	CAGAAACTCTGCACCCTTAACCCCTGCAGCGCTTAGGAAGAACAATTGTGAGTCAGCACCT	2320
D _b	293	-----CCCCAACCCGCGGGCCTGCAGGAGAGACATTTCCGAGTCAACCACT	339
O _y	2321	GCCTGTGTGCCCTCCAAGGAATAATGTTCAGGTTGTCACAGTCAAAATCTCACCAAGACCGTT	2380
D _b	340	GCCTGTGCTGCTCCAAAGAGAAATGTTGCGGCTGGCAGGCAAAACCTACCAAGAGACCGCT	399
O _y	2381	CTATGAGAAAAAGCTTTGACATGGGAGAGAAAACTCTGTTGTCTGTCTGTGCCATGATGTC	2440
D _b	400	CTTTGGCCCAAGAGCTTGCACCTGGGCGGAATAAAGCTGCTGTCTGCTCGGCCGCTGTACT	459
O _y	2441	CGAAGGACTTGGCGAAATCTTTGTCTGTGCAAAAACCTGATCAGGTGACGGAGGAACTGA	2500
D _b	460	CCAAGGAGACTGGGCGAAAGTCTGTGCTGTGCAAAAACCTGATCCGATCGACGGAGGAACTGA	519
O _y	2501	ATATACAAC 2509	
D _b	520	ATACACAGC 528	

RESULT	19		
BF523361/c			
LOCUS	BF523361		
DEFINITION	BF523361	427 bp	mRNA
	UT-R-60-ug-h-09-0-UI.r1		linear EST 11-DEC-2000
	UT-R-60-ug-h-09-0-UI.5,		Rattus norvegicus cdna clone
			mRNA sequence.

ACCESSION	BF523361
VERSION	BF523361.1
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus

REFERENCE AUTHORS TITLE JOURNAL	
1 (bases 1 to 427) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)	

MEDLINE 97044477
Contact: Soares, MB

Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscoar@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1794020
Seq primer: M3 Forward

source	location/quadlens
1. .427	

```

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-G0-ug-h-09-0-UI"
/clone_1fb="UI-R-G0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="vector: pT73D-Pac (pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the

```

BASE COUNT	125 a	92 c	108 g	102 t
ORIGIN	oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. "			

Query Match	11.2%	Score 310.8;	DB 12;	Length 427;
Best Local Similarity	92.4%	Pred. No. 6.9e-62;		
Matches 327; Conservative	0;	Mismatches 27;	Indels 0;	Gaps 0;

[illegible]

QY 832 ATTTTTCGTCCTTCCTGCTATCTCGGTGAAAGCATGCCAAATAAGATTTTTCACA 891
||||||| || ||||||||| ||||| ||||||||| ||||||||| |||
Db 366 ATTTTTCATCTCTCCTGCTATCTGCTGGAAAAGATGCCAAATAAGATTTTTCACA 307

[illegible]

Q7 952 ACTCCCTACTTGGCTGGGAAGATTGCTTTCTCAGAGCTTGCACCTCCTTGCAATTCCT 1011
||| ||||||||| ||||||||| ||||||||| ||| ||| ||||| |||||
Db 246 ACACCCCTAAGTGGCTGGGAAGATTGCTCTCTGTGAGGCTCGGCCCTCTTGTAATTCCT 187

QY 1012 TTCCTTGACATTCCTGCGCGCATCTCTTGACATTTTGACATTAAGTACAGAACAA 1071
Db 186 TTCCTTGACATTCCTGCGCGCATCTCTTGACATTTTGACATTAAGTACAGAACAG 127

QY 1072 CACGCCCAAAACTTTGAGAAAAGAAGAACCCAGCTGCACCTATTTCAG 1125
||||| | | ||||| ||||| ||||| ||||| ||
Db 126 CACGCCCAAAAGCATTTTGAGAAAAGAAGAACCCAGCTGCACCTATTCAG 73

RESULT 20
BF962769

LOCUS	BF962769	515 bp	mRNA	linear	EST	42-UN-200
DEFINITION	QV2-NN0045-181200-560-b10	NN0045	Homo sapiens	CDNA,	mRNA	sequence.
ACCESSION	BF962769					
VERSION	BF962769.1	GI:12380044				

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 515)

Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., ...

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=qv2&t2=qv2-NN0045>)
181200-560-b10&t3=2000-12-18&t4=1)

Seq primer: puc 18 forward	
High quality sequence stop: 73.	
Location/Qualifiers	
1..515	
FEATURES	
source	

DB	602	TACGGGACAGTAGCCCC	620
RESULT 22			
LOCUS	A1589812	634 bp	mRNA
DEFINITION	A1589812	tm4f08.x1	NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2163879 3'
ACCESSION	A1589812		similar to YR:Q99454 Q99454 HNSPC.1; mRNA sequence.
VERSION	A1589812.1	GI:4598860	EST.
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 634)		
TITLE	NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index		
JOURNAL	Unpublished (1998)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnlnl.gov/bdnp/image/image.html Insert length: 1063 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 457 POLYA-No.		
FEATURES			
Source	Location/Qualifiers		
	1..634		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2163879"		
	/clone_idb="NCI-CGAP_Brn25"		
	/tissue_type="anaplastic oligodendroglioma"		
	/ldb_host="DH10B"		
	/note="Organ: brain; Vector: pTR13D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGATGACGTGAGGAGGCGCATAGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	99 a 190 c 187 g 154 t 4 others		
ORIGIN			
Query Match	10.8%; Score 298.8; DB 9; Length 634;		
Best Local Similarity	68.0%; Pred. No. 4.6e-59;		
Matches 414; Conservative	0; Mismatches 195; Indels 0; Gaps 0;		
Y	369 CGGCTGGGCGCTTCAATCAACAGCGCTTTGCTGCTTCTGCTTGGTGGATTTT 428		
Db	1 CGGCTGGGCGCTTCAATCAACAGCGCTTTGCTGCTTCTGCTTGGTGGATTTT 60		
Y	429 GTCAGTGTTCATCAACATCCCTGAGCGACACAAATTTGGCTCAAGTTCCTTGATCT 488		
Db	61 GTCGTGTTCATCAACATCCCTGAGCGAGTTCGAGAGAGCTCGAGGGGCGCTTCAATCT 120		
Y	489 GGAATTCGTGATGATTTGCTCTTTGGTTGGATTCATTCGATTCGTGTCGGG 548		
Db	121 GGAATTCGTGATTCGTGTTGGCTGCGAGATTCGTGCGATTCGCGCGAGG 180		
Y	549 TTGCTGTTCATATAGAGATGCGACAGGACAGCTAGTTTCTTCGAAAGCCCTTCTG 608		

Db	181	CTGCTGCTGC	CGGATACCTGGCTGAGGGGGGGCTCAAGTTTGGCCCGGAACCGTTCTG	240		
Qy	609	TGTTATAGAT	ACCAATTGTTCTTATCGCTTCAATAGCAAGTTGTTTGGCAAAAATCAGAG	668		
Db	241	TGTGTTGACAT	CANAGTGTCTCATCGCTCCATTCGGGTGGCGCCGGGCTCCACAGG	300		
Qy	669	TAATATTTT	GGCAGCTGCAACACAGAAAGTCTCCGTTTCTACAGATCCTCCGATAGT	728		
Db	301	CAAGCTTTT	GGCCACATCTGCGTCCGAGCGCTGGCTTCCTCGCAATTCGGCGGATAT	360		
Qy	729	GCGCATGAC	CGGAAGGGGAGGCACTTGGAAATTA	CTGGGTTCAAGGTTTATGTCACAG	788	
Db	361	CCGATGAG	ACCGGGGAGTGAGCACTGGAAAGCTGCTGGGCTCTG	TGGTCTATGGCCACAG	420	
Qy	789	CAAGAAAT	TAATACAGAGCTGTGATACATAGAAATTTTGGTCTCTTAATTTTGGCTCTTCC	848		
Db	421	CAAGAGCT	GTGCTACTGCTGTACATGCTGTACATGGGCTTCCTTGTCTCAATCCCGGCTGTTCT	480		
Qy	849	TGCTATCT	TGCTGGAAAAAGATGCCAATTAAGAGTTTCTACATATGACAGATGCTCTGTG	908		
Db	481	GGTGTACT	TGGCAGAGAGAGAGAAAGCACCACTNTACACACTTAACGGGAGTACCTGTG	540		
Qy	909	GTGGGGCA	CAATTACATTGACAACTATTGGCTAATGAGACAAAAC	TCCCTTA	CTTGCT	968
Db	541	GTTGNGCT	GTATCAACGCTGACACCACTGGCTACAGTGTACACAAGTAATCC	CCAGACCTGGAA	600	
Qy	969	GGGAAGAT	T	977		
Db	601	CGCAGGCT		609		

```

RESULT 23
BE260338
LOCUS
DEFINITION
601151405F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507553 5',
mRNA sequence.
ACCESSION
BE260338
VERSION
BE260338.1 GI:9131523
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 597)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapds@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: L1CM187 row: 3 column: 02
High quality sequence stop: 597.
Location/Qualifiers
1. 597
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3507553"
/clone_id="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Brain; Vector: pOTS7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```


Db 184 CGAAGAGCTCTGCTCAGCCCTGCTTGGCTTCATTCAGATCCACACTTTTGAATGT 243

QY 1927 GAACAGATCTGACTATCAAG 1949
|||||

Db 244 GAACAGATCTGACTATCAAG 266

RESULT 28
LOCUS A1968605
DEFINITION A1968605 541 bp mRNA linear EST 09-MAR-2000
w90e010.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2514762 3'
similar to TR:Q99454 Q99454 HNSPC.; mRNA sequence.
ACCESSION A1968605
VERSION A1968605.1 GI:5765423
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 541)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D., Bento Soares, Ph.D., M. Fatima
Bonaldio, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldio, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbp/image/image.html
Insert Length: 1029 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 382.
location/Qualifiers
1. 541
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2514762"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldio. "
BASE COUNT 84 a 157 c 173 g 127 t
ORIGIN

Query Match 9.3%; Score 256.8; DB 9; Length 541;
Best Local Similarity 67.2%; Pred. No. 3e-49;
Matches 363; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 418 TGCCTGATTTGTGCTGTTTCTACACCTCGAGACACAAATTTGGCCCTCAAGTGC 477
|||||

Db 2 TGCCTGCTGCTGCTGCTGTTTCCACATCAAGAGACTATGAGAGAGCTGGAGGGGCC 61
|||||

QY 478 CTCCTGATCTGAGATCTGATGATTTGCTCTTTGTTGGAGTTCAATTCGATC 537
|||||

Db 62 CTCCTGATCTGAGATCTGATGATTTGCTCTTTGTTGGAGTTCAATTCGATC 121
|||||

QY 538 TGGTCTGGGGTCTGCTGTTTGTGATATAGAGATGCGAAGAACTAGAGTTGCTCGA 597
|||||

Db 122 TGGCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
|||||

QY 598 AAGCCCTTCTGTTATAGATACATTTCTTATCCGTTCAAGACAGTTGTTCTGCA 657
|||||

Db 182 AAACGCTTCTGTTATAGATACATTTCTTATCCGTTCAAGACAGTTGTTCTGCA 241
|||||

QY 658 AAACCTCAGGGTAAATATTTTGGCAGCTCTGCACTCAGAGCTCTGTTCTCAGATC 717
|||||

Db 242 GGCTCCAGGAGCAACGTCTTGTCCACATCTCGCTCCGAGACCTGCTCTCCGACAT 301
|||||

QY 718 CTCGCAATGTTGGCCATGAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 777
|||||

Db 302 CTGGGATGATCCCATGAGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361
|||||

QY 778 TATGCTCAGCAGCAAGATTAATATCAGAGCTTGTGATAGATTTTGTCTTATTTT 837
|||||

Db 362 TATGCCACAGCAGCAAGAGAGCTGTGATCTGCTGATCATCGGCTTCTGCTCATCCG 421
|||||

QY 838 TCGTCTTCTGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
|||||

Db 422 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
|||||

QY 898 GATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
|||||

Db 482 GATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
|||||

RESULT 29
LOCUS BB635544
DEFINITION BB635544 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus CDNA clone AA30075J21 5', mRNA sequence.
ACCESSION BB635544
VERSION BB635544.1 GI:15400758
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 626)
Arai, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koude
, M., Koyama, S., Matsuyama, T., Miyazaki, K., Nomura, K., Ono, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arai, K., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshihide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
ur:ftp://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a


```

Db      87  TTAATGAATTTTCAGTTCGCAAAACGAGATTAA-GAAACATTACGTCATATGATGTAA 29
Qy      1613 AAGATGTCATTGACA 1628
Db      28  AAGATGTCATTGACA 13

RESULT 31
A1517016
LOCUS   A1517016 771 bp mRNA linear EST 19-APR-2001
DEFINITION GH27636.5,prime GH Drosophila melanogaster head pot2 Drosophila
            melanogaster cDNA clone GH27636 5prime, mRNA sequence.
ACCESSION A1517016
VERSION   A1517016.1 GI:4420116
KEYWORDS EST.
SOURCE    fruit fly.
ORGANISM  Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
            1 (bases 1 to 771)
            Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
            BDGP/HMT Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic sequence AC005974
            Plate: 276 row: C column: 12
            High quality sequence stop: 553.
            Location/Qualifiers
                1..771
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone="GH27636"
                /clone_lib="GH Drosophila melanogaster head pot2"
                /sex="male and female"
                /dev_stage="adult"
                /lab_host="DH5 - alpha"
                /note="Organ: head; Vector: pot2; Site:1: EcoRI; Site:2:
                XhoI; Sized fractionated cDNAs were directly ligated into
                pot2. Plasmid cDNA library."
BASE COUNT 163 a 200 c 213 g 194 t 1 others
ORIGIN
Query Match 8.7%; Score 241; DB 9; Length 771;
Best Local Similarity 61.9%; Pred. No.1.5e-45;
Matches 415; Conservative 0; Mismatches 251; Indels 4; Gaps 2;

Qy      295 AGCCAGAGCTGCACGCGACGTCAGTACGCGCGGTGCAGACACTCTGTACACGTG 354
Db      103 AACCGCGCACCGCGCGGTGTGCGTACCGCGCGCTCCAGAGTCCCTACACACTTC 162
Qy      355 CTGAGAGAGACCCCGCGCTG---CGCTTCATCTACACAGCTTTGCTTTCTCCTTGC 411
Db      163 CTGAGAGCGCGCGCGCTCCACCGCATCTTCTACAGTATGATGATATCTCGATGCG 222
Qy      412 TTTCGTTGCTTATGTTGTCTACGTGTTTCTACATCCCTGAGACACAAATTTGGCTCA 471
Db      223 TTTCACCTGCTGCGCGCTCAGTGTGTCTTTCACCATCAAGAGATACCAAGAGCGCGTC 282
Qy      472 AGTTGCTCTTGATCTGAGTTCGTGATGATGTGCTCTTTGGTTGGAGTTTCATCATT 531
Db      283 TACATTCGTTCCGATGAGATCCTGGTGTTATCTGTTCAACATGAGATTGGAGCT 342
Qy      532 CGAATCTGCTGCGCGGTGCTGCTGTGATATAGAGATGCGCAAGAGACGAGAGTTT 591
Db      343 CGACTCTGCTCATGCGCTCGCATGCGATACAGGAGATGCTGGTGCAGCTGAGAGTTTC 402

```

```

Qy      592 GCTCGAAGACCCCTCTGTTATAGATACATGTTGTTCTATCGCTTCAATAGCAATGTT 651
Db      403 GTGAGGACCATTTCTGTATATATATATATGATATGTCACACATTTTACGCTCATTTGATATA 462
Qy      652 TCTGCAAAAACCTGAGGTAATATTTTGGCAGCTGTCACATCAGAAAGTCCGTTTCTCA 711
Db      463 GGAATGGGACCTCGGGCCAGGTGTCGACAGAGTGTCTTACGTCGCTCGGATCTCTT 522
Qy      712 CAGATCTCTCGCATGTCGTCATGATGACCGAAGGAGGAGGCACTTGGAAATTTACTGGCTCA 771
Db      523 CAGATCTCTTGGAGTGGCGCATGATGATCGGGGACGACCTGGAACTGCTCGGCTCG 582
Qy      772 GTGTTATGCTCTACAGCAAGAAATTAATACACCTTGTACATATGATTTTGGTCTT 831
Db      583 GTTGTATACGACACATACAGAGAACTGATACACACATGATACATGATGATGATGATGAT 642
Qy      832 ATTTTTCGTCCTTCTGCTATCTATCTGATGAGAAAGATGCCAATTAAGATTTTCTACA 891
Db      643 ATCTTTCATCATCTCTGCTATATGTTGAGAGAGACGTCATGATGATGATGATGATGAT 702
Qy      892 TATGCAATGCTCTCTGTCGTCGTCATGATGATGATGATGATGATGATGATGATGATGAT 951
Db      703 TTGCGCCAGCGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 761
Qy      952 ACTCCCTTAA 961
Db      762 GTGCCCATCA 771

```

```

RESULT 32
A1418222
LOCUS   A1418222 502 bp mRNA linear EST 30-MAR-1999
DEFINITION t74803.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2104972 3'
            similar to TR:Q99454 Q99454 HNSPC.; mRNA sequence.
ACCESSION A1418222
VERSION   A1418222.1 GI:4264153
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 502)
            NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BrCAP), Tumor Gene Index
            Unpublished (1998)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonafido, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA sequencing by: Washington University Genome Sequencing Center
            clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNI at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1080 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 322.
            Location/Qualifiers
                1..502
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2104972"
                /clone_lib="NCI CGAP Brn23"
                /tissue_type="gliblastoma (pooled)"
                /lab_host="DH10B"
                /note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
                modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'

```


1. :766

CDS

233 a 154 c 172 g 207 f

Cons

TTCAGG

GCAGT

TCGST

1111

— — — — —

R-GO-1

tus n

ma l i a

COMMENT

FEATURES

IN

tches

35 LT

WORDS

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
human.	Human sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 469)	NCBI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index	Unpublished (1998)
Ph.D.	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	CDNA Library Arrayed by: Greg Lennon, Ph.D.	DNA Sequencing by: Washington University Genome Sequencing Center	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrp/Image/Image.html	Insert Length: 1048	Std Error: 0.00
Seq primer: -400P	from Glbco	High quality sequence stop: 454.	Location/Qualifiers	1..469	/organism="Homo sapiens"	/db_xref="taxon:9606"
/clone="IMAGE:2428714"	/clone_11b="NCI CGAP_Brn25"	/tissue.type="neoplastic oligodendrogloma"	/lab_host="DH10B"	/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer 15' TCTTACCAATCGTAGGCGGCGGCAGATGTTTTTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT	64 a	136 c	148 g	121 t		
ORIGIN						
Query Match	7.98;	Score 217.8;	DB 9;	Length 469;		
Best Local Similarity	69.38;	Pred. No. 3.8e-40;				
Matches 325;	Conservative 0;	Mismatches 142;	Indels 2;	Gaps 2;		
364	CCCCGCGGTGGCGCTCATCTACACACGCTTCTTTCTTCCTGCTCTTGCTGCTG	423				
Db 1	CCGCGCGGTGGCGCTCATCTACACATCTCCATCGTGTCCCTCGTTTCTTCCTGCTC	60				
424	ATTTTGTGAGTATTTTCTACATCCCGAGAGACACAAATTTGGCCTCAAGTTGCCCTTG	483				
Db 61	GTGCTGTCTGTCTTTTCCACATCAAGAGATATAGAAAGAGCTCGAGGGGCGCCCTTAC	120				
484	ATCTGAGTTCTGATGATTTGTCGCTTTGTTTGGAGTTTCATCATTCGAATCTGCTCT	543				
Db 121	ATCTGGAATATGCTGACTATCGGTGTGTGGCTGTGAGTACTGTGGGATCTGGGCG	180				
544	GGGGTTCCTGTTCATATAGAGATGCGAAGAGACGTGAGTTGCTGTGAAGCCG	603				
Db 181	CGAGGCTGCTGTGCGGTACCGTGTGAGGGGGGCGCTCAAGTTGCCGGAACCG	240				
604	TTCTGTATATGATACATTTGTTCTTATGCTTCATATAGAGATGTTTCTGCAAAACT	663				
Db 241	TTCTGTATGATGATCATGTGTGTCTATGCTTCATATGAGATGTTTCTGCAAAACT	300				
664	CAGGTAATATTTTGGCAGCTGTGACTGAGAAGTCTCCGTTTCTACAGATCTCCGC	723				
Db 301	CAGGCAACGCTTTTGGCAGATCTGTGCTCGGAGCGCTCGGCTTCTGCAAGTTCTGGG	360				
724	ATGTTGCGCATGAGACGGAAGGAGGACCTTGGAAATTAATCTGGGTC-AGTGGTTTATGC	782				

[illegible]

Db 535 CGGCTTCCTTGTCTCATCTGCGCTCGTCTGCTGTACTTGCCAGACAGAGGGGAGAA 476
 Qy 876 TAAAGAGTTTCTACATATGAGATGCTCTGTGTGGGACACATTACATTCACACTAT 935
 Db 475 CGACCACCTTTACACACCTACGGGATGCACTGTGTGGGCTGTACACCTGTACCCAT 416
 Qy 936 TGGCTATGAGACAAACTCCCTTACTTGGCTGGAGATTGCTTTCTGCAGGCTTTGC 995
 Db 415 TGGTACGGGAGCAAGTACCCCGACAGCTGTGACAGCTTGTGCGCAACCTTAC 356
 Qy 996 ACCTCTGGACATTCCTTCTTGTGACCTTCCTGCGGACATTCCTGCTCAGATTTCAT 1055
 Db 355 CCTATCGGTCTCTCTTCTTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296
 Qy 1056 AAAAGTACAGACACACCGCCAGAACTTTGAGAAAGAGAACCCAGCTGCCAA 1115
 Db 295 GAAGTTTCAGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 236
 Qy 1116 CCTATTCAGTGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1145
 Db 235 CCTGATCCAGTCGGCTGAGATTTTACGC 206

RESULT 37

LOCUS A1576388 300 bp mRNA linear EST 05-APR-1999
 DEFINITION UI-R-YO-vm-b-07-0-UI.s1 UI-R-YO Rattus norvegicus cDNA clone
 UI-R-YO-vm-b-07-0-UI 3', mRNA sequence.

ACCESSION A1576388
 VERSION A1576388.1 GI:4560764
 KEYWORDS EST.
 SOURCE Norway rat.

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 300)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL discovery
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 COMMENT 97044477

CONTACT: Soares, MB
 PROGRAM: Rat Gene Discovery and Mapping
 UNIVERSITY: University of Iowa
 ADDRESS: 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 TEL: 319 335 8250
 FAX: 319 335 9565
 EMAIL: msoares@blue.weeg.uiowa.edu
 Oligo-dT track not found. Not a site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 37-71,
 >GC-rich#low complexity
 Seq primer: M13 Forward
 Location/Qualifiers
 1..300
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-YO-vm-b-07-0-UI"
 /clone_11b="UI-R-YO"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-YO
 library is a subtracted library derived from an
 individually-tagged normalized whole-eye (minus the lens)
 library. The driver for the subtraction consisted of a
 pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
 UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of

3-5 nucleotides present between the Not I site and the
 oligo-dT track which allows identification of the library
 of origin of a clone within the mixture. The subtracted
 library (UI-R-YO) was constructed as follows: PCR
 amplified cDNA inserts from previous library clones from
 which 3' ESTs had been derived were used as a driver in a
 hybridization with the normalized whole-eye library in
 the form of single-stranded circles. The remaining
 single-stranded circles (subtracted library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-YO
 library. This procedure has been previously described
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 1996).

BASE COUNT 44 a 106 c 109 g 38 t 1 others
 ORIGIN

Query Match 7.8%; Score 217.6; DB 9; Length 300;
 Best Local Similarity 92.0%; Pred. No. 4,1e-40;
 Matches 229; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 152 CAGCCGCCAGGCGGCGAGCGCTGCTACTGCTGGGACACCGCGGCGGACGCTGGGCG 211
 Db 1 CGCCCGCCAGGCGGCGAGCGCTGCTGCTGGGACACCGCGGCGGCGGCGGAG 60
 Qy 212 GCGGCGGCTGAGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 271
 Db 61 GCGGCGGCGGCTGAGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 Qy 272 GGAAGCCGCTCTTCTTACAGAGTACGAGCTGCGGCGGCGGCGGCGGCGGCGG 331
 Db 121 GGAAGCCGCTCTTCTTACAGAGTACGAGCTGCGGCGGCGGCGGCGGCGGCGG 180
 Qy 332 TGCAAGTACTCTTACAGAGTCTGCTGAGAGACCGCGGCGGCGGCGGCGGCGG 391
 Db 181 TGCAAGTACTCTTACAGAGTCTGCTGAGAGACCGCGGCGGCGGCGGCGGCGG 240
 Qy 392 CTTGCGTTT 400
 Db 241 GCTTGTGT 249

RESULT 38

LOCUS BQ285922 438 bp mRNA linear EST 14-MAY-2002
 DEFINITION IK23e09.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5781976 3'
 similar to TR:043796 043796 VOLTAGE GATED POTASSIUM CHANNEL. [2]
 TR:043526 ; mRNA sequence.

ACCESSION BQ285922
 VERSION BQ285922.1 GI:20654890
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 438)
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,D., Cardenas
 , M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE Other_ESTs: IK23e09.Y1
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

TEL: 617-495-1812
 FAX: 617-495-8557


```

Db      122 TGGGGCCGACGGGCTGCTCCGCTACCGCTGGGCTGGAGGGGGCGCTCAAGTTGCCCCG 181
OY      598 AAGCCCTTGTGTTTATGATACCATTTGTTTCTTATCCCTTAATAGCAGTGTCTTGCA 657
Db      132 AAACGGTCTGTGTATGATCATCATGCTCTCATCCCTTCAATGCGCTGCGCCGC 241
OY      658 AAACCTCAGCGTAAATTTTGGCCAGCTCTGACCTAGAACTCCGTTCTTCTACAGATC 717
Db      242 GGCTCCACAGGCAAGCTCTTGGCACATCTGCGCTCCGGAGCCCTGCGCTCTGAGATT 301
OY      718 CTCGGCATGTGGCGCATGAGACGGAAGGGAGCGCATTTGAAATTTACTGGGTTCAGTGT 777
Db      302 CTGCGGATGATCCGATGACCGCGCGGGGCGGACCTGGAAGCTGTGCGCTGTGTGTC 361
OY      778 TATGCTCAGCAGCAAGAAATTAATCAGACGTTGATACATAGGATT 821
Db      362 TATGCGCCACAGCAAGGAGCTGTGCTACTGCTGTGATCATCGGCTT 405

RESULT 42
AV838434/C 448 bp mRNA linear EST 07-NOV-2001
LOCUS      AV838434 Nori Satoh unpublished cDNA library, egg cDNA
DEFINITION Intestinalis cDNA clone rc1eg03115, mRNA sequence.
ACCESSION  AV838434
VERSION     AV838434.1 GI:16782585
KEYWORDS   EST.
SOURCE      Ciona intestinalis.
ORGANISM   Ciona intestinalis.
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Clonidae; Ciona.
REFERENCE   1 (bases 1 to 448)
AUTHORS    Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
TITLE      Expressed genes in Ciona intestinalis
JOURNAL     Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@esclidian.zool.kyoto-u.ac.jp.
FEATURES   Location/Qualifiers
            source          1..448
                        /organism="Ciona intestinalis"
                        /db_xref="taxon:7719"
                        /clone="rc1eg03115"
                        /clone_lib="Nori Satoh unpublished cDNA library, egg"
                        /tissue_type="whole animal"
                        /dev_stage="egg"
                        /note="Vector: pBluescript SK"
BASE COUNT 132 a 110 c 81 g 125 t
ORIGIN
Query Match 73% Score 202; DB 10; Length 448;
Best Local Similarity 68.2%; Pred. No. 1.9e-36;
Matches 296; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

OY      726 GGTCCGATGACGACGAGGAGGAGCACTTGAATTTACTGAGTTGTTTATGCTCA 785
Db      434 GGTATAGATGACAGAGAGAGAGGATCATGAAAGTTTATCTTCTGTTTATGAGCTCA 375
OY      786 CAGCAAGAAATTAATCAGACGTTGTATACATGAGATTTTGTCTTATTTTTCGCTTT 845
Db      374 CAGTAAAGATTGATACAGCATGATGATTTGCTTCCTGCGCTCATATTTGCTTGT 315
OY      846 CCTGTCTATCTGCGGAAAGATG---CAATTAAGAGTTTCTTACATATGACATGC 902
Db      314 TCTTGTCTATCAAGCAAGAAAGATGAAACCAAGATTTTGAACCTTTTGGCGATGC 255
OY      903 TCTCTGTGGGCGCAATTAATCATCTATTTGCTTGTGAGACAAACTCCCGTAAC 962
            TCTCTGTGGGCGCAATTAATCATCTATTTGCTTGTGAGACAAACTCCCGTAAC 962

```

```

Db      254 CTATATGTTGGGATTTGATACACCTTGACACCATCGGGTACGGAGAAAGTTCCATC 195
OY      963 TTGGCTGGGAAGATTGCTTTCTGACAGCTTTGCACTCCTTGCATTTCTTTGCACT 1022
Db      194 ATGGCTGGGTCGTAAATAGCAAGTGTATTTGCAATTTCTGGAATTTCTATTTTTCCT 135
OY      1023 TCCGCGCGGCACTTTGCGCTGAGTTTGTGCAATTAAGTACAAAGAACACCGCCAGAA 1082
Db      134 ACCAGCGGGAATTTCTGGGTTCAAGATTTCCTTTAAAGTTTCAGAACAAACCGTCAGAA 75
OY      1083 ACACCTTTAGAAAAGAAAGAACCAAGCTGCCAACCTTCATTCATGTGTGCTGAGTTA 1142
Db      74 GCATTTGCTGTCGACGAGAAATGCGCGCCGCTATTTATATACATGATGTGGGAGATT 15
OY      1143 CGCAGCTGATGAGA 1156
Db      14 TGCTGGCGATMAAA 1

RESULT 43
BE257127 622 bp mRNA linear EST 13-JUL-2000
LOCUS      BE257127 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349625 5',
DEFINITION mRNA sequence.
ACCESSION  BE257127
VERSION     BE257127.1 GI:9127597
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 622)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LHCMI44 row: e column: 18
            High quality sequence stop: 621.
FEATURES   Location/Qualifiers
            source          1..622
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:3349625"
                        /clone_lib="NIH_MGC_16"
                        /tissue_type="retinoblastoma"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally
                        cloned into EcoRI/XhoI sites using the following 5'
                        adaptor: GGCACGAG(G). Library constructed by Ling Hong
                        in the laboratory of Gerald M. Rubin (University of
                        California, Berkeley) using ZAP-cDNA synthesis kit
                        (Stratagene) and Superscript II RT (Life Technologies).
                        Note: This is a NIH_MGC Library."
BASE COUNT 93 a 205 c 207 g 117 t
ORIGIN
Query Match 72% Score 200.8; DB 10; Length 622;
Best Local Similarity 61.1%; Pred. No. 3.7e-36;
Matches 325; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

OY      169 GGCCTGCTACTGCTGGGCAACCCGCGGCGACAGCTCGTGGCGGCGGTGAGG 228
Db      91 GGCTTGTGTGGGTGAGACCCCGGCGCGGCGGACATCCAGCGGAGCGGCGCTGTATC 150
OY      229 GAGAGCCGCGGGGCAAGCAGGGGGGCCGGATGAGCTCTGTGGGAAAGCCGCTCTTAC 288

```


CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M3 Reverse.

FEATURES

Source

Location/Qualifiers
1. 232
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-AL1-ahk-e-04-0-UT"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7AD-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH-BMAP-MCO-N library is a normalized library constructed
from mouse cortex. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Anne Novakovich, Zivic-Miller
Laboratories."

BASE COUNT 61 a 57 c 57 g 57 t
ORIGIN

Query Match 6.9%; Score 192; DB 12; Length 232;
Best Local Similarity 89.2%; Pred. No. 3.8e-34;

Matches 207; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2239 AGCATTTCTGACGTACCACTGCTGTTGCTTCCCAAGAAATGTTACAGTTGCACAG 2358

DB 1 AGATTTCGTGATGTCACCACTGCTGTTGCTTCCCAAGAAATGTTACAGTTGCACAG 60

QY 2359 TCAATCTCAGCAGACCGTCTATGAGAGAAAGCTTGCATGAGGAGGAAACTGTG 2418

DB 61 TCAACCTGACCAAGACCGTCTATGAGAGAAAGCTTGCATGAGGAGGAAACTGTG 120

QY 2419 TTGCTGCTCTGCTCCATGCTGCGAGAGACTTGGCAATCTTGTCTGTGCAAAACCTG 2478

DB 121 TTGCTGCTGCTCCATGCTGCGAGAGACTTGGCAATCTTGTCTGTGCAAAACCTG 180

QY 2479 ATCAGCTGACGAGAGACTGATATACACTTTCAGGAGTGAAGTCAAGTG 2530

DB 181 ATCAGCTGACGAGAGACTGATATACACTTTCAGGAGTGAAGTCAAGTG 232

RESULT 46

BE703020

LOCUS BE703020 537 bp mRNA linear EST 12-SEP-2000

DEFINITION RC5-NN1089-290600-032-G10 NN1089 Homo sapiens CDNA, mRNA sequence.

ACCESSION BE703020

VERSION BE703020.1 GI:10090762

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=62-RC5-NN1089-290

600-032-610<3-2000-06-29<4-1)

Seq primer: puc 18 forward

High quality sequence stop: 432.

FEATURES

Source

Location/Qualifiers
1. 537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1089"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 93 a 161 c 169 g 114 t
ORIGIN

Query Match 6.9%; Score 191.2; DB 12; Length 537;
Best Local Similarity 68.3%; Pred. No. 6.4e-34;

Matches 265; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 738 CCGAAGGGGAGGACACTTGAATTAATGAGTTCAGTGGTTATGCTACAGAGAGAAAT 797

DB 8 CCGGGCGTGAGGACACCGAAGCGTGGCTGTGTATGCGCCACAGAGAGAGCT 67

QY 798 AATCAGACGCTTGTGATATGAGATTTTGGTCTTATTTTTCGCTTTCCTGTATCT 857

DB 68 GGTCACTGCTTGGGACATCGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127

QY 858 GGTGAAGAGATGCGCAATTAAGATTTTACATATGACATGCTGCTGCTGGGCGAC 917

DB 128 GGCAGAGAGAGGAGAGAGACGACCTTGTACACCTACCGGATGACCTGTGGGGCCT 187

QY 918 AATTACATTGACACTTATGCTATGAGACAAATCCCTAATCTTGGCTGGGAATTT 977

DB 188 GATCAGCGCTGACCAACCACTTGGCTGACGAGACAAAGTACCAGAGCTGGAAGGAGCT 247

QY 978 GCTTTTGCAGGCTTTCGATCTCTTGGCATTTCTTCTTGTGACCTCTCCGCGATCT 1037

DB 248 CTTTGGGCGCAACCTTCACTCATCGGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 307

QY 1038 TGCGTCAAGTTTGCATTAAGATTAAGAACACCGGACGAGAACACTTGAAGAA 1097

DB 308 GGGGTCTGGGTTTGGCTTGAAGGTTTCAGAGACGACGAGGAGAACTTTGAGAGAG 367

QY 1098 AAGGAACCGACGCTGCCAATCTCATTTAG 1125

DB 368 GCGGAACCGGCGAGGACGCTCATTCAG 395

RESULT 47

BE675840

LOCUS BE675840 679 bp mRNA linear EST 08-SEP-2000

DEFINITION 7F17A09, x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3794904 3'

similar to TR:060607 060607 SLOW DELAYED RECTIFIER CHANNEL SUBUNIT.

; contains PTRS: t3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION BE675840

VERSION BE675840.1 GI:10036381

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Search completed: June 19, 2003, 11:07:39
 Job time : 3488 secs

```

ACCESSION   BO340041
VERSION     BO340041.1
KEYWORDS    GI:21000357
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 297)
            Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&tl2=QV2-NN0045-
            261200-569-b11&tl3=2000-12-26&tl4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 50.
            Location/Qualifiers
                1..297
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="NN0045"
                /dev_stage="Adult"
                /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
            BASE COUNT      82 a      73 c      69 g      73 t
            ORIGIN
            Query Match      6.7%; Score 185.4; DB 14; Length 297;
            Best local Similarity 82.1%; Pred. No. 1.4e-32;
            Matches 239; Conservative 0; Mismatches 46; Indels 6; Gaps 2;

QY      1674 TCAACAGCGTGTGATCAATTCCTTGGAAGGGCAATCAGATCAGATA-----AGAAG 1728
DB      1 TCATACACGCTGTGATCAATTCCTTGGAATGCGGCATCTCGACTATCAGATAGTAGAAG 60
QY      1729 AGCCGAGAGAAATTAACAGCAGCAATGAGA-CCAGAGACATCTCAGTATGCTGGTCG 1787
DB      61 AGCCGAGAGAGCATGACTGCAGAGAGAGAGAGCCCAATTAATCTCAGATGCCAGTCC 120
QY      1788 GGTGGTCAAGGTGAAAAAGAGTAGACATGATCCAAAGCTGAGCTGCTACTAGTA 1847
DB      121 GTTGCTCTGGGTTAGCAATAGTAGTAGTCCATAGAAATCCAAAGCTGAGCTGCTACTAGA 180
QY      1848 CATCTATCAACAGCTCTTGGAAGAGCTGCTCAGCCCTCGCTTGGCTTCATTCCA 1907
DB      181 CATCTATCAACAGCTCTTGGAAGAGCTGCTCAGCCCTCGCTTGGCTTCATTCCA 240
QY      1908 GATCCCACTTTGATGATGTAACAGACATGCACTATCAAGCCCTGTGA 1958
DB      241 GATCCCACTTTGATGATGTAACAGACATGCACTATCAAGCCCTGTGA 291

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 04:47:16 ; Search time 595 Seconds
(without alignments)
10491.663 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772
Sequence: 1 atgcccgcaccacacgcggyg.....ctcatcgtcaactgaataa 2772

Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%

Listing first 150 summaries

Database :

N_Geneseq_101002:*

- 1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2772	100.0	2772	22	AAH43633
2	2772	100.0	3111	22	AAH43634
3	2723.8	98.3	3074	22	AAH49499
4	2662.2	96.0	2667	22	AAH49499
5	2635.4	95.1	3071	22	AAH49499
6	2630	94.9	3137	22	AAH49499
7	2625.2	94.7	2694	24	AAH49499
8	2625.2	94.7	2694	24	AAH49499
9	2523.2	91.0	3718	21	AAH49499

10	965	34.8	125910	21	AAH49499	Human KCNQ5 (KCN6g)
11	498.6	18.0	548	24	ABA590234	Human ORF41 coding
12	492.4	17.8	2273	20	AAH57140	Mouse KCNQ2 CDNA.
13	492	17.7	2335	21	AAH47618	KCNQ4 potassium ch
14	478.6	17.3	2159	20	AAH26588	Nucleotide sequenc
15	452.6	16.3	7413	23	AAH74832	DNA encoding novel
16	451.4	16.3	3195	23	AAH74831	DNA encoding novel
17	447	16.1	2565	20	AAH81548	Human brain-derive
18	438.2	15.8	2914	20	AAH57059	Human KCNQ3 CDNA.
19	436.6	15.8	3029	20	AAH81547	Human brain-derive
20	432	15.6	2814	20	AAH57141	Mouse KCNQ3 CDNA.
21	429.4	15.5	1425	24	ABK64418	Human benign prost
22	429.4	15.5	3232	20	AAH57057	Human KCNQ2 CDNA.
23	429.4	15.5	3237	20	AAH57145	Human mutant KCNQ2
24	429	15.5	3232	20	AAH574830	DNA encoding novel
25	428.8	15.5	2565	20	AAH26589	Nucleotide sequenc
26	428.4	15.5	3287	20	AAH26587	Nucleotide sequenc
27	425	15.3	1182	18	ABH85964	Human K+ channel g
28	410.8	14.8	414	24	ABH24166	Human ORF polynuc
29	372	13.4	2900	22	AAH99526	Human protein enco
30	372	13.4	2911	23	AAH73267	DNA encoding novel
31	372	13.4	4154	23	AAH83921	DNA encoding novel
32	331	11.9	735	20	AAH26589	Nucleotide sequenc
33	312.4	11.3	1320	23	AAH73266	DNA encoding novel
34	312.4	11.3	1320	23	AAH83917	DNA encoding novel
35	307.6	11.1	1566	23	AAH567245	DNA encoding novel
36	307.6	11.1	1566	23	AAH567245	DNA encoding novel
37	285.4	10.3	1280	23	ABH28585	Drosophila melanog
38	267.8	9.7	2028	22	AAH30824	Human KVLQT1 gene.
39	267.8	9.7	3181	21	AAH90659	Human KVLQT1 prote
40	267.8	9.7	3181	21	AAH90659	Human long QT synd
41	267.8	9.7	3181	21	AAH89911	Human KVLQT1 codin
42	266.6	9.6	2744	22	AAH89984	Mutant human KVLQT
43	266.6	9.6	2831	18	AAH94004	Human encoding human
44	266.6	9.6	2831	18	AAH90730	Human KVLQT1 full-
45	266.6	9.6	2821	22	ABH86861	Gene #3359 used to
46	258.4	9.3	3182	22	AAH89911	Mutant human KVLQT
47	231	8.3	3335	23	AAH94798	Human full-length
48	208.4	7.5	788	22	AAH92009	Human CDNA 5'-end
49	208.4	7.5	788	22	AAH93662	Human CDNA clone r
50	125.4	4.5	2121	23	AAH74833	DNA encoding novel
51	95.8	3.5	171	20	AAH57151	Human KCNQ2 intron
52	91.2	3.3	705	23	AAH73265	DNA encoding novel
53	90.8	3.3	942	23	AAH83915	DNA encoding novel
54	84.8	3.1	649	20	AAH57167	Human KCNQ3 intron
55	76.4	2.8	5310	23	ABH28584	Drosophila melanog
56	70.8	2.6	1410	23	ABH21467	Drosophila melanog
57	68.8	2.5	1021	20	AAH57176	Human KCNQ3 intron
58	68.2	2.5	1083	20	AAH57170	Human KCNQ3 intron
59	67	2.4	204	20	AAH57150	Human KCNQ2 intron
60	65	2.3	245	20	AAH57164	Human KCNQ3 intron
61	63.4	2.3	211	20	AAH57159	Human KCNQ2 intron
62	60.8	2.2	600	24	ABH52497	Oligonucleotide fo
63	60.8	2.2	600	24	ABH52497	Oligonucleotide fo
64	60.8	2.2	859	20	AAH57166	Human KCNQ3 intron
65	60	2.2	60	24	ABH52497	Human KCNQ3 intron
66	58.8	2.1	320	21	AAH38185	Human spliced tran
67	58.6	2.1	2188	20	AAH77506	Human ovarian tumo
68	58.4	2.1	320	21	AAH38183	Human KCNQ3 intron
69	58.4	2.1	461	24	ABH27494	Human KCNQ3 intron
70	58.4	2.1	1278	24	ABH27494	Human KCNQ3 intron
71	58.4	2.1	1844	24	ABH27494	Human KCNQ3 intron
72	58.4	2.1	2235	24	ABH27494	Human KCNQ3 intron
73	58.4	2.1	2235	24	ABH27494	Human KCNQ3 intron
74	58.4	2.1	2235	24	ABH27494	Human KCNQ3 intron
75	58.4	2.1	2235	24	ABH27494	Human KCNQ3 intron
76	57.4	2.1	1337	20	AAH17263	Human KCNQ3 intron
77	57.2	2.1	318	21	AAH38184	Human KCNQ3 intron
78	56.4	2.0	2106	20	AAH28103	Human KCNQ3 intron
79	56.4	2.0	3289	22	AAH28103	Human KCNQ3 intron
80	56.4	2.0	4158	24	ABH48985	Human KCNQ3 intron
81	56.4	2.0	6458	24	ABH48985	Human KCNQ3 intron
82	56.2	2.0	1117	20	AAH57169	Human KCNQ3 intron

181 CTGGGACCCGGGCGCACGCTCGGTGGGCGGCGGTGGCCCTGAGGAGAGCCGCGG 240
181 CTGGGACCCGGGCGCACGCTCGGTGGGCGGCGGTGGCCCTGAGGAGAGCCGCGG 240
241 GGCAGACAGGGGGCCGGATGAGCCCTGCTGGGAGAGCCGCTCTTACAGAGTAGCCAG 300
241 GGCAGACAGGGGGCCGGATGAGCCCTGCTGGGAGAGCCGCTCTTACAGAGTAGCCAG 300
301 AGCTGCGGGCGCACTCAAGTACCGGCGGGGTGCAAGACTGCTGACAGAGTGTGGAG 360
301 AGCTGCGGGCGCACTCAAGTACCGGCGGGGTGCAAGACTGCTGACAGAGTGTGGAG 360
361 AGACCCCGGGGCTGGGCGCTTCACTACCAAGCTTTCTTTCTCCCTTCTTGGTTGC 420
361 AGACCCCGGGGCTGGGCGCTTCACTACCAAGCTTTCTTTCTCCCTTCTTGGTTGC 420
421 TTGATTTTGTCAAGTCTTCTACCATCCCTGAGCACACAAATTTGGCTCAAGTTGCCTC 480
421 TTGATTTTGTCAAGTCTTCTACCATCCCTGAGCACACAAATTTGGCTCAAGTTGCCTC 480
481 TTGATCCTGAGAGTCTGATGATTTGCTGCTGTTGGTGGAGTTCATCATTCGATCTGG 540
481 TTGATCCTGAGAGTCTGATGATTTGCTGCTGTTGGTGGAGTTCATCATTCGATCTGG 540
541 TCTGGGCGGTGCTGTTGCTGATATAGAGATGGCAAGAGAGTGTGCTCGAAG 600
541 TCTGGGCGGTGCTGTTGCTGATATAGAGATGGCAAGAGAGTGTGCTCGAAG 600
601 CCTTCTGTGTATATAGATACATTTGTTCTATCGCTTCAATAGCAGTTGTTCTGCAAAA 660
601 CCTTCTGTGTATATAGATACATTTGTTCTATCGCTTCAATAGCAGTTGTTCTGCAAAA 660
661 ACTCAGGGAATTTTGGCAGCTCTGCACTCAGAACTCTCCCTTCTCTACATCTCTC 720
661 ACTCAGGGAATTTTGGCAGCTCTGCACTCAGAACTCTCCCTTCTCTACATCTCTC 720
721 CCGATGCTGCGATGAGACCGAAGGGGAGGACTTGAATTTACTGGGTTGAGTGTAT 780
721 CCGATGCTGCGATGAGACCGAAGGGGAGGACTTGAATTTACTGGGTTGAGTGTAT 780
781 GCTCAGCAGCAAGATTAATCAGACCTTGTATAGATAGATTTTGTCTTATTTTTCG 840
781 GCTCAGCAGCAAGATTAATCAGACCTTGTATAGATAGATTTTGTCTTATTTTTCG 840
841 TCTTCTCTGTCTATCTGCTGGGAAAGAGATGCCAATTAAGGTTTCTACATATGCAAT 900
841 TCTTCTCTGTCTATCTGCTGGGAAAGAGATGCCAATTAAGGTTTCTACATATGCAAT 900
901 GCTCTGTGGGGGCAATTTACATTTGACAATTTGGCTATGAGAGCAAACTCCCTTA 960
901 GCTCTGTGGGGGCAATTTACATTTGACAATTTGGCTATGAGAGCAAACTCCCTTA 960
961 ACTTGGCTGGGAAGATTTCTTCTGACAGCTTGTGACCTCTTGGCATTTCTTTTGA 1020
961 ACTTGGCTGGGAAGATTTCTTCTGACAGCTTGTGACCTCTTGGCATTTCTTTTGA 1020
1021 CTTCCTGCGGCGATTTCTTGGCTCAGGTTTGGCATTTAAAGTACAAAGAACACCGCCAG 1080
1021 CTTCCTGCGGCGATTTCTTGGCTCAGGTTTGGCATTTAAAGTACAAAGAACACCGCCAG 1080
1081 AAACACTTTGAGAAAGAAAGAACCCGCTGCAACCTCATTCAGTGTGTTGGGTAGT 1140
1081 AAACACTTTGAGAAAGAAAGAACCCGCTGCAACCTCATTCAGTGTGTTGGGTAGT 1140
1141 TAGCAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCACACTTGAAGCCCTTG 1200
1141 TAGCAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCACACTTGAAGCCCTTG 1200
1201 CACACCTGACGCCCTTACCAATCAGAGCTTAAGTTTAAAGAGCAAGTGGCTGATGC 1260
1201 CACACCTGACGCCCTTACCAATCAGAGCTTAAGTTTAAAGAGCAAGTGGCTGATGC 1260

1261 CCCAGGGCCAGAGTATTAAAGAGCCGACAAAGCTCAGTAGTGACAGAGGTCCCAAGC 1320
1261 CCCAGGGCCAGAGTATTAAAGAGCCGACAAAGCTCAGTAGTGACAGAGGTCCCAAGC 1320
1321 ACCGACATCAGAGCCGAGGCGAGTCCACCAAGTGCAGAAAGCTGTGAGCTTCAACGAC 1380
1321 ACCGACATCAGAGCCGAGGCGAGTCCACCAAGTGCAGAAAGCTGTGAGCTTCAACGAC 1380
1381 GGAACCCGCTTCCGGCCCTCGGCTGCGGCTCAAAAAGTTCTCAGCAAAAACCATGATGAT 1440
1381 GGAACCCGCTTCCGGCCCTCGGCTGCGGCTCAAAAAGTTCTCAGCAAAAACCATGATGAT 1440
1441 GCTGACAGCCCTTGGCAGCTAGATGATATGATGAAAAAGATGCCAGTGTATGTA 1500
1441 GCTGACAGCCCTTGGCAGCTAGATGATATGATGAAAAAGATGCCAGTGTATGTA 1500
1501 TCAAGTGAAGAGCTCACCACCTTAATAAAGTGTATGATGAAAAAGATGCCAGTGTATGTA 1560
1501 TCAAGTGAAGAGCTCACCACCTTAATAAAGTGTATGATGAAAAAGATGCCAGTGTATGTA 1560
1561 TTTCAATGTTGCAAAAACGGAAGTTTAAAGAAACATTCAGTCAATGATGTAAGATGTC 1620
1561 TTTCAATGTTGCAAAAACGGAAGTTTAAAGAAACATTCAGTCAATGATGTAAGATGTC 1620
1621 ATTGAACAATATTTGCTGCTGCTGATCTGACATGTTGTGAATTTAAAGCCCTCAACA 1680
1621 ATTGAACAATATTTGCTGCTGCTGATCTGACATGTTGTGAATTTAAAGCCCTCAACA 1680
1681 CGTGTGATCAAAATTTTGGAAAGGCAAAATACATCAGATTAAGAAAGCCGAGAAA 1740
1681 CGTGTGATCAAAATTTTGGAAAGGCAAAATACATCAGATTAAGAAAGCCGAGAAA 1740
1741 ATTAACAGCAGACATAGACACACAGACATCTGATAGTGTGCGGGGTGTCAGAGTT 1800
1741 ATTAACAGCAGACATAGACACACAGACATCTGATAGTGTGCGGGGTGTCAGAGTT 1800
1801 GAAAAACAGATACAGTCCATAGATCAAGCTGAGTCTGCTACTAGACATCTATCAACAG 1860
1801 GAAAAACAGATACAGTCCATAGATCAAGCTGAGTCTGCTACTAGACATCTATCAACAG 1860
1861 GTTCCTTGGAAAGGCTCTGCTGAGCCCTGCTTGGCTTCATTCAGATCCCACTTTT 1920
1861 GTTCCTTGGAAAGGCTCTGCTGAGCCCTGCTTGGCTTCATTCAGATCCCACTTTT 1920
1921 GAATGGAACAGACATCTGATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCC 1980
1921 GAATGGAACAGACATCTGATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCC 1980
1981 GCACAAACAGTGGCTGCTTATCCAGATCAATAGTCCAAATCTGAGAGGCGCTGAG 2040
1981 GCACAAACAGTGGCTGCTTATCCAGATCAATAGTCCAAATCTGAGAGGCGCTGAG 2040
2041 TTCAATCTACGCGCAATATGATTCAGTGGCCAGACTTCTACGCGCTTACGCCCTATG 2100
2041 TTCAATCTACGCGCAATATGATTCAGTGGCCAGACTTCTACGCGCTTACGCCCTATG 2100
2101 CACAGTCAAGCAACAGAGTGGCCATTTAGTCAAAAGCATGGCTCAGAGTGGCAGCCACC 2160
2101 CACAGTCAAGCAACAGAGTGGCCATTTAGTCAAAAGCATGGCTCAGAGTGGCAGCCACC 2160
2161 AACACCATTTGCAAAACCAATTAATACGGCACCCAGCCAGCCCAACCACTTTACAG 2220
2161 AACACCATTTGCAAAACCAATTAATACGGCACCCAGCCAGCCCAACCACTTTACAG 2220
2221 ATCCACCTCTCTCTCCAGCATCAAGCATCTGCCCCAGGCGCAAAATCTGCAACCTTAAC 2280
2221 ATCCACCTCTCTCTCCAGCATCAAGCATCTGCCCCAGGCGCAAAATCTGCAACCTTAAC 2280
2281 CCTGAGGCTTACAGGAAGCATTTCTGAGCTGACACACCTGCTGTTGGCTCCAAAGAA 2340
2281 CCTGAGGCTTACAGGAAGCATTTCTGAGCTGACACACCTGCTGTTGGCTCCAAAGAA 2340
2341 AATGTTCAAGTTGCAAGTCAATCTCACCAGGACGTTCTATGAGAAAAAGCTTTGAC 2400

Db 2341 AATGTCAGGTTGCACAGTCMAATCTCACAGGACCGCTCTATAGAGAAAAGCTTTGAC 2400
 QY 2401 ATGGAGGAGAAACCTGTTGTCGTCTGTCCTCCATGGTGGCGAGAACTTGGCAAACT 2460
 Db 2401 ATGGAGGAGAAACCTGTTGTCGTCTGTCCTCCATGGTGGCGAGAACTTGGCAAACT 2460
 QY 2461 TTGTCGTGCAAAACCTGATCAGTGCAGCCAGGAACTGATATACAACTTTCAGGAGT 2520
 Db 2461 TTGTCGTGCAAAACCTGATCAGTGCAGCCAGGAACTGATATACAACTTTCAGGAGT 2520
 QY 2521 GAGTCAAGTGGCTCCAGAGGACCCAAAGATTTTACCCTAAAGGAGGAATCCAAATG 2580
 Db 2521 GAGTCAAGTGGCTCCAGAGGACCCAAAGATTTTACCCTAAAGGAGGAATCCAAATG 2580
 QY 2581 TTTATACATGATGAGAGTGGTGGTCCGGAAGACAGACAGACTTTTGTGATGCCCA 2640
 Db 2581 TTTATACATGATGAGAGTGGTGGTCCGGAAGACAGACAGACTTTTGTGATGCCCA 2640
 QY 2641 CCGCAGCTGCCAGGAGACCTGCTTGCATCAGACTCTCTAAGAGCTGGAAGGTCACGA 2700
 Db 2641 CCGCAGCTGCCAGGAGACCTGCTTGCATCAGACTCTCTAAGAGCTGGAAGGTCACGA 2700
 QY 2701 TCATCTCAGAGATTTGTAGGACAGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2760
 Db 2701 TCATCTCAGAGATTTGTAGGACAGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2760
 QY 2761 AAACGTGAATTA 2772
 Db 2761 AAACGTGAATTA 2772

RESULT 2
 ID AAH43634 standard; cDNA; 3111 BP.
 AC AAH43634;
 DT 21-JAN-2002 (first entry)
 DE Human ion-channel forming protein coding sequence.
 XX Ion-channel forming protein; voltage-gated potassium channel;
 KM fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 59..2831
 FT CDS /tag=a
 FT /product="Human ion-channel forming protein"
 WT WO200175108-A1.
 PD 11-OCT-2001.
 PN 03-APR-2001; 2001WO-US10875.
 PE 03-APR-2000; 2000US-194255P.
 PR (LEXI-) LEXICON GENETICS INC.
 PA
 PI Hu Y, Kleke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
 PI Sands AT;
 DR WPI; 2001-656987/75.
 DR P-PSDB; AAB47678.
 XX New human ion channel protein and polynucleotides encoding the protein,
 PT useful in diagnosing or treating diseases, in drug screening, and in
 XX clinical trial monitoring
 PS Disclosure; Page 37-38; 41pp; English.

XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
 CC The protein shares structural similarity with mammalian ion channel
 CC proteins, particularly voltage-gated potassium channel proteins. The
 CC protein is expressed in many human cell lines including fetal brain,
 CC brain, thymus, prostate, heart and skeletal muscle. The novel protein
 CC can be used in the diagnosis or treatment of diseases, in drug
 CC screening, and in clinical trial monitoring. The oligonucleotides may
 CC be used as hybridization probes for screening libraries, and assessing
 CC gene expression patterns (particularly using a micro array or high
 CC throughput chip format). The nucleic acids and novel protein can also be
 CC used in the identification, selection and validation of novel molecular
 CC targets for drug discovery, to screen collections of genetic material
 CC from patients who have a particular medical condition, to identify
 CC mutations associated with a particular disease, as a diagnostic or
 CC prognostic assay, and to screen for drugs which can be used to treat
 CC symptomatic or phenotypic manifestations of perturbing the normal
 CC function of novel human protein. The polypeptides are further used in
 CC generating antibodies.
 XX

Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 other;
 SO

Query Match 100.0%; Score 2772; DB 22; Length 3111;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCCCCGCCACACCGCGGGAGAGAGGCGCGCGCGCTGCGGTGAAGAC 60
 60 ATGCCCCGCCACACCGCGGGAGAGAGGCGCGCGCGCTGCGGTGAAGAC 119
 61 GCGCAGCG 120
 120 GCGCAGCG 179
 121 TCGGCG 180
 180 TCGGCG 239
 181 CTGGGACCG 240
 240 CTGGGACCG 299
 241 GGCACAGCG 300
 300 GGCACAGCG 359
 301 AGCTGCG 360
 360 AGCTGCG 419
 361 AGACCG 420
 420 AGACCG 479
 421 TTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTTGGCTCAAGTTC 480
 480 TTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTTGGCTCAAGTTC 539
 481 TTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTTGGCTCAAGTTC 540
 540 TTGATTTTGTCACTGTTTCTACATCCCTGAGCACACAAATTTGGCTCAAGTTC 599
 541 TCTGCGGCTTGTGTTGTGATATAGAGATGCGACAGAGACTGAGTTTGTGGAAG 600
 600 TCTGCGGCTTGTGTTGTGATATAGAGATGCGACAGAGACTGAGTTTGTGGAAG 659
 601 CCTTCTGTGTTATATATACATATTTCTTATATGCTTCAATAGCAGTTTTCGAAAA 660
 660 CCTTCTGTGTTATATATACATATTTCTTATATGCTTCAATAGCAGTTTTCGAAAA 719
 661 ACTCAGGATATATTTTGGCAGCTGCGACTGAGAGTCTCGCTTCTCAATCTCTC 720
 720 ACTCAGGATATATTTTGGCAGCTGCGACTGAGAGTCTCGCTTCTCAATCTCTC 779

QY 721 CGATGTGGGCATGAGCCGAAGGGGAGGCACTTGGAAATTACTGGGTTCACTGAGTTTAT 780
 DB 780 CGCATGTGGGCATGAGCCGAAGGGGAGGCACTTGGAAATTACTGGGTTCACTGAGTTTAT 839
 QY 781 GCTCACAGCAAGAAATTATACAGCTTGGTACATAGATATTTTGGTTCTATTTTTCG 840
 DB 840 GCTCACAGCAAGAAATTATACAGCTTGGTACATAGATATTTTGGTTCTATTTTTCG 899
 QY 841 TCTTTCCTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTTACATATGAGAT 900
 DB 900 TCTTTCCTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTTACATATGAGAT 959
 QY 901 GCTCTGTGTGGGGACAAATTAATGCAACTATTTGGTATGAGACAAACTCCCTTA 960
 DB 960 GCTCTGTGTGGGGACAAATTAATGCAACTATTTGGTATGAGACAAACTCCCTTA 1019
 QY 961 ACTTGGCTGGGAAGATCTTCTTCTGAGGCTTGGCACTCTTGGCATTTCTTCTTTCGA 1020
 DB 1020 ACTTGGCTGGGAAGATCTTCTTCTGAGGCTTGGCACTCTTGGCATTTCTTCTTTCGA 1079
 QY 1021 CTTCCTGCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAGACACACCCGAC 1080
 DB 1080 CTTCCTGCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAGACACACCCGAC 1139
 QY 1081 AAACACTTGAAGAAAGAAAGGAAAGCCAGCTGCCAACCCTATTCAGTGTGTTGGCTAGT 1140
 DB 1140 AAACACTTGAAGAAAGAAAGGAAAGCCAGCTGCCAACCCTATTCAGTGTGTTGGCTAGT 1199
 QY 1141 TACGAGCTGATGAGAAATCTGTTCATTTGCACTTGGACCTGGAGCCACTTGAAGGCTTGG 1200
 DB 1200 TACGAGCTGATGAGAAATCTGTTCATTTGCACTTGGACCTGGAGCCACTTGAAGGCTTGG 1259
 QY 1201 CACACCTGAGGCTTACCAATATAGAAAGTAAAGTTTAAAGAGGAGTGGCCATGGCTAGC 1260
 DB 1260 CACACCTGAGGCTTACCAATATAGAAAGTAAAGTTTAAAGAGGAGTGGCCATGGCTAGC 1319
 QY 1261 CCCAGGGGCGAAGATTAATTAAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGC 1320
 DB 1320 CCCAGGGGCGAAGATTAATTAAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCAAGC 1379
 QY 1321 ACCGACATCACAGCCGAGGAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGAC 1380
 DB 1380 ACCGACATCACAGCCGAGGAGTCCACCAAAAGTGCAGAAAGCTGAGCTTCAACGAC 1439
 QY 1381 CGAACCCGCTGCGGCTCGCTGCGCTCAAAAGTTTTCAGGCCAAACAGATGATGAT 1440
 DB 1440 CGAACCCGCTGCGGCTCGCTGCGCTCAAAAGTTTTCAGGCCAAACAGATGATGAT 1499
 QY 1441 GCTGACACAGCCCTTGGCACTGATGATATGATGAAAAAGATGCCAGTGTGATGTA 1500
 DB 1500 GCTGACACAGCCCTTGGCACTGATGATATGATGAAAAAGATGCCAGTGTGATGTA 1559
 QY 1501 TTAGTGGAAAGACCTCACCCACACCTTAAACCTGCTATTTGAGCTATACAAATATGAAA 1560
 DB 1560 TTAGTGGAAAGACCTCACCCACACCTTAAACCTGCTATTTGAGCTATACAAATATGAAA 1619
 QY 1561 TTTTCATGTTGCAAAAGGAAAGTTTAAAGAAACATTAAGCTCATATGATGATTAAGATGTC 1620
 DB 1620 TTTTCATGTTGCAAAAGGAAAGTTTAAAGAAACATTAAGCTCATATGATGATTAAGATGTC 1679
 QY 1621 ATTGAACAATATTTCTGCTGCTATCTGTGACATGTTGTGAGATTAATAAGCTTCAACA 1680
 DB 1680 ATTGAACAATATTTCTGCTGCTATCTGTGACATGTTGTGAGATTAATAAGCTTCAACA 1739
 QY 1681 CGGTGTGATCAAAATTTCTGAAAAAGGCAATACATCAGATAGAAAGAGCGAGAGAAA 1740
 DB 1740 CGGTGTGATCAAAATTTCTGAAAAAGGCAATACATCAGATAGAAAGAGCGAGAGAAA 1799
 QY 1741 ATTAACAGCAAGAAATGAGACAGACAGATCTCAGTATGCTCGGTTGGGTGCTCAAGGTT 1800
 DB 1800 ATTAACAGCAAGAAATGAGACAGACAGATCTCAGTATGCTCGGTTGGGTGCTCAAGGTT 1859

QY 1801 GAAAAACAGGTACAGTCCATAGAAATCCAGCTGACCTGACTTACATCTATCTACAG 1860
 DB 1860 GAAAAACAGGTACAGTCCATAGAAATCCAGCTGACCTGACTTACATCTATCTACAG 1919
 QY 1861 GTCTTTGGAAAGGCTCTGCTCCAGCCCTGCTTGGCTTATTCATTCAGATCCACCTTTT 1920
 DB 1920 GTCTTTGGAAAGGCTCTGCTCCAGCCCTGCTTGGCTTATTCATTCAGATCCACCTTTT 1979
 QY 1921 GAATGTACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 1980
 DB 1980 GAATGTACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 2039
 QY 1981 GCACAAAAACAGTGGCTGTTATCCAGATCAAACTAGTGGCCACATCTCCAGAGGCTGCGAG 2040
 DB 2040 GCACAAAAACAGTGGCTGTTATCCAGATCAAACTAGTGGCCACATCTCCAGAGGCTGCGAG 2099
 QY 2041 TTCAATTTGAGCCCAAAATGATTTGAGTCCCAAGACTTTCATAGGCTTAGCCCTACTAG 2100
 DB 2100 TTCAATTTGAGCCCAAAATGATTTGAGTCCCAAGACTTTCATAGGCTTAGCCCTACTAG 2159
 QY 2101 CACAGTCAAGCAACAGTGGCCATTAATAGTCAAAAGGCTCAGAGCTGAGAGGCTGAGCCACC 2160
 DB 2160 CACAGTCAAGCAACAGTGGCCATTAATAGTCAAAAGGCTCAGAGCTGAGAGGCTGAGCCACC 2219
 QY 2161 AACACCAATTTGCAAAACCAATTAATATCGGCAACCCAGCCAGCCGCAAACTTTACAG 2220
 DB 2220 AACACCAATTTGCAAAACCAATTAATATCGGCAACCCAGCCAGCCGCAAACTTTACAG 2279
 QY 2221 ATCCACCTCTCTCCGACCAATCAAGATCTGCCAGGCTGAGGCTGAGGCTGAGGCTGAGG 2280
 DB 2280 ATCCACCTCTCTCCGACCAATCAAGATCTGCCAGGCTGAGGCTGAGGCTGAGGCTGAGG 2339
 QY 2281 CCTGAGGCTTACAGAAAGCATTTCTGACGTACACACCTGCTGCTGCTGCTGCTGCTGCTG 2340
 DB 2340 CCTGAGGCTTACAGAAAGCATTTCTGACGTACACACCTGCTGCTGCTGCTGCTGCTGCTG 2399
 QY 2341 AATGTTCAAGTTGTCACAGTCAAAATCTCACCAGAGGACCTGCTATGAGGAAAGCTTGGAC 2400
 DB 2400 AATGTTCAAGTTGTCACAGTCAAAATCTCACCAGAGGACCTGCTATGAGGAAAGCTTGGAC 2459
 QY 2401 ATGGAGAGGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
 DB 2460 ATGGAGAGGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2519
 QY 2461 TTGCTGTGCAAAACCTGATCAGTGTGACGACCGAGAACTGAAATATACACTTTTAGGAGAT 2520
 DB 2520 TTGCTGTGCAAAACCTGATCAGTGTGACGACCGAGAACTGAAATATACACTTTTAGGAGAT 2579
 QY 2521 GAGTCAAGTGGCTCCAGAGGCGCAAGATTTTACCAGAAATGGAGGAAATCCAAATTTG 2580
 DB 2580 GAGTCAAGTGGCTCCAGAGGCGCAAGATTTTACCAGAAATGGAGGAAATCCAAATTTG 2639
 QY 2581 TTTATTAACGATGAAGAGGTGGGTCCGGAAGACAGAGACAGACACTTTTGTATGCCGCA 2640
 DB 2640 TTTATTAACGATGAAGAGGTGGGTCCGGAAGACAGAGACAGACACTTTTGTATGCCGCA 2699
 QY 2641 CCGCAGCCTGCCAGGAGAGCTGCTTTCATCAGACTCTCTAAGGACTGGAAGTCCAGCA 2700
 DB 2700 CCGCAGCCTGCCAGGAGAGCTGCTTTCATCAGACTCTCTAAGGACTGGAAGTCCAGCA 2759
 QY 2701 TCATGTCAGAGCATTTGTAAGGAGAGGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2760
 DB 2760 TCATGTCAGAGCATTTGTAAGGAGAGGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2819
 QY 2761 AAACCTGAATTA 2772
 DB 2820 AAACCTGAATTA 2831

RESULT 3
 AAH49499
 ID AAH49499 standard; DNA; 3074 BP.
 XX

QY 1294 TCAGTAGTGACAGAGAGTCCCAAGCAGCAGATCAGAGCCGAGGAGTCCCAACCAA 1353
 |||||
 Db 1430 TCAGTAGTGACAGAGAGTCCCAAGCAGCAGATCAGAGCCGAGGAGTCCCAACCAA 1489
 |||||
 QY 1354 GTGCAGAGAGCTGAGAGCTTCAACGACGAAACCGCTTCCGGCCCTGCTGCTCAAA 1413
 |||||
 Db 1490 GTGCAGAGAGCTGAGAGCTTCAACGACGAAACCGCTTCCGGCCCTGCTGCTCAAA 1549
 |||||
 QY 1414 AGTTCACGCAAAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1473
 |||||
 Db 1550 AGTTCACGCAAAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
 |||||
 QY 1474 GATGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
 |||||
 Db 1610 GATGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1669
 |||||
 QY 1534 GTTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1593
 |||||
 Db 1670 GTTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1729
 |||||
 QY 1594 TTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
 |||||
 Db 1730 TTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
 |||||
 QY 1654 TTGTGTAGATTAATAAGCTTCAACACAGTGTGATGATGATGATGATGATGATGATGAT 1713
 |||||
 Db 1790 TTGTGTAGATTAATAAGCTTCAACACAGTGTGATGATGATGATGATGATGATGATGAT 1849
 |||||
 QY 1714 ACATCAGATTAAGAGAGCCGAGAGAAATAACAGACAGATGATGATGATGATGATGAT 1773
 |||||
 Db 1850 ACATCAGATTAAGAGAGCCGAGAGAAATAACAGACAGATGATGATGATGATGATGAT 1909
 |||||
 QY 1774 AGTATGCTGGTGGGGGTGCTCAAGGTTGAAAAACAGATGATGATGATGATGATGATGAT 1833
 |||||
 Db 1910 AGTATGCTGGTGGGGGTGCTCAAGGTTGAAAAACAGATGATGATGATGATGATGATGAT 1969
 |||||
 QY 1834 GACTGCTACTAGACATCTATCAACAGAGTCTCTGGAAGGCTCTGCTCAAGCCCTGCT 1893
 |||||
 Db 1970 GACTGCTACTAGACATCTATCAACAGAGTCTCTGGAAGGCTCTGCTCAAGCCCTGCT 2029
 |||||
 QY 1894 TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCTGATCTCAAAAGCCCT 1953
 |||||
 Db 2030 TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCTGATCTCAAAAGCCCT 2089
 |||||
 QY 1954 GTGGATTAAGCAAAAGTCTTTCGGGGTTCGCAAAAACAGTGGTGTTCATCCAGATCACT 2013
 |||||
 Db 2090 GTGGATTAAGCAAAAGTCTTTCGGGGTTCGCAAAAACAGTGGTGTTCATCCAGATCACT 2149
 |||||
 QY 2014 AGTGCCAAATCTCGAGAGGCTGAGTTCATTCGAGCCCAATGAGTTCAAGTCCAG 2073
 |||||
 Db 2150 AGTGCCAAATCTCGAGAGGCTGAGTTCATTCGAGCCCAATGAGTTCAAGTCCAG 2209
 |||||
 QY 2074 ACTTTTACGCGCTTACGCTTACTATGACAGTCAAGACACAGAGTGGCAATTAGTCAA 2133
 |||||
 Db 2210 ACTTTTACGCGCTTACGCTTACTATGACAGTCAAGACACAGAGTGGCAATTAGTCAA 2269
 |||||
 QY 2134 AGCGATGCTCAGAGAGTGGAGCCACCAACACATTCGAAACCAATTAATTAATTAATTA 2193
 |||||
 Db 2270 AGCGATGCTCAGAGAGTGGAGCCACCAACACATTCGAAACCAATTAATTAATTAATTA 2329
 |||||
 QY 2194 AAGCCAGCAGCCCAACACTTTACAGATCCACCTCTCTCCAGCCATCAAGATCTG 2253
 |||||
 Db 2330 AAGCCAGCAGCCCAACACTTTACAGATCCACCTCTCTCCAGCCATCAAGATCTG 2389
 |||||
 QY 2254 CCAGAGCCAGAACTCTGACACCTTAACCTCTGAGGCTTACAGAGAAAGATTTCTGACGTC 2313
 |||||
 Db 2390 CCAGAGCCAGAACTCTGACACCTTAACCTCTGAGGCTTACAGAGAAAGATTTCTGACGTC 2449
 |||||
 QY 2314 ACCAGCTGCTTTGGCTTCAAGAAATGTTGAGTTGACAGTCAATTCACCAAG 2373
 |||||
 Db 2450 ACCAGCTGCTTTGGCTTCAAGAAATGTTGAGTTGACAGTCAATTCACCAAG 2509
 |||||
 QY 2374 GACCGTTCTATGAGAAAGCTTTGACATGGAGAGAAACTCTGTTGCTGTCTGCC 2433
 |||||

Db 2510 GACCGTTCTATGAGAAAGCTTTGACATGGAGAGAAACTCTGTTGCTGTCTGCC 2569
 |||||
 QY 2434 ATGTGCCCCAAGACTTTGGCAAACTTTTCTCTGTGCAAAACCTGATCAGGTGACGAG 2493
 |||||
 Db 2570 ATGTGCCCCAAGACTTTGGCAAACTTTTCTCTGTGCAAAACCTGATCAGGTGACGAG 2629
 |||||
 QY 2494 GAACATATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGCAGCAAGATTTT 2553
 |||||
 Db 2630 GAACATATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGCAGCAAGATTTT 2689
 |||||
 QY 2554 TACCCCAATGAGAGGAATCCAAATTTTATACAGTGAAGAGTGGTCCCGAAGAG 2613
 |||||
 Db 2690 TACCCCAATGAGAGGAATCCAAATTTTATACAGTGAAGAGTGGTCCCGAAGAG 2749
 |||||
 QY 2614 ACAGAGACAGACCTTTTATGAGCCGACCGCAGCTGCGCGAGGAGTGGCTTTGATCA 2673
 |||||
 Db 2750 ACAGAGACAGACCTTTTATGAGCCGACCGCAGCTGCGCGAGGAGTGGCTTTGATCA 2809
 |||||
 QY 2674 GACTCTTAAGAGCTGGAAGGTGACATCTCAGAGCATTTTGTAAAGCAGAGAAAGT 2733
 |||||
 Db 2810 GACTCTTAAGAGCTGGAAGGTGACATCTCAGAGCATTTTGTAAAGCAGAGAAAGT 2869
 |||||
 QY 2734 ACAGATGCCCTCAGCTTGGCTCTCATGTCAAACTGAATTA 2772
 |||||
 Db 2870 ACAGATGCCCTCAGCTTGGCTCTCATGTCAAACTGAATTA 2908
 |||||

RESULT 4
 AAS14653
 ID AAS14653 standard; cDNA; 2667 BP.
 XX
 AC AAS14653;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
 XX
 KW Human; ss; voltage-gated potassium channel; KCNQ5-2; noctropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; splice variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..2967
 FT /*tag= a
 FT /product= "hKCNQ5-2"
 XX
 PN MO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001MO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TU;
 XX
 DR WPI: 2001-611467/70.
 DR P-PSDB; AA009021.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 XX
 PS Claim 5; Page 63-64; 78bp; English.
 XX

CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a splice variant of hKCNQ5 encoding hKCNQ5-2.

CC XX Sequence 2667 BP: 701 A: 667 C: 660 G: 639 T: 0 other;

Query Match 96.0%; Score 2662.2; DB 22; Length 2667;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 ATGAAGATGTGGAGTGGGGCCGGGAGGAGTGCTCTGAATCGGAGCCGCGAGGGC 165
DB 1 ATGAAGATGTGGAGTGGGGCCGGGAGGAGTGCTCTGAATCGGAGCCGCGAGGGC 60
QY 166 GAGGAGCCGTACTGCTGGGAGCCGGGAGGAGCTGGTGGGCGGGCGGGGCGGCTG 225
DB 61 GAGGAGCCGTACTGCTGGGAGCCGGGAGGAGCTGGTGGGCGGGCGGGGCGGCTG 120
QY 226 AGGAGAGAGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
DB 121 AGGAGAGAGCCCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 286 TACACGAGTACCCAGAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345
DB 181 TACACGAGTACCCAGAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 346 TACACGAGTACCCAG 405
DB 241 TACACGAGTACCCAG 300
QY 406 CTGTGCTTTGGTCTGATGATTTTGTCAAGTGTCTTACCATCCCTAGAGACACAAATG 465
DB 301 CTGTGCTTTGGTCTGATGATTTTGTCAAGTGTCTTACCATCCCTAGAGACACAAATG 360
QY 466 GCCCAGAGTGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
DB 361 GCCCAGAGTGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 526 ATCATTCGAGTCTGCTGCGGGTGTGCTGATGATGATGATGATGATGATGATGATGAT 585
DB 421 ATCATTCGAGTCTGCTGCGGGTGTGCTGATGATGATGATGATGATGATGATGATGAT 480
QY 586 AGGTTTCTCGAAGAGCCCTTCTGTATATAGATACATGTTCTTATCCCTCAATAGCA 645
DB 481 AGGTTTCTCGAAGAGCCCTTCTGTATATAGATACATGTTCTTATCCCTCAATAGCA 540
QY 646 GTTGTCTTCGAAAGAACTCAGAGGATATTTTGGCAGTCTGCACTGCAAGTCTCCGT 705
DB 541 GTTGTCTTCGAAAGAACTCAGAGGATATTTTGGCAGTCTGCACTGCAAGTCTCCGT 600
QY 706 TTCTCAGAGATCCCTCCGATGCTGCGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAG 765
DB 601 TTCTCAGAGATCCCTCCGATGCTGCGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAG 660

QY 766 GTTTCAGTGTATATGCTACAGCAGAGAAATTAATCACAGCTGTGTACATGATTTTGG 825
DB 661 GTTTCAGTGTATATGCTACAGCAGAGAAATTAATCACAGCTGTGTACATGATTTTGG 720
QY 826 GTTCTATATTTTTCGCTTCTGCTGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGG 885
DB 721 GTTCTATATTTTTCGCTTCTGCTGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 886 TCTACATATGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
DB 781 TCTACATATGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 946 GACAAAGTCCCTTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1005
DB 841 GACAAAGTCCCTTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 1006 ATTTCTTTCTTTCACCTTCTGCGGAGATTTCTGCTGAGGTTTGCATTAAGATACNA 1065
DB 901 ATTTCTTTCTTTCACCTTCTGCGGAGATTTCTGCTGAGGTTTGCATTAAGATACNA 960
QY 1066 GAACAAACACCGCCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCACCTCATTCAG 1125
DB 961 GAACAAACACCGCCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCACCTCATTCAG 1020
QY 1126 TGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAAGCA 1185
DB 1021 TGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAAGCA 1080
QY 1186 CACTTGAAGGCTTTGACACACCTGACAGCCCTACCAATGAGAACTTAAGTAAAGAGGGA 1245
DB 1081 CACTTGAAGGCTTTGACACACCTGACAGCCCTACCAATGAGAACTTAAGTAAAGAGGGA 1140
QY 1246 GTGCGATAGGCTAGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305
DB 1141 GTGCGATAGGCTAGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1306 AGGAGTCCCGCAAGACCCGACATCACAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1365
DB 1201 AGGAGTCCCGCAAGACCCGACATCACAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1366 TGGAGCTTCAAGCAGCCGAGCCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1425
DB 1261 TGGAGCTTCAAGCAGCCGAGCCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1426 AAACCAATGATGATGCTGACACAGCCCTTGGGACATGATGATGATGATGATGATGAT 1485
DB 1321 AAACCAATGATGATGCTGACACAGCCCTTGGGACATGATGATGATGATGATGATGAT 1380
QY 1486 TGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1545
DB 1381 TGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1546 ATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1605
DB 1441 ATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1606 GATGTAAAAAGATGCTTGAACAAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
DB 1501 GATGTAAAAAGATGCTTGAACAAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1666 AAAAGCCTTCAACAGTGTGATCAAAATTCCTGGAAAAAGGCAAAATCACATCAGATTAAG 1725
DB 1561 AAAAGCCTTCAACAGTGTGATCAAAATTCCTGGAAAAAGGCAAAATCACATCAGATTAAG 1620
QY 1726 AAAGCCGAGAGAAATTAACAGCAGAACTGAGACCAAGATCTCAGTATGCTCGGT 1785
DB 1621 AAAGCCGAGAGAAATTAACAGCAGAACTGAGACCAAGATCTCAGTATGCTCGGT 1680
QY 1786 CGGAGTCAAGGTTGAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1845
DB 1681 CGGAGTCAAGGTTGAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

QY 1846 GACATCTATACACAGAGTCCCTCGGAAAGGCTGCTGACCCCTCGCTTGGCTTCATTC 1905
 DB 1741 GACATCTATACACAGAGTCCCTCGGAAAGGCTGCTGACCCCTCGCTTGGCTTCATTC 1800
 QY 1906 CAGATCCACACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 1965
 DB 1801 CAGATCCACACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA 1860
 QY 1966 GATCTTTGGGGTCCGACACAAAACAGTGGCTTATCCAGATCACTAGTGGCAACATC 2025
 DB 1861 GATCTTTGGGGTCCGACACAAAACAGTGGCTTATCCAGATCACTAGTGGCAACATC 1920
 QY 2026 TCGAGAGGCTCAGTTCATCTGACGCCCAATGATGTCAGTCCGACGACTTCTACGCG 2085
 DB 1921 TCGAGAGGCTCAGTTCATCTGACGCCCAATGATGTCAGTCCGACGACTTCTACGCG 1980
 QY 2086 CTTAGCCCTACTATGACAGTCAAGCAGACAGAGTGGCAATTAATGTCAAAGCGATGGCTCA 2145
 DB 1981 CTTAGCCCTACTATGACAGTCAAGCAGACAGAGTGGCAATTAATGTCAAAGCGATGGCTCA 2040
 QY 2146 GAGAGTGGCCACCAACACACATGTCGAACCAATTAATGTCGAACCAACCAACGACGACCC 2205
 DB 2041 GAGAGTGGCCACCAACACACATGTCGAACCAATTAATGTCGAACCAACCAACGACGACCC 2100
 QY 2206 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGATCTGCCAGGCGCAAA 2265
 DB 2101 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGATCTGCCAGGCGCAAA 2160
 QY 2266 ACTCTGACACCTTACCCCTGCAAGCTTACAGAAAGCATTTTCTGACGTACACCTGCTT 2325
 DB 2161 ACTCTGACACCTTACCCCTGCAAGCTTACAGAAAGCATTTTCTGACGTACACCTGCTT 2220
 QY 2326 GTTGCCTCCAAAGAAATGTCTGAGTTCAGTCACTCAATCTCCAAAGGACCCGTTATAG 2385
 DB 2221 GTTGCCTCCAAAGAAATGTCTGAGTTCAGTCACTCAATCTCCAAAGGACCCGTTATAG 2280
 QY 2386 AGGAAAGCTTTGACATGGAGAGAGAAACTCTGTTGTCTGTCTGCTCCATGGTCCGAG 2445
 DB 2281 AGGAAAGCTTTGACATGGAGAGAGAAACTCTGTTGTCTGTCTGCTCCATGGTCCGAG 2340
 QY 2446 GACTTGGCAATCTTGTCTGTGCAAAACCTGATCAGGTGACCGAGAACTGAAATTA 2505
 DB 2341 GACTTGGCAATCTTGTCTGTGCAAAACCTGATCAGGTGACCGAGAACTGAAATTA 2400
 QY 2506 CAACCTTACAGGAGTGTGATGAGTGGCTCCAGAGGCGCAAGATTTTACCCCAATGG 2565
 DB 2401 CAACCTTACAGGAGTGTGATGAGTGGCTCCAGAGGCGCAAGATTTTACCCCAATGG 2460
 QY 2566 AGGGAATCCAAATTTTATTAATGATGAAGAGTGGTCCGGAAGAGACAGAGACAGAC 2625
 DB 2461 AGGGAATCCAAATTTTATTAATGATGAAGAGTGGTCCGGAAGAGACAGAGACAGAC 2520
 QY 2626 ACTTTTGAATGCCGACCGACGCTCCAGAGGAGCTGCTTGTGATCAGACTCTCTAAG 2685
 DB 2521 ACTTTTGAATGCCGACCGACGCTCCAGAGGAGCTGCTTGTGATCAGACTCTCTAAG 2580
 QY 2686 ACTGGAAGGTCAGATCATCTCAGAGACTTTGTAAGGAGGAGAAAGTACAGATGCCCTC 2745
 DB 2581 ACTGGAAGGTCAGATCATCTCAGAGACTTTGTAAGGAGGAGAAAGTACAGATGCCCTC 2640
 QY 2746 AGCTTGCCTCATGTCAAACTGAATAA 2772
 DB 2641 AGCTTGCCTCATGTCAAACTGAATAA 2667
 RESULT 5
 AASI4651
 ID AASI4651 standard; cDNA; 3071 BP.
 XX AASI4651:
 AC AASI4651:
 XX
 DT 18-DEC-2001 (first entry)
 XX

DE Human cDNA for voltage gated potassium channel hKCNQ5.
 XX
 KW Human; ss: voltage-gated potassium channel; hKCNQ5; natriotic;
 KW cerebrioprotective; natriotic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W0200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PE 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 DR WPI; 2001-611467/70.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 XX
 PS Claim 5; Page 61-62; 78pp: English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a representative cDNA for hKCNQ5.
 CC
 SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other:
 Query Match 95.1%; Score 2635.4; DB 22; Length 3071;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
 QY 97 GGCAGCGGATGAAGATGTGAGTGGGCGGAGGAGTGTCTGAACCTCGGACGCC 156
 DB 1 GGCAGCGGATGAAGATGTGAGTGGGCGGAGGAGTGTCTGAACCTCGGACGCC 60
 QY 157 GCCAGGGGCGAGCGCTCTGCTGCTGAGGACACCGCGGCGACGCTCGGTGGGGGGC 216
 DB 61 GCCAGGGGCGAGCGCTCTGCTGCTGAGGACACCGCGGCGACGCTCGGTGGGGGGC 120
 QY 217 GGTGGGCTGAGGAGAGCGCGCGGAGCAAGGAGGAGCGGATGACCTGCTGGGGAAG 276
 DB 121 GGTGGGCTGAGGAGAGCGCGCGGAGCAAGGAGGAGCGGATGACCTGCTGGGGAAG 180

QY	277	CCGGCTCTCTTACACGAGTACCCAGAGCTGCCGGCGCAACGTCAAGTACCCGGCGGTGAC	336
Db	181	CCGGCTCTCTTACACGAGTACCCAGAGCTGCCGGCGCAACGTCAAGTACCCGGCGGTGAC	240
QY	337	AACTACTGTACACGTGTGAGAGACCCCGGGCTGGGGGTTCATCTACCAAGCTTTC	396
Db	241	AACTACTGTACACGTGTGAGAGACCCCGGGCTGGGGGTTCATCTACCAAGCTTTC	300
QY	397	GTTTTTCCTCTGTCTTGGTGGCTTGATTTTGTCAAGTCTTTCATCCCTGAGAC	456
Db	301	GTTTTTCCTCTGTCTTGGTGGCTTGATTTTGTCAAGTCTTTCATCCCTGAGAC	360
QY	457	ACAAATATGGCCCTCAAGTGGCCCTTGATCTCGAGTTCGATGATGTGTCTTTGGT	516
Db	361	ACAAATATGGCCCTCAAGTGGCCCTTGATCTCGAGTTCGATGATGTGTCTTTGGT	420
QY	517	TTGAGTTCATTCATTGAACTGTGCTGGCGGTTGCTGTGTCTCATATAGAGATGGCAA	576
Db	421	TTGAGTTCATTCATTGAACTGTGCTGGCGGTTGCTGTGTCTCATATAGAGATGGCAA	480
QY	577	GGAAGACTGAGGTTTGGCTGGAAAGCCCTCTGTATATAGTACCATTGTCTTATCGT	636
Db	481	GGAAGACTGAGGTTTGGCTGGAAAGCCCTCTGTATATAGTACCATTGTCTTATCGT	540
QY	637	TCAATAGCAGTGTCTTTCGCAAAAACCTCAGGGTAAATTTTTCACAGTCTGCACCTAGA	696
Db	541	TCAATAGCAGTGTCTTTCGCAAAAACCTCAGGGTAAATTTTTCACAGTCTGCACCTAGA	600
QY	697	AGTCTCGGTTCCCTACATCCCTCCGCAATGTCCGATGGACATGGACCGAAGGGAGCACTTGG	756
Db	601	AGTCTCGGTTCCCTACATCCCTCCGCAATGTCCGATGGACATGGACCGAAGGGAGCACTTGG	660
QY	757	AAATTAAGTGGTTCAGTGGTTATGTCTACAGCAGAGAAATTAATCACAGTGTGGACATA	816
Db	661	AAATTAAGTGGTTCAGTGGTTATGTCTACAGCAGAGAAATTAATCACAGTGTGGACATA	720
QY	817	GGATTTTGGTCTTATTTTTCGTCCTTTCCTTGTCTATCTGTGGAAAGAGATGCCAAT	876
Db	721	GGATTTTGGTCTTATTTTTCGTCCTTTCCTTGTCTATCTGTGGAAAGAGATGCCAAT	780
QY	877	AAAGAGTTTCTACATATGACAGATCTCTGTGTGGGGCAAAATTAATTAATTAACATCTAAT	936
Db	781	AAAGAGTTTCTACATATGACAGATCTCTGTGTGGGGCAAAATTAATTAATTAACATCTAAT	840
QY	937	GGCTATGGAGACAACAACTCCCTAACTTGGCTGGGAAGATTCCTTCTGCAGGCTTTCGA	996
Db	841	GGCTATGGAGACAACAACTCCCTAACTTGGCTGGGAAGATTCCTTCTGCAGGCTTTCGA	900
QY	997	CTCCTTGGCAATTTCTTCTTGTGCACCTCCCTGGCGGGAATTCCTTGGCTCAGGTTTGCATTA	1056
Db	901	CTCCTTGGCAATTTCTTCTTGTGCACCTCCCTGGCGGGAATTCCTTGGCTCAGGTTTGCATTA	960
QY	1057	AAAGTACAGACACACACCGCCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAAC	1116
Db	961	AAAGTACAGACACACACCGCCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAAC	1020
QY	1117	CTCATTCAGTGTGTGGCTGATGATTAACGACGCTGATGAGAAATCTGTTCATTTGCACAC	1176
Db	1021	CTCATTCAGTGTGTGTGGCTGATGATTAACGACGCTGATGAGAAATCTGTTCATTTGCACAC	1080
QY	1177	TGGAGCCACACTTGAAGGCTTGCACACCTTCAGGCCCTTACCAA-----1220	
Db	1081	TGGAGCCACACTTGAAGGCTTGCACACCTTCAGGCCCTTACCAA-----1220	
QY	1221	-----TAGAAGCTAAGTTTAAAGAGCGAGTCCGATGGCTAAGCCCGAGGGGC	1286
Db	1141	GCATTCAGCAGCTCAGAGCTAAGTTTAAAGAGCGAGTCCGATGGCTAAGCCCGAGGGGC	1200
QY	1270	CAGAGTATTAAGAGCCGACAAAGCTCACTAGTGTGACAGAGAGTCCCAACACGACGATTC	1329
Db	1201	CAGAGTATTAAGAGCCGACAAAGCTCACTAGTGTGACAGAGAGTCCCAACACGACGATTC	1260
QY	1330	ACAGCCGAGGCACTCCACCAAAAGTGCAGAAAGACTGAGCTTCAACGACGGAACCCGC	1389

Db	1261	ACAGCCGAGGCGAGTCCACCACCAAAATGCAGAGAGGCTGGAGGCTTCAACGACCGAACCCGC	1320
QY	1390	TTGGGCGCCCTGCGTGGCGGCTCAAAAGTCTCTGACCCAAAACCAAGTATAGATGCTGACACA	1449
Db	1321	TTCCGGCCCTGCGTGGCGGCTCAAAAGTCTCTGACCCAAAACCAAGTATAGATGCTGACACA	1380
QY	1450	GCCCTTGGCACTGATGATGATATATATATATAAAAGATGCGACGTATGATGATGATGAA	1509
Db	1381	GCCCTTGGCACTGATGATGATATATATATATAAAAGATGCGACGTATGATGATGATGAA	1440
QY	1510	GACCTCACCCCACTTAAAACTGTCAATTGACGTATCAGAATTATGAAATTTCAATGTT	1569
Db	1441	GACCTCACCCCACTTAAAACTGTCAATTGACGTATCAGAATTATGAAATTTCAATGTT	1500
QY	1570	GCAAAAGGAAAGTTAAAGAAATACATAGCTCATATGATGTAAAGATGTCATTGAAACA	1629
Db	1501	GCAAAAGGAAAGTTAAAGAAATACATAGCTCATATGATGTAAAGATGTCATTGAAACA	1560
QY	1630	TATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGCTGTTGAT	1689
Db	1561	TATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGCTGTTGAT	1620
QY	1690	CAAAATTTTGGAAAAAGGCAATACATCAGATAGAAAGAGCCGAGAGAAATTAACAGCA	1749
Db	1621	CAAAATTTTGGAAAAAGGCAATACATCAGATAGAAAGAGCCGAGAGAAATTAACAGCA	1680
QY	1750	GAACATGAGACCCACAGACGATCTCAGTATGCTGGTGGGGGTGTCAAAGTTGAAAAACAG	1809
Db	1681	GAACATGAGACCCACAGACGATCTCAGTATGCTGGTGGGGGTGTCAAAGTTGAAAAACAG	1740
QY	1810	GTCAGTGCATAGAAATCCAGCTGGACTGGCTACTAGACATATATCAACAGGTCCTTCGG	1869
Db	1741	GTCAGTGCATAGAAATCCAGCTGGACTGGCTACTAGACATATATCAACAGGTCCTTCGG	1800
QY	1870	AAAGGCTCTGCTCAGGCTTGTGGCTTATTCAGATCCACCTTTTGAATGTGAA	1929
Db	1801	AAAGGCTCTGCTCAGGCTTGTGGCTTATTCAGATCCACCTTTTGAATGTGAA	1860
QY	1930	CACACATCTGACTATCAAAAGCCCTGGATAGCAAAAGTCTTTGGGGTTCCGCACAAAAC	1989
Db	1861	CACACATCTGACTATCAAAAGCCCTGGATAGCAAAAGTCTTTGGGGTTCCGCACAAAAC	1920
QY	1990	AGTGGCTCTTATCCAGATCAACTAGTGGCCAAACATCTTGAGNAGGCTGCACTTCAATCTCG	2049
Db	1921	AGTGGCTCTTATCCAGATCAACTAGTGGCCAAACATCTTGAGNAGGCTGCACTTCAATCTCG	1980
QY	2050	AGCCCAAAATGATTCAGTGGCCAGACTTTTCTACGCGCTTAGACCTTACTATGACAGTCAA	2109
Db	1981	AGCCCAAAATGATTCAGTGGCCAGACTTTTCTACGCGCTTAGACCTTACTATGACAGTCAA	2040
QY	2110	GCAACACAGGTGCCAATTAGTCAAAAGGATGGCTCAGAGTGGGAGCCACCAACACATTT	2169
Db	2041	GCAACACAGGTGCCAATTAGTCAAAAGGATGGCTCAGAGTGGGAGCCACCAACACATTT	2100
QY	2170	GCAACACAAATTAATATAGGAGCCAGCCAGCCAGCCACCAACTTTACAGATCCOACT	2229
Db	2101	GCAACACAAATTAATATAGGAGCCAGCCAGCCAGCCACCAACTTTACAGATCCOACT	2160
QY	2230	CCCTCTCCAGACATCAAGCATCTGCGCCAGGACAGAAACTGTGCAACCCCTAACCCGACGC	2289
Db	2161	CCCTCTCCAGACATCAAGCATCTGCGCCAGGACAGAAACTGTGCAACCCCTAACCCGACGC	2220
QY	2290	TTACAGAGAAAGCATTTCTGACGTACACACCTGCTTGTGCTCCAGAGAAATGTTGAG	2349
Db	2221	TTACAGAGAAAGCATTTCTGACGTACACACCTGCTTGTGCTCCAGAGAAATGTTGAG	2280
QY	2350	GTTGACACATGCAAAATCTCACCAAGGACCGTTCTATAGGAAAAACCTTTGACATGGGAGGA	2409
Db	2281	GTTGACACATGCAAAATCTCACCAAGGACCGTTCTATAGGAAAAACCTTTGACATGGGAGGA	2340
QY	2410	GAACATCTGTTCTGCTGTGCTCCATAGTGGCCGAAGACCTTGGCAATCTTTGTCTGTG	2469

Db 2341 GAAACTGTGTCTGTCTGTCCATGTGCGGAGACTTGGGCAATCTTGTCTGTG 2400
 QY 2470 CAAACCTGATCAGGTGACCGAGAGAACTGATATACACTTTAGGGAGTCAAGT 2529
 Db 2401 CAAACCTGATCAGGTGACCGAGAGAACTGATATACACTTTAGGGAGTCAAGT 2460
 QY 2530 GGCTCCAGAGGCGCAAGATTTTACCCCAATGAGGGGAAATCCAAATTTGTTTAACT 2589
 Db 2461 GGCTCCAGAGGCGCAAGATTTTACCCCAATGAGGGGAAATCCAAATTTGTTTAACT 2520
 QY 2590 GATGAAGAGTGGTCCCGAAGACAGACAGACACTTTTGAATGCCAGCCAGCCT 2649
 Db 2521 GATGAAGAGTGGTCCCGAAGACAGACAGACACTTTTGAATGCCAGCCAGCCT 2580
 QY 2650 GCCAGGGAACCTGCTTTCATCAGACTCTTAAGAGATGGAAGGTACAGATCACTAG 2709
 Db 2581 GCCAGGGAACCTGCTTTCATCAGACTCTTAAGAGATGGAAGGTACAGATCACTAG 2640
 QY 2710 AGCATTTGTAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2769
 Db 2641 AGCATTTGTAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
 QY 2770 TAA 2772
 Db 2701 TAA 2703

RESULT 6
 AAC85414
 ID AAC85414 standard; cDNA: 3137 BP.
 AAC85414:

20-APR-2001 (first entry)

Human KCNQ5 potassium channel subunit coding sequence.

Human: KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
 central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
 CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
 compulsive behaviour; dementia; depression; Huntington's disease;
 mania; memory impairment; memory dysfunction; spinal cord damage;
 phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;
 epilepsy; ds.

OS Homo sapiens.

Key Location/Qualifiers
 CDS 1..2694
 /*tag= a
 /product= "KCNQ5 subunit"

W0200077035-A2.

21-DEC-2000.

29-MAY-2000; 2000MO-DK00289.

11-JUN-1999; 99DK-0000828.

(NEUR-) NEUROSEARCH AS.

Jentsch TJ.

WPI: 2001-080678/09.

P-PSDB: AAB47046.

Novel genes encoding KCNQ5 potassium channel subunits, useful for
 treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
 depression, Huntington's disease, schizophrenia and Parkinson's disease

Claim 2; Page 44-48; 50pp; English.

XX This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
 CC heteromeric channels with other KCNQ channel subunits, in particular
 CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
 CC chromosome 6 (q14). Chemicals which have the ability to bind to
 CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
 CC of diseases related to diseases or adverse conditions of the central
 CC nervous system (CNS), including affective disorders, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders, motor dysfunction, motion disorders, motor
 CC disorders, neurodegenerative diseases, Parkinson's disease and
 CC Parkinson-like motor disorders, phobias, pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
 CC convulsions and epilepsy.

Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 other;

Query Match 94.9%; Score 2630; DB 22; Length 3137;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 106 ATGAGAGATGTGAGTGGGCGGCGAGGTGCTGTAAGTGGCGAGCCGCGAGGGGC 165
 Db 1 ATGAGAGATGTGAGTGGGCGGCGAGGTGCTGTAAGTGGCGAGCCGCGAGGGGC 60
 QY 166 GACGGCCCTGCTAGCTGGGCGACCGCGCGCGACGCTGGTGGCGGCGGCTGGCCTG 225
 Db 61 GACGGCCCTGCTAGCTGGGCGACCGCGCGCGACGCTGGTGGCGGCGGCTGGCCTG 120
 QY 226 AGGAGAGACCGCGCGGCGAAGCAGAGGGGCGCGATGAGCTGCTGGGAGACCGCTCT 285
 Db 121 AGGAGAGACCGCGCGGCGAAGCAGAGGGGCGCGATGAGCTGCTGGGAGACCGCTCT 180
 QY 286 TACACGAGTACCCAGAGTGGCGGCGAAGTACCGGCGGCGGAGAGTACCTG 345
 Db 181 TACACGAGTACCCAGAGTGGCGGCGAAGTACCGGCGGCGGAGAGTACCTG 240
 QY 346 TACAAGTGTGAGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 405
 Db 241 TACAAGTGTGAGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 406 CTGTCTTGTGCTGCTGATTTTGTGCAATGTTTTCATACATCCCGAGAGACCAAAATTG 465
 Db 301 CTGTCTTGTGCTGCTGATTTTGTGCAATGTTTTCATACATCCCGAGAGACCAAAATTG 360
 QY 466 GCGTCAGTGGCCTGCTGATGCTGAGTTCGATGATTTGCTTTGGTGGAGTTC 525
 Db 361 GCGTCAGTGGCCTGCTGATGCTGAGTTCGATGATTTGCTTTGGTGGAGTTC 420
 QY 526 ATCATTCGAATCTGCTGCGGGTGTGTTGCGATATAGAGATGCGAAGAGACTG 585
 Db 421 ATCATTCGAATCTGCTGCGGGTGTGTTGCGATATAGAGATGCGAAGAGACTG 480
 QY 586 AGGTTTGTGCGAAGACCTTCTGCTTATAGATACATGTTCTTATGCTTCAATAGCA 645
 Db 481 AGGTTTGTGCGAAGACCTTCTGCTTATAGATACATGTTCTTATGCTTCAATAGCA 540
 QY 646 GTTGTGTTGCGAAGAACTCAGGGTAAATTTTGGCACGCTGCACTAGAACTCCGT 705
 Db 541 GTTGTGTTGCGAAGAACTCAGGGTAAATTTTGGCACGCTGCACTAGAACTCCGT 600
 QY 706 TTCTACAGATCCCTCGCATGCTGCGCATGACCGAAGGGAGGCACTTGGAAATTAACG 765
 Db 601 TTCTACAGATCCCTCGCATGCTGCGCATGACCGAAGGGAGGCACTTGGAAATTAACG 660
 QY 766 GGTGAGAGTATAGCTACAGCAAGAAATTAATACAGCTTGTGACATAGGATTTTG 825
 Db 661 GGTGAGAGTATAGCTACAGCAAGAAATTAATACAGCTTGTGACATAGGATTTTG 720
 QY 826 GTTCTATTTTTCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885


```

Db 721 GTTCTTATTTTTCGCTTCCTTCTCTATCTGTGGTGGAAAAAGATGCCAATAAAGATTT 780
QY 886 TCTACATATGACAGATGCTCTCTGTGGGGGACAAATTAATGACAACTATGGCTATGGA 945
Db 781 TCTACATATGACAGATGCTCTCTGTGGGGGACAAATTAATGACAACTATGGCTATGGA 840
QY 946 GACAAAACCTCCCTAACTTGGCTGGGAGAAATGCTTTCGAGAGCTTTGCACTCCCTGGC 1005
Db 841 GACAAAACCTCCCTAACTTGGCTGGGAGAAATGCTTTCGAGAGCTTTGCACTCCCTGGC 900
QY 1006 ATTCTCTTTCGACATCTCCCTGGGCAATCTTGGGCAAGTTCCTTTCGATTAAGTACAA 1065
Db 901 ATTCTCTTTCGACATCTCCCTGGGCAATCTTGGGCAAGTTCCTTTCGATTAAGTACAA 960
QY 1066 GAACAACACCGCCAGAAACACTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1125
Db 961 GAACAACACCGCCAGAAACACTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1020
QY 1126 TGTGTTGGCGTATGATGACAGCTGATGAGAAATCTGTTTCATTCGACACCTGGAGGCCA 1185
Db 1021 TGTGTTGGCGTATGATGACAGCTGATGAGAAATCTGTTTCATTCGACACCTGGAGGCCA 1080
QY 1186 CACTTGAAGGCGCTTGACACCTGACAGCCCTTACCAA----- 1220
Db 1081 CACTTGAAGGCGCTTGACACCTGACAGCCCTTACCAA----- 1220
QY 1221 --TGAAGAGCTTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGGCGAGAGTAT 1278
Db 1141 AGTGAAGAGCTTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGGCGAGAGTAT 1200
QY 1279 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCGAAGCCGACATTCACAGCCGAG 1338
Db 1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCCGAAGCCGACATTCACAGCCGAG 1260
QY 1339 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCCGACCCCTTCCGGCCC 1398
Db 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCCGACCCCTTCCGGCCC 1320
QY 1399 TCGGTGGCGCCCAAAAGTTCACAGCCAAACAGATATGATCTGACACAGCCCTTGGC 1458
Db 1321 TCGGTGGCGCCCAAAAGTTCACAGCCAAACAGATATGATCTGACACAGCCCTTGGC 1380
QY 1459 ACTGATGATGATATGATGAGAAAAAGAGTGCAGTGTGATGATCAGTGGAGACCTTACC 1518
Db 1381 ACTGATGATGATATGATGAGAAAAAGAGTGCAGTGTGATGATCAGTGGAGACCTTACC 1440
QY 1519 CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTATGAATTTTCATGTTGCAAAAACG 1578
Db 1441 CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTATGAATTTTCATGTTGCAAAAACG 1500
QY 1579 AAGTTTAAAGAAACATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Db 1501 AAGTTTAAAGAAACATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1639 GGTTCATCTGACATGTTGTGTGAATTTAAAGCCTTCAACACAGTGTGATCAAAATTCCT 1698
Db 1561 GGTTCATCTGACATGTTGTGTGAATTTAAAGCCTTCAACACAGTGTGATCAAAATTCCT 1620
QY 1699 GGAAGAGGGAATACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGAACATGAG 1758
Db 1621 GGAAGAGGGAATACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
QY 1759 ACCACAGAGCATGCTATGATGCTGGTGGGAGGCAAGGTTGAAAGAAAGAGTACAGTGC 1818
Db 1681 ACCACAGAGCATGCTATGATGCTGGTGGGAGGCAAGGTTGAAAGAAAGAGTACAGTGC 1740
QY 1819 ATAGAATCCAGCTGACCTGCTACTAGACATCTATCAACAGTCTTTCGAGAAAGCTCT 1878
Db 1741 ATAGAATCCAGCTGACCTGCTACTAGACATCTATCAACAGTCTTTCGAGAAAGCTCT 1800
QY 1879 GCGTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTAACAGACATCT 1938
Db 1801 GCGTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTAACAGACATCT 1860

```

```

QY 1939 GACTATCAAAACCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAAACAGTGGCTG 1998
Db 1861 GACTATCAAAACCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAAACAGTGGCTG 1920
QY 1999 TTATCCAGATCACTAGTGGCAACATCTGAGAGGCTTCGCAATTCATTTGACGCCAAT 2058
Db 1921 TTATCCAGATCACTAGTGGCAACATCTGAGAGGCTTCGCAATTCATTTGACGCCAAT 1980
QY 2059 GAGTTGAGTGGCCAGACTTTTCTAGCGGCTTAAAGCCCTTACTATGACAGTCAAGCAACAG 2118
Db 1981 GAGTTGAGTGGCCAGACTTTTCTAGCGGCTTAAAGCCCTTACTATGACAGTCAAGCAACAG 2040
QY 2119 GTGGCAATTTGATCAAAAGGATGCTGACAGTGGCAGCCACCAACCAATTCGAAACCA 2178
Db 2041 GTGGCAATTTGATCAAAAGGATGCTGACAGTGGCAGCCACCAACCAATTCGAAACCA 2100
QY 2179 ATAAATACGGCACCACCAAGCCAGCCCAACCAATTTAAGATGCCACCTCTCCCA 2238
Db 2101 ATAAATACGGCACCACCAAGCCAGCCCAACCAATTTAAGATGCCACCTCTCCCA 2160
QY 2239 GCCATCAAGCATCTGCCAGGCGAGAAACCTGCAACCTTACAGGCTTACAGGAA 2298
Db 2161 GCCATCAAGCATCTGCCAGGCGAGAAACCTGCAACCTTACAGGCTTACAGGAA 2220
QY 2299 AGCATTTGACGTGACACCTGCTTGGGCTTCCCAAGGAAATGTTTACAGTTGACAG 2358
Db 2221 AGCATTTGACGTGACACCTGCTTGGGCTTCCCAAGGAAATGTTTACAGTTGACAG 2280
QY 2359 TCAAAATCTCACAAGACCGCTTATGAGAAAGCTTTGACATGGAGAGAAACTCTG 2418
Db 2281 TCAAAATCTCACAAGACCGCTTATGAGAAAGCTTTGACATGGAGAGAAACTCTG 2340
QY 2419 TTGTCTGTCTGCTCCATGTTGCGGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2478
Db 2341 TTGTCTGTCTGCTCCATGTTGCGGAGAGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2400
QY 2479 ATCAGGTGACCGAGGAACTGATATATCACTTTCAAGGAGTGTGATCAAGGCTCCAGA 2538
Db 2401 ATCAGGTGACCGAGGAACTGATATATCACTTTCAAGGAGTGTGATCAAGGCTCCAGA 2460
QY 2539 GGCAGCAAGATTTTAAACCCCAATGAGAGGAATCAAAATGTTTATTAACATGATGAAG 2598
Db 2461 GGCAGCAAGATTTTAAACCCCAATGAGAGGAATCAAAATGTTTATTAACATGATGAAG 2520
QY 2599 GTGGGTCCGAGAGACAGAGACACTTTTGTATGATCCGACCGAGCTGCCAGGAA 2658
Db 2521 GTGGGTCCGAGAGACAGAGACACTTTTGTATGATCCGACCGAGCTGCCAGGAA 2580
QY 2659 GCTGCTTTGATCAGACTCTTAAGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2718
Db 2581 GCTGCTTTGATCAGACTCTTAAGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2640
QY 2719 AAGGAGAGAGAAATGACATATGCTCAGCTTGCCTCATGTCAAACTGAATAA 2772
Db 2641 AAGGAGAGAGAAATGACATATGCTCAGCTTGCCTCATGTCAAACTGAATAA 2694

RESULT 7
AAS14652
ID AAS14652 standard: cDNA: 2694 BP.
XX AAS14652;
XX 18-DEC-2001 (first entry)
DE Human cDNA encoding a voltage gated potassium channel hKvN05-1.
XX
KW Human; ss; voltage-gated potassium channel; hKvN05-1; nontropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.

```


Db	1261	GGCAGTCCACCAAGGTGAGAAAGAGCTGGAGCTTACAGACCCGACCCGCTTCGGGCC	1320
QY	1399	TCGGTGGCCCTCAAAAGTTCTAGCCAAAACAGATGATGATGCTGACACAGCCCTTGGC	1458
Db	1321	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACAGTATGATGATGCTGACACAGCCCTTGGC	1380
QY	1459	ACTGATGATGATATGATGATAAAAAAGATGCCAGTGGTGAATGATCAGTGGAAAGCTTACC	1518
Db	1381	ACTGATGATGATATGATGATAAAAAAGATGCCAGTGGTGAATGATCAGTGGAAAGCTTACC	1440
QY	1519	CCACCACCTTAAAACTGTCTATTGAGCCTATCAGAAATTTATGAATTTTCATGTTGCCAAAACGG	1578
Db	1441	CCACCACCTTAAAACTGTCTATTGAGCCTATCAGAAATTTATGAATTTTCATGTTGCCAAAACGG	1500
QY	1579	AAGTTTAAAGAAACATTTACGTCATGATGATGTAAGAAAAGTGCATTCATAACAATTTCTGCT	1638
Db	1501	AAGTTTAAAGAAACATTTACGTCATGATGATGTAAGAAAAGTGCATTCATAACAATTTCTGCT	1560
QY	1639	GGTCATCTGCAGATGTTGTTGTAGAATTTAAAGCCCTTCAAAACAGTGTTCATCAATTTCTT	1698
Db	1561	GGTCATCTGCAGATGTTGTTGTAGAATTTAAAGCCCTTCAAAACAGTGTTCATCAATTTCTT	1620
QY	1699	GGAAAAAGGCAAAATCACATCAGATTAAGAAAGGCCAGAGAAAATTAACAGCAGAACTAG	1758
Db	1621	GGAAAAAGGCAAAATCACATCAGATTAAGAAAGGCCAGAGAAAATTAACAGCAGAACTAG	1680
QY	1759	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAAACAGTACAGTCC	1818
Db	1681	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAAACAGTACAGTCC	1740
QY	1819	ATGAAATCGAAGCTGGAGCTGCGCTACTATACACTCTATCAACAGCTCTTGGAAAGCTCT	1878
Db	1741	ATGAGATCGAAGCTGGAGCTGCGCTACTATACACTCTATCAACAGCTCTTGGAAAGCTCT	1800
QY	1879	GCCTCAGCCCTCGCTTGGCTTCATTCAGAGATCCACCTTTTGAATGTTAAACAGACATCT	1938
Db	1801	GCCTCAGCCCTCGCTTGGCTTCATTCAGAGATCCACCTTTTGAATGTTAAACAGACATCT	1860
QY	1939	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCCCAAAAACAGTGGCTGC	1998
Db	1861	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCCCAAAAACAGTGGCTGC	1920
QY	1999	TTATTCAGATCAACTAGTGCACACATCTCGAGAGGCCGCGAGTTGATTTGACGCCAAAT	2058
Db	1921	TTATTCAGATCAACTAGTGCACACATCTCGAGAGGCCGCGAGTTGATTTGACGCCAAAT	1980
QY	2059	GAGTTACGTGCCAGACTTTCTACGCGCTTAAGCCCTACTATGACACAGTCAAGCAACACAG	2118
Db	1981	GAGTTACGTGCCAGACTTTCTACGCGCTTAAGCCCTACTATGACACAGTCAAGCAACACAG	2040
QY	2119	GTGCCAATTAGTCAAAAGCGATGGCTGACGAGTGGCAGCCACCAACACCATTTGCCAACCA	2178
Db	2041	GTGCCAATTAGTCAAAAGCGATGGCTGACGAGTGGCAGCCACCAACACCATTTGCCAACCA	2100
QY	2179	ATPAATAGGCGACCCCAAGCCAGACGCCCAACAACATTTACAGATCCCACTCTCTCCCA	2238
Db	2101	ATPAATAGGCGACCCCAAGCCAGACGCCCAACAACATTTACAGATCCCACTCTCTCTCCCA	2160
QY	2239	GGCATCAACATCTGCCAGGCGCCAGAAACTCTGCACCTTAACCTGCAAGGCTTACAGGAA	2298
Db	2161	GGCATCAACATCTGCCAGGCGCCAGAAACTCTGCACCTTAACCTGCAAGGCTTACAGGAA	2220
QY	2299	AGCATTTCTGAGCTCACCACTGCTGTTGGCTTGCCTCAAGGAAATGTTCAAGTTGACACAG	2358
Db	2221	AGCATTTCTGAGCTCACCACTGCTGTTGGCTTGCCTCAAGGAAATGTTCAAGTTGACACAG	2280
QY	2359	TCAAATCTACCAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGAGAAACTCTG	2418
Db	2281	TCAAATCTACCAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGAGAAACTCTG	2340
QY	2419	TTGTGTGTGTGCCCTGATGGCCGAAGGATTTGGGCAAAATCTTGTCTGTGCCAAACCTG	2478
Db	2341	TTGTGTGTGTGCCCTGATGGCCGAAGGATTTGGGCAAAATCTTGTCTGTGCCAAACCTG	2400

QY	2479	ATCAGGTGACCGAGGAAGTGAATATACAACTTTCAGGAGTGAATCAAGTGGCTCCAGA	2538
Db	2401	ATCAGGTGACCGAGGAAGTGAATATACAACTTTCAGGAGTGAATCAAGTGGCTCCAGA	2460
QY	2539	GGCAGCCAAAGATTTTACCCTCAATGAGAGGAATCCAAATTTGTTAACTGATGAAGAC	2598
Db	2461	GGCAGCCAAAGATTTTACCCTCAATGAGAGGAATCCAAATTTGTTAACTGATGAAGAG	2520
QY	2599	GTCGGTCCCGAAGACACAGACACACATTTTGATGCGCACCGGAGCCTGCCAGGAA	2658
Db	2521	GTGGGTCCCGAAGACACAGACACACATTTTGATGCGCACCGGAGCCTGCCAGGAA	2580
QY	2659	GCTGCTTTGCATCAGACTCTCTTAAGACTGGAAGTCAAGATCATCTCAGACCAATTTGT	2718
Db	2581	GCTGCTTTGCATCAGACTCTCTTAAGACTGGAAGTCAAGATCATCTCAGACCAATTTGT	2640
QY	2719	AAGCAGAGAAATACAGATGCCCTGAGCTTGCCGTCATGTCAAACTGAAATTA	2772
Db	2641	AAGCAGAGAAATACAGATGCCCTGAGCTTGCCGTCATGTCAAACTGAAATTA	2694
RESULT 8			
AAD27192			
XX	AAD27192	standard; cDNA; 2694 BP.	
XX	AAD27192:		
XX	09-APR-2002	(first entry)	
DE	Human potassium channel polypeptide, KCNQ5 cDNA.		
XX	Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;		
KW	dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;		
KW	ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;		
KW	anxiety disorder; bipolar disorder; sleep disorder; eating disorder;		
KW	addiction; myokymia; Alzheimer's disease; age-associated memory loss;		
KW	learning deficiency; cognitive disorder; motor disease; neuron disease;		
KW	neurophysiological disorder; neuropsychological disorder; asthma;		
KW	neuron cell death; brain tumour; gene therapy; antisense therapy;		
KW	synaptic transmission; electrical excitability; ss.		
XX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
EH	CDS	1..2694	
FT		/tag= a	
FT		/product= "Human KCNQ5 protein"	
XX	WO200192526-A1.		
XX	06-DEC-2001.		
XX	24-MAY-2001; 2001WO-US17314.		
XX	26-MAY-2000; 2000US-207389P.		
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PA	Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CS;		
XX	Gridkoff VK;		
PI	WPI: 2002-122069/16.		
XX	P-PSDB; AAL16599.		
DR			
XX	Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding		
PT	it, for diagnosing, treating and identifying modulators useful in		
PT	treating neurological, neurophysiological and neuropsychological		
XX	diseases		
PS	Claim 3; Fig 1; 128pp; English.		
CC	The invention relates to potassium channel polypeptides referred to		

Db 1801 GCCTCAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGAATGGAACAGACATCT 1860
 QY 1939 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGGGCTGC 1998
 Db 1861 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGGGCTGC 1920
 QY 1999 TTATTCAGATCAACTAGTGGCAACATCTCGAGAGGCTGAGTTCATCTGAGCCCAAT 2058
 Db 1921 TTATTCAGATCAACTAGTGGCAACATCTCGAGAGGCTGAGTTCATCTGAGCCCAAT 1980
 QY 2059 GAGTTACAGTGGCCACACTTTTACGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2118
 Db 1981 GAGTTACAGTGGCCACACTTTTACGGCTTAGCCCTACTATGACAGTCAAGCAACAG 2040
 QY 2119 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCCAGCCACCAACCATTTGCAACCAA 2178
 Db 2041 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCCAGCCACCAACCATTTGCAACCAA 2100
 QY 2179 ATAAATACGGCAACCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2238
 Db 2101 ATAAATACGGCAACCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
 QY 2239 GCCATCAAGCATCTGCCCCAGGCGCAAAATCTGCAACCCCTACCCCTGAGCTTACAGGAA 2298
 Db 2161 GCCATCAAGCATCTGCCCCAGGCGCAAAATCTGCAACCCCTGAGCTTACAGGAA 2220
 QY 2299 AGCATTTCTGACGTACACCACTGCTTGTGCTCCAGAGAAATGTTTCAGTGGTGCAG 2358
 Db 2221 AGCATTTCTGACGTACACCACTGCTTGTGCTCCAGAGAAATGTTTCAGTGGTGCAG 2280
 QY 2359 TCAATATCTACCAAGAGACCGTTCTATGAGGAAAGCTTTGACATGGAGAGAAACTCTG 2418
 Db 2281 TCAATATCTACCAAGAGACCGTTCTATGAGGAAAGCTTTGACATGGAGAGAAACTCTG 2340
 QY 2419 TTGTCGTGCTGCTCCATGCTGCGGCAAGACTTGGCAATCTTTGCTGCGCAAACTG 2478
 Db 2341 TTGTCGTGCTGCTCCATGCTGCGGCAAGACTTGGCAATCTTTGCTGCGCAAACTG 2400
 QY 2479 ATCAGGTGACCGAGAACTGATATACACTTTCAGGAGTGAAGTGCCTCCAGA 2538
 Db 2401 ATCAGGTGACCGAGAACTGATATACACTTTCAGGAGTGAAGTGCCTCCAGA 2460
 QY 2539 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAACGTGAGAGAG 2598
 Db 2461 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAACGTGAGAGAG 2520
 QY 2599 GTGGGTCCCGAAGAGAGAGACACTTTTGAATGCGCAGCCGAGGCTGCGCAAGGAA 2658
 Db 2521 GTGGGTCCCGAAGAGAGAGACACTTTTGAATGCGCAGCCGAGGCTGCGCAAGGAA 2580
 QY 2659 GCTGCTTTGCTGATGACACTCTCTAAGAGCTGGAAGGTCAAGATCTCAGAGCATTTGT 2718
 Db 2581 GCTGCTTTGCTGATGACACTCTCTAAGAGCTGGAAGGTCAAGATCTCAGAGCATTTGT 2640
 QY 2719 AAGGAGAGAGAAAGTACAGATGCCCTGAGTGGCTCATGTCAACTGAAATTA 2772
 Db 2641 AAGGAGAGAGAAAGTACAGATGCCCTGAGTGGCTCATGTCAACTGAAATTA 2694
 RESULT 9
 AAC64371
 ID AAC64371 standard; cDNA; 3718 BP.
 XX AAC64371:
 DT 07-FEB-2001 (first entry)
 XX Human KCNQ5 (KCN6q) cDNA sequence SFO ID NO:2.
 DE Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;

KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; ss.
 OS Homo sapiens.
 PN MO200061606-A1.
 XX 19-OCT-2000.
 PD 10-APR-2000; 2000MO-US09587.
 PF 14-APR-1999; 99US-0129274.
 PR (MERI) MERCK & CO INC.
 PA Petrukhin K, Caskey CT, Li W, Metzker ML,
 XX WPI: 2000-647417/62.
 DR P-PSDB: AAB24241.
 XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, salla disease, deafness, and epilepsy -
 PS Claim 3; Fig 2; 99pp; English.
 CC The present sequence encodes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.
 XX Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
 SO
 Query Match 91.0%; Score 2523.2; DB 21; Length 3718;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 2562; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
 QY 208 GCGGCGCGCGGTGCTGAGGAGAGCCCGCGGCAAGCAGAGGCGCCGAGTACGCTG 267
 Db 87 GACTGCGCGGTGCTGAGGAGAGCCCGCGGCAAGCAGAGGCGCCGAGTACGCTG 146
 QY 268 CTGGGAGCGCGCTCTTACACAGATGACAGAGTGGCGGCAACGTCAGTACCGG 327
 Db 147 CTGGGAGCGCGCTCTTACACAGATGACAGAGTGGCGGCAACGTCAGTACCGG 206
 QY 328 CGGTCAGAACTACCTGTACACAGTGTGAGAGAGCCCGCGGCTGAGTAC 387
 Db 207 CGGTCAGAACTACCTGTACACAGTGTGAGAGAGCCCGCGGCTGAGTAC 266
 QY 388 CACGCTTGGTTTCTCCTTCTGCTTGTGCTGCTTATTTTGCATGTTTCTACATC 447
 Db 267 CACGCTTGGTTTCTCCTTCTGCTTGTGCTGCTTATTTTGCATGTTTCTACATC 326
 QY 448 CCTGAGCACAAAATTTGGCCTCAAGTTCCTTGTATCTGAGTTCGATGATGTC 507
 Db 327 CCTGAGCACAAAATTTGGCCTCAAGTTCCTTGTATCTGAGTTCGATGATGTC 386
 QY 508 GTCTTTGGTTTGGATTCATTCGAATCTGCTGCGGTTGCTGTTGCGATATAGA 567
 Db 387 GTCTTTGGTTTGGATTCATTCGAATCTGCTGCGGTTGCTGTTGCGATATAGA 446
 QY 568 GGATGGCAAGAGAGCTGAGTTCCTGGAAGCCCTTGTGCTTATGATACATTTGT 627
 Db 447 GGATGGCAAGAGAGCTGAGTTCCTGGAAGCCCTTGTGCTTATGATACATTTGT 506

QY	628	CTATGCGCTTCATPAGAGTGTGTTCTGCAAAAACTCAGGGTAATATTTTGGCAGCTCT	687
Db	507	CTATATGCTTCATAGACAGTGTGTTCTCAAAAACATCAGGGTAATATTTTGGCAGCTCT	566
QY	688	GCACCTCAGAAAGTCTCCGTTTCTCTACAGATFCCCTCCCATGCTGGCGCATGGAACCGAAGGGGA	747
Db	567	GCACCTCAGAAAGTCTCCGTTTCTCTACAGATFCCCTCCCATGCTGGCGCATGGAACCGAAGGGGA	626
QY	748	GGCATTGGCAAATTTACTGGGTTCACTAGTGGTTATGCTCACAGCAGGAATTTAATCACAGCT	807
QY	808	TGGTACATAGAGATTTTGGTCTTATTTTTCGTTTCGTTTCCCTGCTATCTCGGTGGGAAG	867
Db	627	GGCAGCTGGAAATTAAGTGGGTTCACTAGTGGTTATGCTCACAGCAGGAATTTAATCACAGCT	686
QY	868	GATGCCAATTAAGAGTTTTCATATATGACAGATGCTCTCTGGTGGGGCACAAATTAATCTTG	927
Db	747	GATGCCAATTAAGAGTTTTCATATATGACAGATGCTCTCTGGTGGGGCACAAATTAATCTTG	806
QY	928	ACAACATTTGGCTATGAGACAAAACCTCCCTAATTGGCTGGGAAGATTGCTTTCTGCA	987
Db	807	ACAACATTTGGCTATGAGACAAAACCTCCCTAATTGGCTGGGAAGATTGCTTTCTGCA	866
QY	988	GGCTTTGACACTCCTTGGCATTTCCTTCTTTCGACTTCTCCGACCGGCAATCTTGCTCAGGT	1047
Db	867	GGCTTTGACACTCCTTGGCATTTCCTTCTTTCGACTTCTCCGACCGGCAATCTTGCTCAGGT	926
QY	1048	TTTGCAATTAAGATACAGAACACACCGCCAGAAAACACTTTGAGAAAAAGAAAGAACCA	1107
Db	927	TTTGCAATTAAGATACAGAACACACCGCCAGAAAACACTTTGAGAAAAAGAAAGAACCA	986
QY	1108	GGCGCAACCTCAFTTCAGTGTGTTGGGTGGTGGTACGAGCTGANTAGAAAATCTGTTTCC	1167
Db	987	GCTGCCAACCTCAFTTCAGTGTGTTGGGTGGTGGTACGAGCTGANTAGAAAATCTGTTTCC	1046
QY	1168	ATTGCAACCTGGAAGCCACACTTGAAGGCTTTGCACACTGAGCCCTACCA	1220
Db	1047	ATTGCAACCTGGAAGCCACACTTGAAGGCTTTGCACACTGAGCCCTACCA	1106
QY	1221	-----TCAGAGCTAAAGTTTAAAGAGCAGAGTGGCAGTGCTAGC	1280
Db	1107	CAGGGGAAGCATCAAGCAAGCTCAAAAGCTAAAGTTTAAAGAGCAGAGTGGCAGTGCTAGC	1166
QY	1261	CCCAGGGGCCAGAGTATTAAAGCGGACAGCCTCAGTAGGTGACAGGGGTCCCAAGC	1320
Db	1167	CCCAGGGGCCAGAGTATTAAAGCGGACAGCCTCAGTAGGTGACAGGGGTCCCAAGC	1226
QY	1321	ACCGACATCACAGCCCGAAGGGCAGTCCCAACAAAGTGACAGMAAGCTGAGCTTCAAGAC	1380
Db	1227	ACCGACATCACAGCCCGAAGGGCAGTCCCAACAAAGTGACAGMAAGCTGAGCTTCAAGAC	1286
QY	1381	CGAACCCTGCTCGGGGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATAGAT	1440
Db	1287	CGAACCCTGCTCGGGGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATAGAT	1346
QY	1441	GGTGACACAGCCCTTGGCAGCTGATGATGTATATGATGAAAAAAGAGTGCAGTGTGATGA	1500
Db	1347	GCTGACACAGCCCTTGGCAGCTGATGATGTATATGATGAAAAAAGAGTGCAGTGTGATGA	1406
QY	1501	TCAGTGGAAAGACCTCAACCCCAACCACTTAAAACTGTCATTCGAGCTATCAGAAATATGAAA	1560
Db	1407	TCAGTGGAAAGACCTCAACCCCAACCACTTAAAACTGTCATTCGAGCTATCAGAAATATGAAA	1466
QY	1561	TTTTCAATGTCGCAAAAGCGAAGTTTAAAGAAACATTAGCTCCATATGATGTAAAAAGATGTC	1620
Db	1467	TTTTCAATGTCGCAAAAGCGAAGTTTAAAGAAACATTAGCTCCATATGATGTAAAAAGATGTC	1526
QY	1621	ATTGAACAATATTTCTGCTGTCATCTGGACATGTTGTGTAGAAATTAAGAGCCCTTCAACA	1680
Db	1527	ATTGAACAATATTTCTGCTGTCATCTGGACATGTTGTGTAGAAATTAAGAGCCCTTCAACA	1586

QY	168	CGGTTGATCAAAATCTTGGAAAAAGGGCAAAATCACATCCAGATATAGAAAGACCCGAGAAAA	1748
Db	1587	CGGTTGATCAAAATCTTGGAAAAAGGGCAAAATCACATCCAGATATAGAAAGACCCGAGAAAA	1648
QY	1741	ATAACAGCAGAACATGAGACCACAGACGATCTAGTATGCTCGGTGGGTGTCMAAGTT	1800
Db	1647	ATAACAGCAGAACATGAGACCACAGACGATCTAGTATGCTCGGTGGGTGTCMAAGTT	1708
QY	1801	GAATAACAGGTACGCTCATGAAATTCAAAGCTGGACTGGCTACTATGACATCTATCAACAG	1866
Db	1707	GAATAACAGGTACGCTCATGAAATTCAAAGCTGGACTGGCTACTATGACATCTATCAACAG	1766
QY	1861	GTGCTTCGAGAAAGGCTCTGCTCCAGCCCTCGCTTGGCTTCATCTCCAGATCCCACTTTT	1920
Db	1767	GTGCTTCGAGAAAGGCTCTGCTCCAGCCCTCGCTTGGCTTCATCTCCAGATCCCACTTTT	1828
QY	1921	GAATGTGAACAGACATCTGACTATATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGGTTCC	1988
Db	1827	GAATGTGAACAGACATCTGACTATATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGGTTCC	1888
QY	1981	GCACAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTCTCGAAGGCTCGAG	2048
Db	1887	GCACAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTCTCGAAGGCTCGAG	1948
QY	2041	TTTCATTCGTACGCCCAAAATGAGTTCAAGTCCGACGCTTTCTACGGCTTACGCCCTTACATG	2100
Db	1947	TTTCATTCGTACGCCCAAAATGAGTTCAAGTCCGACGCTTTCTACGGCTTACGCCCTTACATG	2006
QY	2101	CACAGTCAACACACAGAGTGGCCAAATGATCAAGAGATGGCTCAGACAGTGGGAGGCCAC	2166
Db	2007	CACAGTCAACACACAGAGTGGCCAAATGATCAAGAGATGGCTCAGACAGTGGGAGGCCAC	2066
QY	2161	AACACCATTTGCAAAACCAAAATTAATACGGCACCACCAAGCCAGACGCCCCCAACACTTTACG	2220
Db	2067	AACACCATTTGCAAAACCAAAATTAATACGGCACCACCAAGCCAGACGCCCCCAACACTTTACG	2128
QY	2221	ATGCCACCTCCTCTCCCAAGCATCAAGCATCTGGCCAGGGCCAGAAACTCTGCACCCCTAAC	2288
Db	2127	ATGCCACCTCCTCTCCCAAGCATCAAGCATCTGGCCAGGGCCAGAAACTCTGCACCCCTAAC	2188
QY	2281	CCTGCAGGCTTACAGGAAGACATTTCTACGTCACACACCTGGCTTTGGCTCCCAAGAA	2340
Db	2187	CCTGCAGGCTTACAGGAAGACATTTCTACGTCACACACCTGGCTTTGGCTCCCAAGAA	2246
QY	2341	AATGTTCAAGTTGACAGCTCAAAATCTCACCAAGACCTGTTCTATGAGAAAAAGCTTTGAC	2400
Db	2247	AATGTTCAAGTTGACAGCTCAAAATCTCACCAAGACCTGTTCTATGAGAAAAAGCTTTGAC	2306
QY	2401	ATGGGAGGAAGAACTGTTGCTGCTGTGCTCCATGAGTCCGGAAGACTTGGGCAAAATCT	2466
Db	2307	ATGGGAGGAAGAACTGTTGCTGCTGTGCTCCATGAGTCCGGAAGACTTGGGCAAAATCT	2366
QY	2461	TTGTCTGTGCAAAAACCTGATCAGGTGCAACGAGAACTGAATATACAACTTTACAGGAGT	2520
Db	2367	TTGTCTGTGCAAAAACCTGATCAGGTGCAACGAGAACTGAATATACAACTTTACAGGAGT	2428
QY	2521	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTATCCCAATGGAGGGAATCCAAATTG	2580
Db	2427	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTATCCCAATGGAGGGAATCCAAATTG	2486
QY	2581	TTTATTAACGTATAAGAGTGGGTGCCCAAGAGACAGACAGACACTTTTGTATGCCGA	2640
Db	2487	TTTATTAACGTATAAGAGTGGGTGCCCAAGAGACAGACAGACACTTTTGTATGCCGA	2546
QY	2641	CCGACAGCTGCCAGGGAAGCTGCTTTGCATCAGACTCTTAAGACTGGGAAGTCAAGA	2700
Db	2547	CCGACAGCTGCCAGGGAAGCTGCTTTGCATCAGACTCTTAAGACTGGGAAGTCAAGA	2606
QY	2701	TCATCTCAGAGCACTTTGTAAAGGAGGAAAGTACAGATGCCCTCAGCTTGGCTCATGTC	2760
Db	2607	TCATCTCAGAGCACTTTGTAAAGGAGGAAAGTACAGATGCCCTCAGCTTGGCTCATGTC	2666
QY	2761	AAACTGAATAAA 2772	

XX Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 16 other;
 SQ Query Match 17.8%; Score 492.4; DB 20; Length 2273;
 Best Local Similarity 57.2%; Pred. No. 2.5e-119;
 Matches 1022; Conservative 2; Mismatches 665; Indels 99; Gaps 4;

169 GGCCTGCTACTGCTGGGACCCGCGGCGCACGCTGCTGGCGCGGCTGAGCTAGG 228
 67 GGCCTGCTGGGCTGAGCCCGCGGCGGANTCCACACGCGACGCGCNCNCTACTATC 126
 229 GAGAGCCCGCGGCGGACGAGGCGCGGAGTACCTGCTGGGAAAGCCGCTCTTAC 288
 127 GCGGCGCTCCGAGGCGCGGACGCGGACANMTTGTAGCAAGCGCGGAGGCGGCGG 186
 289 ACAGATACCAAGAGCTGCGCGGCGGACGTCAGTACCGGCGGCGGAGACTACCTAC 348
 187 GGAGCCGGGAAAGCCCGCNAACGACGCTCTTACGCAAGCTGCGAATTTCTCTAC 246
 349 AACGTGCTGAGAGAGACCCCGCGGCTGGGCTCATACACGCTTCTCTCTCTCT 408
 247 AACGTGCTGAGAGCGCGCGGCTGGGCTCATACACGCTTCTCTCTCTCTCT 306
 409 GTCCTTGGTCTGATTTTGTACAGTCTTCTACATCCTTACGACACACAAATTGGCC 468
 307 GTTCTCTCTGCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
 469 TCAAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
 367 GAGGCGGCGCTCTTACATCTTGAATCGAGTATCTGCTGCTGCTGCTGCTGCT 426
 529 ATTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 427 GTGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 589 TTGCTGGAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 487 TTTTCCAGGAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
 649 GTTCTGCAAAACCTGAGGATTAATTTTGGCAGCTGCTGCTGCTGCTGCTGCT 708
 547 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 709 CTACAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 607 TTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 769 TCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 667 TCGGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 829 CTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
 727 CTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 889 ACATATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
 787 ACCTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
 949 AAAATCTCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
 847 AAGTACCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
 1009 TCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 907 TCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
 1069 CAACACCGCGAAGAACTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1128
 967 CACATCTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1026
 1129 GTTGGCGTAGTACGAGCTAT----- 1152

Db 1027 GCCTGAGATTTATAGTACTAACCCTCTCAACGACGACCTGACACTGCGAGTAC 1086
 QY 1153 ----GAGAAATCTTTTCCATTGCAACCTGGAGCCACACTTGGAGCCTTGCACACTGC 1209
 Db 1087 TACGACGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
 QY 1210 AGCCCTTAC-----AATCAGAAAGTAACTTTTA 1237
 Db 1147 AGACTATCTCCACTCTGAAACAGCTGAGCTGCTGAGGAATCTCAAGCAAAATCTGA 1206
 QY 1238 AGAGCGAGTGCAGTCTGAGCCCGAGGCGCAGAGTATTAAAGCCAGCAAGCTCAG 1297
 Db 1207 CTACCTTACGAGAGGACACAGCCAGAGCCATACCAAGCCCGAGGATGCTGCC 1266
 QY 1298 TAGGTACAGAGAGTCCCAAGCAAGCCAGCATACAGC----- 1334
 Db 1267 AAGGAAAGGCTCTCCCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCT 1326
 QY 1335 --GAGGCGAGTCCCAAGTGCAGAGAGTGCAGAGCTTCAACGACCGAAGCCGCTTC 1392
 Db 1327 CTGATGACAGAGCCGAGCAAGTGCAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1386
 QY 1393 CGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
 Db 1387 CGCAGGCTTCCGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
 QY 1453 CTGGCAGTATGAT 1512
 Db 1447 CTTGGGAGAGACATCTGATGAGACACAGAGCTGATGCTGAGTCTGATGATGAT 1506
 QY 1513 CTACCCGACACTTAAATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1572
 Db 1507 CTACCCGCTGCTCAAGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1566
 QY 1573 AAACGAAATTTAAGAAACATTTAGTCTGATGCTGATGCTGATGCTGATGCTGAT 1632
 Db 1567 AAGCGAAATTTAAGAAACATTTAGTCTGATGCTGATGCTGATGCTGATGCTGATG 1626
 QY 1633 TCTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
 Db 1627 TCGGCTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1686
 QY 1693 ATTCTTGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGAT 1752
 Db 1687 ATTGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1743
 QY 1753 CATGAGACACAGAGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1812
 Db 1744 ACGGAGCTGCGGAG 1803
 QY 1813 CAGTCCATGAAATCCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
 Db 1804 TTGTCAATGAAAGAAAGAGCTCGACTTCTGCTGAGCATCTATACAGAG 1851

RESULT 13
 AAA47618
 ID AAA47618 standard; cDNA; 2335 BP.
 XX
 XX AAA47618;
 DT 08-NOV-2000 (first entry)
 DE
 XX
 XX KCM04 Potassium channel gene.
 KW KCM04; potassium channel; cardiac arrhythmia; neonatal epilepsy;
 KW deafness; probes; treatment; therapy; transgenic animal; antibody;
 KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
 KW presbycusis; affective disorder; Alzheimer's disease; anxiety;
 KW ataxia; cognitive deficits; compulsive behavior; dementia;
 KW depression; Huntington's disease; mania; memory impairment;
 KW motor disorders; neurodegenerative disease; Parkinson's disease;
 KW Pick's disease; psychosis; schizophrenia; spinal cord damage;

KM stroke; tremor; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 83..2170
 FT /tag- a
 FT /product- KCNQ4 Potassium channel polypeptide
 XX
 XX MO200044786-A1.
 XX
 XX 03-AUG-2000.
 XX
 XX 19-JAN-2000; 2000MO-DK00024.
 XX
 XX 26-JAN-1999; 99DK-0000076.
 XX 19-MAY-1999; 99DK-0000593.
 XX
 XX (NEUR-) NEUROSEARCH AS.
 XX
 XX Jentsch TJ;
 XX
 XX WPI: 2000-548813/50.
 XX P-PSDB; AAB01476.
 XX
 XX Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
 PT useful e.g. for treating tinnitus, deafness, Alzheimer's and
 PT Parkinson's diseases
 PS
 PS Claim 1; Page 43-48; 65pp; English.
 XX
 XX Mutations in 3 known genes of the KCNO branch of the potassium
 CC channel gene family underlie inherited cardiac arrhythmia's, neonatal
 CC epilepsy and in some cases associated with deafness. KCNQ4 has been
 CC mapped to the DFNA2 locus for autosomal dominant hearing loss, and
 CC a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
 CC pedigree has been identified. KCNQ4 is the first potassium channel
 CC gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
 CC channels with other KCNQ channel subunits, especially KCNQ3.
 CC Nucleotides encoding the KCNQ4 protein and the protein itself may be
 CC used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate KCNQ4 expression. The nucleotides may
 CC also be used as DNA probes in diagnostic assays (e.g. polymerase
 CC chain reactions (PCR)) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function
 CC of KCNQ4 polypeptides and their role in metabolism, for example
 CC through the production of transgenic animals. The KCNQ4 polypeptides
 CC may be used as antigens in the production of antibodies and to
 CC identify modulators (agonists and antagonists) of KCNQ4 expression
 CC and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may
 CC also be used to down regulate KCNQ4 expression and activity. They may
 CC be used in this way to treat tinnitus, loss of hearing (especially
 CC progressive hearing loss, neonatal deafness and presbycusis
 CC (deafness of the elderly)) and disease or adverse conditions of the
 CC central nervous system (CNS) such as affective disorder, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders and dysfunctions, motion disorders, motor disorders,
 CC neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
 CC disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
 CC cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
 CC molecules may be administered to down regulate KCNQ4 expression by
 CC binding with the cells own KCNQ4 genes and preventing their
 CC expression.
 XX
 XX Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 other;
 SQ
 Query Match 17.7%; Score 492; DB 21; Length 2335;
 Best Local Similarity 59.3%; Pred. NO. 3.3e-119;
 Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

QY 322 TACCGGCGGGTGACAGAACTACCTGATCAACAGTGTGAGAGACCCCGCGCTGGCGCTTC 381
 DB 320 TACCGCGGCTGACAGAACTAGGGGTCTACAAAGTCTGGAGCGGCCCGCGGCTGGCTTC 379
 QY 382 ATCTACACAGCTTTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 441
 DB 380 GTCTACACAGCTTCTCATATTTTGTGTCGTCTAGCTGCTGGTGTCTCTGCTCTCTCTCT 439
 QY 442 ACCATCCCTGAGACACACAAATTTGGCCTCAAGTTGCCTCTTGAATCCCGAGTTCGTATG 501
 DB 440 ACTATCCAGAGACACACAGAACTGATCCCAAGAGTGTCTCTCAATCTTGGATTCGTATG 499
 QY 502 ATTGTCGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 561
 DB 500 ATCTGCTTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 559
 QY 562 TATAGAGATGGCAG 621
 DB 560 TACCGAGATGGAG 619
 QY 622 ATTGTTCTTATGCTTCAATAGAGTGTCTTGCAGAAATCTGAGGTTAATATTTTGGC 681
 DB 620 ATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
 QY 682 ACCTGCACTCAGAGTCTCCGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
 DB 680 ACCTGCGGCTGCGGACGATGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 739
 QY 742 AGGGAGGACCTTGGAAATTTACTGGGTTCAAGTGTATGCTACAGCAAGAAATTAATC 801
 DB 740 CCGGCGGCGACCTGGAGAGTGGGCTGAGTGTCTACCGAGATACAGAGAGAGAGAGAGAG 799
 QY 802 ACAGCTTGTATCTAGAGATTTTGGTTCTATTTTGGTTCTTCTCTCTCTCTCTCTCTCTCT 861
 DB 800 ACCGCTGTGATCTGCGGTCTCTGCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
 QY 862 GAAAGAGATCCCAATTAAGAGTTTCTTACATATGACAGATGCTCTGTGGGGGACAAAT 921
 DB 860 GAG 919
 QY 922 ACATTGACAACTTTGGCTATGAGACAAATCTCCCTAACTTGGCTGGGAAATTTGCTT 981
 DB 920 ACATTGACAACTTTGGCTATGAGACAAATCTCCCTAACTTGGCTGGGAAATTTGCTT 979
 QY 982 TCTGAGGCTTGTGACCTCTGAGATTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1041
 DB 980 GCTGCTGGCTTGTGACCTCTGAGATTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1039
 QY 1042 TCAGTTTGTGCAATTAAGATGACAAAGACACCGCCAGAAACCTTTGAGAAAGAGAG 1101
 DB 1040 TCCGGCTTGTGCAATTAAGATGACAAAGACACCGCCAGAAACCTTTGAGAAAGAGAG 1099
 QY 1102 AACCCAGCTGCAACCTCATCTAGTGTGTTGGGTAGTATGAGAGAGAGAGAGAGAGAG 1161
 DB 1100 ATCCGCGGACCACTCATCTAGTGTGTTGGGTAGTATGAGAGAGAGAGAGAGAGAG 1159
 QY 1162 GTTTCATTGCACTGGAAGCACTTGAAGGCTTTGACAC----- 1205
 DB 1160 GCTTACTGACAGCACTGTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
 QY 1206 ----- 1205
 DB 1220 GCGCTTGTGTTGAGCAGTGAACAGGGCCCGCAATG666GCTTACGGCCCTGGAAGGTG 1279
 QY 1206 ----- 1205
 DB 1280 CCGCGGCGCGGCTACCCGAGAGACACCTCCCGTTACCGCGCGCTTGGACCTGCGAC 1339
 QY 1206 -----CTGAGCGCTTACCAATGAGAGCTTAAGTTTAAAGAGAGCA 1245
 DB 1340 CCGCGGCGGACGACCT 1399

QY 1248 GCGATGGCTAGCCGCCAGGCGCAGATATTAGAGCCGCAAGCCTCAGTAG-----G 1301
 Db 1450 ---CTTCTCCAGCCCCCGAGGGGTGGCTGCCAAGGGAGGGGTCCCCGAGGCCAGAC 1506
 QY 1302 TGACAGAGAGTCCCAAGCAGCATCAAGCCGAGGGAGTCCCAACAAATGACAGAA 1361
 Db 1507 TGTGAGGGGCTCACCAGCGCCAGACAGACCTGAGAGACAGCCCCAGAGGTGCCAA 1566
 QY 1362 GAGCTGAGCTTTCACAGCCGACCGCTTCCGGCCCTCGCTCGCTCAAAAGTTCTCA 1421
 Db 1567 GAGCTGAGCTTTCGAGGAGCCGAGCCGAGCCGAGCTTCCGAGTCAAGGGTGCAGC 1626
 QY 1422 GCCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1481
 Db 1627 GTACAGGAGAACTCAGA---AGAAGCAAGCCTCCCCGAGAGACATTTGTGATGACAA 1663
 QY 1482 AGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1541
 Db 1684 GAGCTGCCCCCTGCGAGTTGTGACCGAGACCTGACCCGCGCTCAAAAGTCAGATCAG 1743
 QY 1542 AGCTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1601
 Db 1744 AGCGGTGTGTCTACGCGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1803
 QY 1602 ATATGATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1661
 Db 1804 CTACGAGCTGATGAGACGCTATGACGACGATGACGACGACGACGACGACGACGACG 1863
 QY 1662 AATTAAGACCTTCAAAACAGCTGATGATGATGATGATGATGATGATGATGATGATG 1721
 Db 1864 AATTAAGACCTTCAAAACAGCTGATGATGATGATGATGATGATGATGATGATGATG 1923
 QY 1722 TAAGAGAGCCGAGAGAAATTAACAGCATGATGATGATGATGATGATGATGATGATG 1781
 Db 1924 CAAGGA---CCGACCAAGAGGCGCGGAGGCGAGGAGCGCGGAGGAGCGCGGAGGAG 1980
 QY 1782 CGGCTGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1841
 Db 1981 GGGAGCGGCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
 QY 1842 ACTAGACATCTATCAACAG 1860
 Db 2041 GGTGAATATCTACTACGACG 2059
 RESULT 17
 AAX81548
 ID AAX81548 standard; DNA; 2565 BP.
 AC AAX81548:
 XX 25-AUG-1999 (first entry)
 DE Human brain-derived potassium channel DNA structural DNA.
 XX
 KW Human: brain-derived potassium channel; neurophysiology;
 KW cognitive disorder; behavioural disorder; psychiatric disorder;
 KW neurodegenerative disorder; developmental disorder; mental retardation;
 KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
 KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 OS Homo sapiens.
 XX
 XX W09931232-A1.
 PN

XX
 PD 24-JUN-1999.
 XX
 PF 11-DEC-1998; 98MO-GB03720.
 XX
 PR 13-DEC-1997; 97GB-0026339.
 XX
 PA (ZENRE) ZENRECA LTD.
 XX
 PI Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 DR WPI; 1999-395178/33.
 XX
 PS New isolated potassium channel polypeptide
 PS Claim 2: Fig 2; 151pp; English.
 CC
 CC The present sequence represents brain-derived potassium channel DNA.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 S0 Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other;
 Query Match 16.1%; Score 447; DB 20; Length 2565;
 Best Local Similarity 56.8%; Pred. No. 2,7e-107;
 Matches 1038; Conservative 0; Mismatches 645; Indels 144; Gaps 6;
 QY 169 GGCCTGCTACTGCTGCGACCCGCGCGGCGGCTGCGGCGGCGGCGGCTGAG 228
 Db 67 GCGTTCGTGGGCTGAGACCCCGCGCGCGGCGGCGGCGGCGGCGGCGGCTGATC 126
 QY 229 GAGAGCCCGCGGCGGAGCAGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCTCTTAC 288
 Db 127 GCGGCTCCGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
 QY 289 ACGAGTACCGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 Db 187 GCGGCGGCGGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
 QY 349 AACGCTGTGAGAGAGACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 Db 247 AACGCTGTGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
 QY 409 GTCTTTGGTCTGCTGATTTTGTCACTGTTTGTACCATCCCTGAGACACAAATTTGGCC 468
 Db 307 GTTTTCT 366
 QY 469 TCAGATGGCCCTTGATCTGAGAGTTTCTGATGATTTGTCTTTGGTTGGAGTTTCATC 528
 Db 367 GAGGGGCGGCTCTATCATCTCTGAAATCTGATATCTGTTGTTGGCGGTGACTTTC 426
 QY 529 ATTGGAATCTGCTGTGCGGTTGCTGTTGCTGATATAGAGATGCAAGAGACGAGAG 588
 Db 427 GTCCGAAATCTGCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
 QY 589 TTTCCTGAAAGGCCCTTCTGTGTTATATAGATACCATTTCTTATGCTTCAATAGAGATT 648

Db	487	TTTTGCCCGGAACCGTTTCTGTGTGATTTGACATATATGTGTCTATCCGCTCCATTTGGGGT	546
QY	649	GTTTTCGCAAAAACCTCAGGGTAATATTTTTCGCCAGCTGTGCACTCAGAAAGTCTCGTTTC	708
Db	547	CTGGCCGGCCGGCTCCCAAGGGCAACGCTTTTGTCCACATCTGTGCGTCCGGAGCCCTGCCTTC	606
QY	709	CTACAGATCTCTCCGCATGTGGTCCGATATGACACCGAAGGGGAGGACCTTGAAATATCTGGGT	768
Db	607	CTCAGATTTTGTGGGATGATCCCATATGGACCGCGGGGAGGACCTTGGAGCTGTCTGGG	666
QY	769	TCAGTGGTTTATCTCTCACAGCAAGAAATTAATACAGCTTGTATAGATTTTGGT	828
Db	667	TCGTGGTCTATATGCCACACGAAAGAGCTGTGACTGTGATCCCTGTATATCGGCTCTCTTGT	726
QY	829	CTTATTTTTCGTCCTTTCCTTGTCTATCTGTGTGAAAAGGATGCCAATAAAGATTTC	888
Db	727	CTATCTCTGGCCCTCGTTCCTGCTGTACTTGTGGCAGAGAGGGGAGAAACGACCACTTTGAC	786
QY	889	ACATATGCAGATGCTCTGTGTGGGGACCAATTAACATTTGCAACTATTTGGCTATGGAGAC	948
Db	787	ACCTACGGCGATGACACTCTGTGTGGGCGCTATACGCTGTACACACATTTGGCTACGGGAC	846
QY	949	AAAATCCCTCTAACCTTGGCTGGGGAAGATGTCTTTCGACAGCTTGTGCATCTTGGCATT	1008
Db	847	AAGTACCCCAAGACTGTGAAACGGACGAGCTCTTTCGCGCAACCTTCACTCATCTGGTGT	906
QY	1009	TCTTTCTTTTGACCTTCTCGCGGCAATCTTGGCTCAGTTTGTGATTAAGATACAAAGAA	1068
Db	907	TCTCTCTTCTGGCTGCTCGACAGGATCTTGGGGCTGTGGTTTGCCTTGAAGTTTCAAGAG	966
QY	1069	CACACACGCGCAGAAACACTTTGAGAAAAAGAAAGAACACAGCTGCGCAACCTATTCAGTGT	1128
Db	967	CAGACACAGGCAAGAGCACTTTGAGAAAGAGGGGGAACCCGGACGACGCTGATCAGATCG	1026
QY	1129	GTTTGGCGTAGTTCGCACTGTAT-----	1152
Db	1027	GCTGTGGAGATTCTAGCGCACCAACACCTCTCGGCGACAGACCTGCACCTCAGCTGGCAGTAC	1086
QY	1153	---GAGAAATCTGTTTCCATTTGCAACCTGGAAGCGACACTTGAAGGCTTTCGCAACCTGC	1209
Db	1087	TACGAGCGAAGGTTCACCGTGTCCCATGTACAGTTTCGCAAACTCAACCTACGGGGCGTCC	1146
QY	1210	AGCC-----	1213
Db	1147	AGACTTATCCCCCGCTGTGAACCAAGCTGTGAGAGAACTCAAGAGTAATCTGGA	1206
QY	1214	-----CTACACATTCAGAAAGCTAATTTAAG	1239
Db	1207	CTCGCTTTAGGAAGAGACCCCCCGCGGAGCCGTCTTCCAAACCCAGAAAGTATAGTTTGAAA	1266
QY	1240	GAGCAGTAGCGCATGTGCTAGGCCCGAGGGCCAGAGTAATTAAGAGCCGCAACAAAGCTCAGTA	1299
Db	1267	GATGTGTG---CTTCTCCAGCCCCCGAGGCTGTGCGTGCAGAGGGGAAGGGGTCCCGCGAG	1323
QY	1300	G-----GTGACAGGAGGTCCCCCAAGACCCGACATCAAGCCGAGGGAGTGTCCACACAA	1355
Db	1324	GCCCACTGTGAGGCGGTGTACCCAGCCGCAACAGACCTGTGAGAGACAGCCCAACGCAAG	1383
QY	1354	GTGCGAAGAGGTGTGAGCTTCAACAGCGAAACCGCTTCCGAGCCCTGCTCGCTCTCAAA	1413
Db	1384	GTGCCCAAGAGCTGTGAGCTTCCGGGAGCCGCAACCGGAGACCGCAGAGCTTTCCGATCAAG	1443
QY	1414	AGTTCTCAGCCAAAACAGATAGATGTCTGACACAGCCCTTGGCAGCTGATGATGTATAT	1473
Db	1444	GGTGCGCGGTG---ACGGCAGAACTCAAGAAAGAAAGAAACCTCCCGGAGAGGACATTTGTG	1500
QY	1474	GATGAAAAAGATGTGCAGTGTATATACAGTGTGAAGACCTTACCCCAACCTTAATACT	1533
Db	1501	GATGACAAAGAGCTGCCCTCTCGAGTTTGTGACCGGAGACCTGACCCCGGGCTCAAAAGTC	1566
QY	1534	GTCAATTCGAGCTATCAGAAATTAATTAATTTCAATGTTCAAAACGGAAGTTTAAGAAACA	1599

Db	1561	AGATTCAGAGCCGCTGTGTGCATCCGGTCTCGTGTCCAAAGCGGAATTCAGAGAGAGC	1620
QY	1594	TTAGCTCCAAATGATGTATAAAGATGTCTATTAAACAATATTCTGCTGGTCATCTGAACTG	1653
Db	1621	CTGGGGCCCTTCGACGTGTATGGACTGTCTTCAGCGATCTAAGCCGGCCACTTGGACATG	1680
QY	1654	TTGTGTAGAAATTAAGAAGCCTTCAAACACAGTGTTCATCAAAATCTTGGAAAAAGGCAAAATC	1713
Db	1681	CTGTCCGAAATTAAGAGGCTCGACGCCAGAGTGCACCGATCTGTGGGCGGGGCCCAACGG	1740
QY	1714	ACATTCAGATTAGAAGAGCCGAGAGAATAATACAGAGAAATCTGAGACACAGACGATGCT	1773
Db	1741	ATCACGGGCAAGGA---CCGACCCAGAGGCCCGGCCGAGGGGAGACTCCCGAAGGAAACCC	1799
QY	1774	AGTAGTCTCGGTGCGGTGATCAAGGTTGAAAAACAGGTACAGTCCATGTGAATCCAAAGCTG	1833
Db	1798	AGCATGATGAGGACGCGCTCGGGGAAGGTGGAGAAGCAGGTCTTGTCCATGGAGAAGAAAGCTG	1857
QY	1834	GACTGCTACTAGACATCTATCAACAG	1860
Db	1858	GACTTCTGTGTAATATCTACTACTGAG	1884

CC	nucleic acids are used as probes or primers, either for detecting
CC	treat or prevent these forms of epilepsy. Fragments of the encoding
CC	in cell-free form) are used to screen for agents that can be used to
CC	that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC	epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC	prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
CC	KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC	KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC	This invention describes novel human and mouse potassium channel proteins
XX	Claim 1; Page 131-136; 195pp; English.
PS	Nucleic acid encoding potassium channels KCNQ2 and 3
DR	P-PsDB; AAY08344.
XX	WPI: 1999-312938/26.
XX	Charlier C, Leppert MF, Singh NA;
XX	(UTAH) UNIV UTAH RES FOUND.
XX	PR 24-OCT-1997; 97US-0063147.
XX	PF 23-OCT-1998; 98WO-US22375.
XX	PD 06-MAY-1999.
XX	PN WO921875-A1.
XX	Key Location/Qualifiers
FT	CDS 19..2637
FT	/tag= a
FT	/product= "KCNQ3"
OS	Homo sapiens.
XX	
KM	JME: rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW	detection; gene therapy; drug screening; ss.
KW	benign familial neonatal epilepsy; BFNE; juvenile myoclonic epilepsy;
KW	KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
XX	Human KCNQ3 cDNA.
DE	
DT	22-JUL-1999 (first entry)
XX	
AC	AAX57059;
ID	AAX57059 standard; DNA; 2914 BP.
RESULT 18	

ID	Accession	Standard	DNA	Length (BP)
YY	1354	gTGCAGAAAGCTGGAGCTTCAAGCAGCAACCCGCTTCCGGCCCTGCTGCGCCCTCAAA	1413	
Db	1393	gTCCCCCAAGAGCTGGAGCTTGGGGACCGCACCGCCGACGCTTTCCCATCAAG	1452	
QY	1414	AGTTCACAGCCAAACCAAGTATAGATCTGTGACAGAGCCCTTGGCACTGATGATATAT	1473	
Db	1453	GGTCCGCGCTCACGGCAGAACTCAGAAAG---AAGCAAGCTCCCGGAGAGGACATTTGTG	1509	
QY	1474	GATGAAAAAAGATGCCAGTGTGATGTATCATGTGTAAGAGACCTCACCCACCACTTAAACT	1533	
Db	1510	GATGACAAAGAGCTGCCCTTCGAGCTTGTGACCCGAGGACCTGACCCCGGCTTCAAAATC	1569	
QY	1534	GTCATTCGAGCTATCAGAAATTTGAAATTTTCATGTTGCAAAAGGAAGTTTAAGAAACA	1593	
Db	1570	AGCATGAGAGCCCGTGTGTGTCATGGGGTTCCTGTGTGTCCAAAGCGAAATTCAAAGGAGC	1629	
QY	1594	TTACGTCATATGATGTTAAAAAGATGTCATTGAAACAATATTCTGTGTCATCTGGACATG	1653	
Db	1630	CTGCGGCGCCCTACGACGATGATGAGCTCATCGAGCTACTGACCCGGCCACCTGGACATG	1689	
QY	1654	TTGTGTAAGATTTAAAGCCTTCAAAACAGCTGTGTATTCAAATCTGGAAAAAGGGCAATC	1713	
Db	1690	CTGTCCCGATTTAAGAGCCTCTCAGTCCAGAGTGGACCCAGATGCTGGGGCGGGCCCAAGC	1749	
QY	1714	ACATCGATTAAGAAAGACCCGAGAAAAATAACAGCAGAAATGAGACCAAGAGATCTC	1773	
Db	1750	ATCACCGACACAAGA---CCGACCAAGGGCCCGCGGAGCGGAGCTGCCGAGGACCC	1806	
QY	1774	AGTATCTCGTGGTGGGTGTGTCAAGCTTGAATAAACAGGTACAGTCCATAGATCCAAGCTG	1833	
Db	1807	AGCATATGAGGAGGCTCGGGAAAGTGGAAGACAGGTCTTGTGCATGGAAGAAAGCTG	1866	
QY	1834	GACTGCTACTAGACATCTATCAACAG	1860	
Db	1867	GACTTCTGCTGTAATATCTCATGTCAG	1893	
RESULT 20				
YY	AAK57141	standard	DNA	2814 BP
AC	AAK57141			
XX	AAK57141			
DT	22-JUL-1999	(first entry)		
DE	Mouse KCNQ3 cDNA			
KW	KCNQ3; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;			
KW	benign familial neonatal epilepsy; BFNK; juvenile myotonic epilepsy;			
KW	JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;			
KW	detection; gene therapy; drug screening; ss.			
OS	Mus musculus			
FT	Key	Location/Qualifiers		
FT	CDS	202..2814		
FT		/tag= a		
FT		/product= "KCNQ3"		
PN	W09921875-A1			
PD	06-MAY-1999			
PE	23-OCT-1998	98WO-US22375		
PR	24-OCT-1997	97US-0063147		
PA	(UTAH) UNIV UTAH RES FOUND			
PI	Charlier C, Leppert MF, Singh NA;			
PI	WPI; 1999-312938/26			
PI	P-PSDB; AAY08346			

XX Nucleic acid encoding potassium channels KCNQ2 and 3
PT
XX
PS Claim 1; Page 159-163; 195pp; English.
XX
XX This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available.
XX

50 Sequence 2814 BP; 667 A; 753 C; 796 G; 590 T; 8 other;

Query Match	Score	DB	Length
15.68;	432;	20;	2814;

Matches 962; Conservative 3; Mismatches 673; Indels 58; Gaps 7;

OY		50	GAGGTAAACAGCGGACCACAGCGCGGGCGGCGCGGGCGGGCGCTTGGGCAGCGGCATGA	109
Db		225	GGCTGGCGGGGGCGCGCGGAGAGGGGGCCGCCGAGCGCGGCCGCTAACCTCCTCTGG	284
OY		110	AGGATGTGGACTCGGGCGGGGCGAAGGTCTCTGTCAACTCGGCAGCGCCAGAGGGCGACG	169
Db		285	AGG-GGAACTCGGGCGGTGGCGCGCGCGACGAGAGAACGGAAAAATGGGGCTGGCGCCAGGAGACG	343
OY		170	GCTGCTCTCTCTGTGGGCAACCGCGGGGCGCACCTCGGTGGCGGGCGGGCTGGACG	229
Db		344	TGGAGCAAGTCACCTTTGGCGCTTAGGGGGCCGGAGCCGACAAAAGCGGAGCCCTGTCTGG	403
OY		230	AGAGCCGGCGGGGCGCAAGCAGGGGGCGCCGGATTAGCTGTGCGGGAGAAGCCGCTCTCTTACA	289
Db		404	AGGGCGGGTGCGCGGGAAGAGGGGCGACAGAGAGAACCCCGAGGGCATCTGGGCTCTCTGGCAA	463
OY		290	CGAGTAGCCAGACTGCC-----GGCCAGCTCAAGTACCGGGCGGGTGCGAAGACT	340
Db		464	AGACCCCCCTGAGCGCCGCACTGCAAGAGAAACAAACGCCAAGTACAGGGCATCCAACACTT	523
OY		341	ACCTGTACAACTGCTGTGGAGAGACCCCGCGGTGGGGCTTATCAACACGCTTTCGTTT	400
Db		524	TGATCTATGACGCCCTTGAGAGAACCGCGGGGGTGGGCCCTGCTCTTACACAGCGCTTGT	583
OY		401	TTCTCTCTTCTTGGTTGTTGTTGTAATTTGTCAAGTTTTCTACCAATCCCTGAGCACANA	460
Db		584	TCTGATTTGTCTGGAGTCTTGATTCTTGGCGCTCACACACTTCAAGGAATATGAGA	643
OY		461	AATGGCCCTCAAGTTGCCCTCTTGATCCTGGAGTTCTGATGATTTGCTCTTGGTTTGG	520
Db		644	CTGTGTTGGAGACTGGCTTTTGTCTGCGAATAATTGTCAATTTTCACTTTTGGAGCG	703
OY		521	AGTTCAATCATTCGAATCTGGTCTCGCGGGTTCTGTGTGCAATATAGAGAGTGGCAAGAA	580
Db		704	AGTTTGCCTTGGAGATCTGGCTCAGAGATTTGTCTGCAATACAAAGCTGGCGTGGAC	763
OY		581	GACTGAGTTTGTCTGAAAGCCCTTCTGTGTTATAGATATCATATGTTTATATTCCTTCAA	640
Db		764	GGCTAAAGTTTGGCAAGAGCCCTCTGACATGTTGGACATCTTGTAATGATGCTCTCG	823
OY		641	TACACAGTTCTTTCGCAAAAACCTAGGGTAATATTTTGGCAGCGTCTGACTCAGAACTC	700
Db		824	TGCGAGTGTGTTGCGGTGGGAAACCAAGGACAAATGTTCTGGCCACCT--CCCTGGCAACC	880

```

OY 701 TCGTTTCCAGACATCTCCGATGGTGGCATGAGCCGAGGAGGACCTTGAAT 760
DB 881 TTGCTTCCGCGAGATCTCCGATGCTTGAATGATGAGAGGGGTGGACCTGGAAAC 940
OY 761 TACTGGGTCAGTGGTTTATGCTACAGCAAGAAATTAATCAGCTGTGATAGAT 820
DB 941 TCGTGGGCTGGCTATCTGTGCCACAGCAAGAAATCATGCTGGTACATAGCT 1000
OY 821 TTTTGGTCTTATTTTCTTCTTCTTCTTCTATCTGTGGTGAAGAAAGATG----- 871
DB 1001 TCGTACACTCATCTCTTCTTCTTCTTCTTCTTCTGCTGAGAGAGATGTGCGAGAA 1060
OY 872 -----CCAATAAGAGTTTCTACATATGAGATCTGCTGTG 910
DB 1061 TGGATGCCAGAGAGAGATGAGAGAGTTTGAAGACCTATGAGATCTGTGTGT 1120
OY 911 GGGGCAATTTACATTTGACATATTTGGTATGAGAGCAAAATCCCTTAATTTGGCTGG 970
DB 1121 GGGGCTGATCACACCTGGCCACCATTTGTTATGAGAGACACCTAAACCTGGGAAG 1180
OY 971 GAGATTTGCTTGTGAGGCTTGTGACATCTGTGCACTTTCTTCTTGTGCACTTCTGCG 1030
DB 1181 GAGCTGTGATGTGCTGACCTTTCTTAACTGCGCTCTCTTTTGTGCTCCGAG 1240
OY 1031 GCATCTTGTGCTGAGTGTGCTTGAATTAAGTACAGAAACACCGCAGAAACCTTTG 1090
DB 1241 GCATCTTGTGCTGAGTGTGCTGAGTGTGCTGAGAGACACCGCTGAGAAAGCTTTG 1300
OY 1091 AGAAAGAGAGAAACCCAGCTGCGACCTCATTCAGTGTGCTTGTGCTGATAGCAGCTG 1150
DB 1301 AGAAGAGAGAGAAACCCAGCTGCGACCTCATTCAGTGTGCTGATAGCAGCTG 1360
OY 1151 A---TGAAATCTGTTTCAATGCAACCTGGA-----AGCCACACTGGAAGGCTGCG 1201
DB 1361 ACCCCAGAGAGTGTGCTGCTGCTGCAACCTGAGATCTTATGATCACTGTCTCTTCC 1420
OY 1202 ACACCTGCAAGCCCTACCAATCAGAACTAAAGTTTAAAGGAGCGAGTGGCATGCGTACC 1261
DB 1421 CATTTTCAAGAAAGAAACCACTGAGAGAGAGCGCAAGCAAGCTGTGCTGTGATC 1480
OY 1262 CCAGGGGCGCAGATATTAAAGCCGACAAAGCTCAGTAGTACAGAGAGGTCGCCAAGCA 1321
DB 1481 GGGTGGCTTTTAACTCTGCTGCTGAGCAATTAAGGAAAGCTATTTACCCCTGGA 1540
OY 1322 CCGACATCAAGCGAGGAGAGTCCCAAGAGTGAAGAGCGAGCTTCAAGCAGC 1381
DB 1541 ATGTAGATGCCATAGAAAGAAAGCCCTTCCAAAGAGCCAAAGCTGTGCTTAAACAATA 1600
OY 1382 GAACCGGCTTCCGGCCCTGCTGCGCTCAAAAGTTCTACAGCAAAACAGTATAGATG 1441
DB 1601 AAGAGGCTTCCGGAGCCCTTCCGCAAGAAAGCTTCTTGGCAGAGGCTGTAAG 1660
OY 1442 CTGACACAGCCCTTGGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1501
DB 1661 ATCTGCGAGAGCGAGCCCATGCA-----GAAGAGAGGGGCTATGGGATGCAATGCC 1714
OY 1502 CAGTGAAGAGCTCAACCAACCACTTAAAGTGTCACTGAGTATGCAATTAAGAAT 1561
DB 1715 TCAATTGAGACATGATCCCTRCCTTAAAGCTTGAAGCTCGAGCTGCAAAATTCACAGT 1774
OY 1562 TTGATGTTGCAAAACGAGAGTTTAAAGAAACATTACGCTCATGATGATGATGATGATGAT 1621
DB 1775 TCGGCTATATTAATAAAAGTTCAAGAGAGAGCTTGAAGCTTGAAGATGATGATGATGAT 1834
OY 1622 TTGAACAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681
DB 1835 TTGAGCAGATTTGGCGGAGCATCTGACATCTTCCAGATTAAGTACCTACAGACAA 1894
OY 1682 GTGTGATCAAAATCT 1697
DB 1895 GAATGATATGATTTT 1910

```

```

RESULT 21
ABK64418
ID ABK64418 standard; DNA: 1425 BP.
XX
AC ABK64418;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #313.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001MO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
XX
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
XX
PA (NISH) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarini P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI: 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
XX
PT detecting expression levels of one or more genes in prostate cells from
XX
PT patient that are differentially regulated compared to normal prostate
XX
PT cells.
XX
PS Disclosure; Page 188; 444pp; English.
XX
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of at least one gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
XX
Sequence 1425 BP; 231 A; 462 C; 439 G; 293 T; 0 other;
XX
Query Match 15.5%; Score 429.4; DB 24; Length 1425;
Best Local Similarity 61.5%; Pred. No. 8,7e-103;
Matches 707; Conservative 0; Mismatches 436; Indels 6; Gaps 1;
OY 3 GCCCCGACACACGCGGAGAGAGAGGCGCGCGCGCTGTGGTGAAGCGG 62
DB 72 GCCATGCGGCTCCCGCGGCGGCGCTGTGGTGGCGCGCGCGCGCTCGC 131
OY 63 CGAGCGGCGGCGGCGGCGGCGGCGGCGCTGTGGAGGAGTGTGAGTCT 122
DB 132 CCCCCTGAGCTGAGCCGACCCGCGGCGGCGCTTCCGCGAGGACCATGTGTGCAAGTCT 191

```

QY	123	GGCGCGGGGACAGGATGCTCTGTGAACCTCGGACAGCCGCA-----GGGGGAGCGCGCTGCT	176
Db	123	GGCGCGGGGACAGGATGCTCTGTGAACCTCGGACAGCCGCA-----GGGGGAGCGCGCTGCT	176
QY	129	GGGCAACGGCGGGCTGTATACCCGGGCGGAGCGGGGAGAAAGAAAGCTGAAGGTGGCTTCGT	251
Db	129	GGGCAACGGCGGGCTGTATACCCGGGCGGAGCGGGGAGAAAGAAAGCTGAAGGTGGCTTCGT	251
QY	177	ACTGCTGGGACACCGCGCGGGCAACGCTCGGTGGCGGGCGGGTGGCTTAGAGGAGAGCCG	236
Db	177	ACTGCTGGGACACCGCGCGGGCAACGCTCGGTGGCGGGCGGGTGGCTTAGAGGAGAGCCG	236
QY	252	GGGGGCTGGACCCCGGGGGCGCCGACCTCCACCCGGGAGCGGGGGCGCTGTATGGCCGGCTC	311
Db	252	GGGGGCTGGACCCCGGGGGCGCCGACCTCCACCCGGGAGCGGGGGCGCTGTATGGCCGGCTC	311
QY	237	CCGGGGGCAAGAGGGGGGCCGGATGAGCTGCTGGGGGAAGCCGCTCTTTACACGATG	296
Db	237	CCGGGGGCAAGAGGGGGGCCGGATGAGCTGCTGGGGGAAGCCGCTCTTTACACGATG	296
QY	312	CGAGGCCCCCAAGCGCGGGAGCATCCTCCAGCAAAACCTCGCGGGGGGGCGCGGCGCCG	371
Db	312	CGAGGCCCCCAAGCGCGGGAGCATCCTCCAGCAAAACCTCGCGGGGGGGCGCGGCGCCG	371
QY	297	CCAGAGCTGCGCGGCGCAACGTCAGATCGGCGGGGCGAGAACTACCTGTACACGCTGCT	356
Db	297	CCAGAGCTGCGCGGCGCAACGTCAGATCGGCGGGGCGAGAACTACCTGTACACGCTGCT	356
QY	372	GAAAGCCCCCAAGCGGCAAGCGCTTCTACCGCAAGCTGCGAGAAATTCCTCTACACGCTGCT	431
Db	372	GAAAGCCCCCAAGCGGCAAGCGCTTCTACCGCAAGCTGCGAGAAATTCCTCTACACGCTGCT	431
QY	357	GGAGAGACCCCGCGGCTGGGGCTTCACTTACCAACGCTTTCGTTTTCTCCCTGCTTTGG	416
Db	357	GGAGAGACCCCGCGGCTGGGGCTTCACTTACCAACGCTTTCGTTTTCTCCCTGCTTTGG	416
QY	432	GGAGGGGGCGCGCGGCTGGGGCTTCACTTACCAACGCTTTCGTTTTCTCCCTGCTTTTC	491
Db	432	GGAGGGGGCGCGCGGCTGGGGCTTCACTTACCAACGCTTTCGTTTTCTCCCTGCTTTTC	491
QY	417	TTGCTGATTTTGTGAGTGTTCACCAATCCCTAGACACAAAAATTGGCCTCAAGTTG	476
Db	417	TTGCTGATTTTGTGAGTGTTCACCAATCCCTAGACACAAAAATTGGCCTCAAGTTG	476
QY	492	CTGCTCTGCTGCTGTGTGTGTTTCCACCAATCAAGGAGATGAGAAAGCTCGAGGGGCG	551
Db	492	CTGCTCTGCTGCTGTGTGTGTTTCCACCAATCAAGGAGATGAGAAAGCTCGAGGGGCG	551
QY	477	CCCTTGATTCCTGAGATTCGTGATGATTTGCTCTTTGGTTTGGATTCATTCGAT	536
Db	477	CCCTTGATTCCTGAGATTCGTGATGATTTGCTCTTTGGTTTGGATTCATTCGAT	536
QY	552	CCCTACATCTCGGAAATCGTACATGCTGTTGTTTGGCGTGGATTCCTGTGGGAT	611
Db	552	CCCTACATCTCGGAAATCGTACATGCTGTTGTTTGGCGTGGATTCCTGTGGGAT	611
QY	537	CTGGTCTCGGGGTCTGCTGTTCGATATAGAGATGGCAGAGAACGATGAGTTGCTCG	596
Db	537	CTGGTCTCGGGGTCTGCTGTTCGATATAGAGATGGCAGAGAACGATGAGTTGCTCG	596
QY	612	CTGGGCGCGAGGCTCTGCTGCGGATACCCTGGCGGAGAGGGGCGGCTCAGCTGACGTTG	671
Db	612	CTGGGCGCGAGGCTCTGCTGCGGATACCCTGGCGGAGAGGGGCGGCTCAGCTGACGTTG	671
QY	597	AAAGCCCTCTGCTGTATAGATACCATTTGTTTCGCTTAAATAGACGTTGTTCTG	656
Db	597	AAAGCCCTCTGCTGTATAGATACCATTTGTTTCGCTTAAATAGACGTTGTTCTG	656
QY	672	GAAACCGTTCTGTGTGATGTGATCATGTGTGCTCATGCGCTCATTTGCGGTGCTGGCCG	731
Db	672	GAAACCGTTCTGTGTGATGTGATCATGTGTGCTCATGCGCTCATTTGCGGTGCTGGCCG	731
QY	657	AAAAACTAGGCTAATPATTTTTGCCACGCTGCTACCTCAGAGCTCCGTTTCCCTACGAT	716
Db	657	AAAAACTAGGCTAATPATTTTTGCCACGCTGCTACCTCAGAGCTCCGTTTCCCTACGAT	716
QY	732	CGGCTCCAGGGCAACGCTTGTGCCACATCTCGCTCCGAGACCTGCGCTTCTCGACGAT	791
Db	732	CGGCTCCAGGGCAACGCTTGTGCCACATCTCGCTCCGAGACCTGCGCTTCTCGACGAT	791
QY	717	CTCCGCAATGGGCGCATGGACCGAAGGGGAGGACCTTGGAATATACCTGGTTCAGTGT	776
Db	717	CTCCGCAATGGGCGCATGGACCGAAGGGGAGGACCTTGGAATATACCTGGTTCAGTGT	776
QY	792	TCTGGGATGATCCCATGATGACCGCGGGGAGGACCTGGAAGCTGTGTGGCTCTGTGTGT	851
Db	792	TCTGGGATGATCCCATGATGACCGCGGGGAGGACCTGGAAGCTGTGTGGCTCTGTGTGT	851
QY	777	TTATGCTCACAGCAAGGAATTATTCACAGCTTGATACATAGGATTTTGGTCTCTAATTT	836
Db	777	TTATGCTCACAGCAAGGAATTATTCACAGCTTGATACATAGGATTTTGGTCTCTAATTT	836
QY	852	CTATGCCCAACAGCAGGAGCTGTGATCGCTGATACATCGGCTTCTTGTCTCATCT	911
Db	852	CTATGCCCAACAGCAGGAGCTGTGATCGCTGATACATCGGCTTCTTGTCTCATCT	911
QY	837	TTGCTGTTTCCCTGTCTATGCTGTGGAAGGAAGATCCCATTAAGATTTTCTACATATG	896
Db	837	TTGCTGTTTCCCTGTCTATGCTGTGGAAGGAAGATCCCATTAAGATTTTCTACATATG	896
QY	912	GCGCTCGTTCTTGTTGTTACTGTGGCAGAGAGGGGAGAACGACCACTTGGACACCTACCG	971
Db	912	GCGCTCGTTCTTGTTGTTACTGTGGCAGAGAGGGGAGAACGACCACTTGGACACCTACCG	971
QY	897	AGATGCTCTGTTGGGGGACAAATTCATTCATTTGAGTATGGAGCAAAACATCC	956
Db	897	AGATGCTCTGTTGGGGGACAAATTCATTCATTTGAGTATGGAGCAAAACATCC	956
QY	972	GGATGCACTGTGTGGGGCGTGATCAGCTGTACCAACATTTGGCTACGGGGGAACAATACCC	1033
Db	972	GGATGCACTGTGTGGGGCGTGATCAGCTGTACCAACATTTGGCTACGGGGGAACAATACCC	1033
QY	957	CCTACTGTGCTGGGGAATGTTCTTTCGACAGCTTTCGACTCCTTGGCATTTCTTCTT	1011
Db	957	CCTACTGTGCTGGGGAATGTTCTTTCGACAGCTTTCGACTCCTTGGCATTTCTTCTT	1011
QY	1032	CCAGAACCTCGAGACGGCAGCTTCCTGCGCAACCTTCACCCCTGAGTGTCTCCCTCT	1091
Db	1032	CCAGAACCTCGAGACGGCAGCTTCCTGCGCAACCTTCACCCCTGAGTGTCTCCCTCT	1091
QY	1017	TGCATTCCTGCGGCAATTCCTGGCTCGAGTTTTCATTAAGATACAAAGAACACACCG	1076
Db	1017	TGCATTCCTGCGGCAATTCCTGGCTCGAGTTTTCATTAAGATACAAAGAACACACCG	1076
QY	1092	CGCGCTGCTCTCAGGCAATCTTGGGGTCTGGGTTTTCCTGAAAGGTTAGAGACACACAG	1155
Db	1092	CGCGCTGCTCTCAGGCAATCTTGGGGTCTGGGTTTTCCTGAAAGGTTAGAGACACACAG	1155
QY	1077	CCAGAAACCTTTGAGAAAGAGAAACCAACGCTGCGCAACTCATTCAGTGTGTT	

ID	AAK57057 standard; DNA; 3232 BP.
XX	
AC	AAX57057;
DT	22-JUL-1999 (first entry)
XX	
DE	Human KCNQ2 cDNA.
KW	KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis; benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME; rolandic epilepsy; mutant; treatment; screening; epilepsy; detection; gene therapy; drug screening; ss.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers CDS 128..2746 /tag= a /product= "KCNQ2"
FT	
PX	WO921875-A1.
PN	
PD	06-MAY-1999.
PF	23-OCT-1998; 98WO-US22375.
PR	24-OCT-1997; 97US-0063147.
PA	(UTAH) UNIV UTAH RES FOUND.
PI	Charlier C, Leppert MF, Singh NA: wpi. 1999-312938/26. P-PsDB: AAK08341.
DR	Nucleic acid encoding potassium channels KCNQ2 and 3
PS	Claim 1; Page 117-122; 195pp; English.
CC	This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. Antibodies specific for mutant or wild-type proteins are used as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are useful in rational design of drugs and therapeutically (in replacement therapies). The forms of epilepsy associated with mutations in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available.
SQ	Sequence 3232 BP; 577 A; 1054 C; 1061 G; 533 T; 7 other;
Dt	Query Match 15.5%; Score 429.4; DB 20; Length 3232; Best Local Similarity 61.5%; Pred No. 1.3e-102;
Matches	707; Conservative 0; Mismatches 436; Indels 6; Gaps 1
OY	3 GCCCGGCCAACGAGGGAGAAGAGAGGCACC CGCGGTCTTGAGTGAAGACGG 62 Db GCATGCGGCTCCGGCGCGGGGGCGTCGGGTGGGGCCCCCGCCCGCGCTCGCG 81
OZ	63 CGCAGCGCGCGCGCGCGCGCGCGCGCTTGTTGGCACAGCATGAAGATGTGAATC 122 Dz CCCGCTTAGCGCTGAGCCCAGACCGCGCGCGCTCCCGCAGGCAACCATGTCACAAGTC 141

```

QY 123 GGGCCGGGGGCGAGGGTGTGCTGAAGTGGGAGCCGCCA-----GGGGCGAGGGCTGCT 176
DB 142 GCGGACGGGGGGGCTATATACCCCGGCCGAGGAGAGAAAGTGAAGTGGGCTTCCT 201
QY 177 ACTGCTGGGACCCCGCGCGGCGACGCTGCGTGGCGGGCGGCTGGAGGAGAGCCG 236
DB 202 GGGGCTGGAGCCCGCGCGGCGGAGCTCCACCCGGGAGGGGGGCGTGTATGCGCGGCTC 261
QY 237 CCGGGGCGAGGAGGGGGCGCGAGTGAAGCTGCTGGGGAAGCCGCTCTTACACAGTGA 296
DB 262 CGAGAGCCCCCAAGGCGCGGCGACATCTCAGCAAACTCGCGGGGCGCGCGCGCCG 321
QY 297 CCAGAGGCGCGGGGCGAGCTCAAGTACCGGGGGGCGAGAACTACATCTACAGCTGCT 356
DB 322 GAAAGCCCCCAAGGCGAGAGCCCTTACCGCAAGCTGCGAAGATTTCTCTACAGCTGCT 381
QY 357 GAGAGAGCCCGCGCGGCTGGGGTTCATCTACACAGCTTTCGTTTCTCTGCTTGG 416
DB 382 GAGAGGGCGCGCGGCTGGGGTTCATCTACACAGCTTTCGTTTCTCTGCTTGG 441
QY 417 TTGCTTATTTTGTAGTGTCTTACCATCTCCCTGAGCAGCAAAATTTGGCTCAAGTGG 476
DB 442 CTGCTCTGCTGTCTGTCTGTTCACCAATCAAGGAGTATGAGAAAGCTCGGAGGGGCG 501
QY 477 CCTCTGATCTGAGTGTGATGATGATGCTCTTTGGTTTGGAGTTTCAATCAATCAAT 536
DB 502 CCTCTACATCTCTGAAATCTGATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 561
QY 537 CTGCTCTGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 596
DB 562 CTGGGCGCGAGGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 621
QY 597 AAAGCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 656
DB 622 GAAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 681
QY 657 AAAACCTGAGTATATATATATATATATATATATATATATATATATATATATATATAT 716
DB 682 CGGCTCCGAGGCGAAGCTTTGGCAGCATCTGGCGTCCGAGGCTGGCTTCTGCGAGAT 741
QY 717 CCTCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 776
DB 742 TCTGCGGATGATGCCCATGACCGCGGGGAGGACCTGTGAGCTGTGTGTGTGTGTGTGT 801
QY 777 TTATCTCAGCAGCAAGATTAATACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 836
DB 802 CTATGCCACAGCAGAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
QY 837 TTGCTCTTCTCTGTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 896
DB 862 GGGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 921
QY 897 AGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
DB 922 GATGCTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 981
QY 957 CCTATCTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
DB 982 CGAGACCTGGAAGGAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1041
QY 1017 TGCACCTTCTGCGGCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
DB 1042 GCGGCTGCTGTGAGGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1101
QY 1077 CCAGAAACCTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTGAGTGTGTGTGTGT 1136
DB 1102 GCGAAGGACTTTTGAAGAGAGCGGAGAACCGGACGAGGCTGTATCCAGGCTGTGAG 1161
QY 1137 TAGTTACGC 1145
DB 1162 ATTTACGC 1170

```

```

RESULT 23
AAK57145
ID AAK57145 standard; DNA; 3237 BP.
XX
AC AAK57145;
DE 22-Jul-1999 (first entry)
XX
DE Human mutant KCNQ2 cDNA.
XX
KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BPNE; juvenile myotonic epilepsy;
KW JME; Rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW detection; gene therapy; drug screening; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 128..2920
FT /tag="a
FT /product="KCNQ2"
XX
PN MO9921875-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US22375.
XX
PR 24-OCT-1997; 97US-0063147.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Charlier C, Leppert MF, Singh NA;
XX
DR WPI; 1999-312938/26.
DR P-PSDB; AAY08347.
XX
PT Nucleic acid encoding potassium channels KCNQ2 and 3
XX
PS Claim 1: Page 168-172; 195pp; English.
XX
CC This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or Rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available.
XX
SQ Sequence 3237 BP; 577 A; 1056 C; 1064 G; 533 T; 7 other;
XX
Query Match 15.5%; Score 429.4; DB 20; Length 3237;
Best Local Similarity 61.5%; Pred. No. 1,3e-102;
Matches 707; Conservative 0; Mismatches 436; Indels 6; Gaps 1;
QY 3 GCGCCGCGACACAGCGGAGAGAGAGGAGGCGCGCGCGGCTGTGGGTGAAGACGG 62
DB 22 GCCATGCGGCTCCGCGCGGCGGCGCTGGGCTGGGCGCGCGCGCGCGCGCGCTCCG 81
QY 63 GCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 122

```


Db	82	CCCCGCTGAGCTGAGCCCGACCCCGGGGCGCCTCCCGCCAGGACCATGGTGGAGAAGTC	141
Qy	123	GGGCGGGGGAGGGGTGCTGCTGAACCTCGGACGCCCA-----GGGGCGAGCGCTGCT	176
Db	142	GGCGAAGCGGGGCTATATACCCCGGCGGAGCGGAGAAAGACTGAAGGTGGCTTTCG	201
Qy	177	ACTGCTGGGACCCCGCGGCGCAAGCTCGGCTGGCGGGGGGGGCGCTGAGGGAGAGCGC	236
Db	202	GGGGCTGGACCCCGGCGCCCACTCCACCCGGAGGGGGCGCTGTGTATGCCCGGCTC	261
Qy	237	CCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGTGGGAACCGCTCTTACACAGTAG	296
Db	262	CGAGGGCCCAAGGGGGGCAAGATTCCTACAGAAACCTCGGCGGGGGCGCGCGGCGCGG	321
Qy	297	CCAGAGCTGCCGGCGCAAGTCAAGTACCGGCGGGGTGACAACTACTGTACAAAGTGT	356
Db	322	GAAGCCCCCAAGGCGCAAGCCCTTTCACCGCAAGCTGCAGAAATTCCTCTACAAAGTGT	381
Qy	357	GGAGAGACCCCGGGGCGGGGCTTCATCTACAGCGCTTGTGTTTCCCTTCCTTCTTGG	416
Db	382	GGAGCGGCGCGCGGCTGGCGCTTACATCTACAGCGCTAGCTGTCTCTGGTTTCTC	441
Qy	417	TTGCTGATTTTGTCAAGTGTTTTCTACATCCCTGAGCACAAATTTGGCTCAAGTTG	476
Db	442	CTGCGCTGCTGCTGTGTGTTTCCACATCAAGAGATAGAGAGAGCTCGAGGGGGC	501
Qy	477	CCCTTGATCCTGGAGTTCGATGATGTGCTGTTGGTTTGGAGTTCATCTCAAT	536
Db	502	CCCTTACCTCTGGAATATCGACTATGTGTGTTGGCGTGAAGTCTGTGCGGAT	561
Qy	537	CTGTCTTCGCGGGTTCGTGTGTCATATAGAGATGGCAAGGAAGCTGAGGTTTGTCTG	596
Db	562	CTGGGCGCGAAGCTGCTGCTCGCGGTACCGGCTGGAGGGGGCGGCTCAAGTTTGGCCG	621
Qy	597	AAAGCCCTCTGTGTATAGTACCATTTGTCTTATGCTTCAATAGCAGTGTTTCTGC	656
Db	622	GAAGCCGTTCTGTGTGATTGACATCATGTGCTCATGCTCCCATTTGCGGTGCGCGC	681
Qy	657	AAAACTAGGATATATTTTGGCAGCTCGACTGAGAGTCTCGTTTCTTACAGAT	716
Db	682	CGGCTCCCAAGGGCAACGCTTTGGCAATCTGGCGTCCGAGGCGCTTCCGCAAGAT	741
Qy	717	CTCCGCAATGGTGGCATGAGCCGAAGGGAGGCACTTGAATTTACTGGGTTCAGTGT	776
Db	742	TCTGGGATGATCCGCATGAGCAGCGGGGGAGGACCTGGAAGGCTGCGGGCTCTGTGT	801
Qy	777	TTATGCTACAGCAAGGAATTAATCACAGCTGGGACATTTAGATTTTGGTTCTTATTT	836
Db	802	CTATGCCCAACGCAAGAGAGCTGTGTACTGCTCGTGTACATCGGCTTCTTGTCTCATCT	861
Qy	837	TTGCTCTTCCCTGTCTATCTGTGTGGAAAGAGATGCAATAAAGAGTTTCTACATATGC	896
Db	862	GGCCTCGTTCCTGTCGTACTTGGCGAGAAAGGGGAGAACACCACTTTGACACCTCATGC	921
Qy	897	AGATGCTCTCTGTGTGGGACAAATTAATTAATTAATTAATTTGGCTATGGAGCAAAACCTC	956
Db	922	GGATCACACTGTGTGGGCGTGTATCAGCTATCACCACTATGTGCTACGGGGCAAGTACC	981
Qy	957	CCTAATTTGGCTGGGAGAAATTTGCTTTCGAGAGGCTTTCACCTCTTGGCATTTTCTTCT	1016
Db	982	CCAGACCTGTGAACGGCAGGCTCTTTGGCGCAACCTTCAACCTCATCGGTGTCTCTCTT	1041
Qy	1017	TGCACCTCTCGCGGCATTTCTGGCTCAGGTTTTCATTTAAAGTACAAAGAACACCGC	1076
Db	1042	CGCGCTGCTGAGGACCTTTGGGCTGTGGGTTTCCCTGAAGTTTCAGGAGCACACAG	1101
Qy	1077	CCAGAAACCTTTGAGAAAGAGAACCCACAGCTCCAAACCTTCAAGTGTGTTGGCG	1138
Db	1102	GCAGAAAGCTTTGAGAAAGGCGGAAACCGGACAGGCGTGTATCAGTGTGGCTGGAG	1163
Qy	1137	TAGTACGC	1145

[illegible]


```

QY 298 CAGAGCTGCC-----GGCGCAACGTCACTACCGGGGCGGATGAGAACTACCTGTATC 348
Db 223 CTGAGCCCGCCAGTCAAGAGAAACAAGCCAAAGTACGGGCGATCAAACTTGTATCAG 282
QY 349 AACGCTGAGAGAGAGCCCGGGGCTGGGCTTATCTACGAGCTTTCGTTTCTCTT 408
Db 283 GACGCGCTGAGAGAGAGCCGGGGGCTGGGCTCTTATACAGCGGTTGGTCTCTGAT 342
QY 409 GCTTTGGTGGCTGATTTTGTACAGTGTTCATCCATCCCTGAGCACAAATTTGGCC 468
Db 343 GTCCCTGGGGTGTGATTTCTGGCTGTCCGACACATTCAGAGATGTAGAGCTGTCCG 402
QY 469 TCAAGTCCCTCTTATCTGAGATTCGATGATTTGCTGCTTGGTGGAGCTTATC 528
Db 403 GGAAGCTGGCTTCTTACTGTAGAGATTTGCTATTTTCATCTTGGAGCGAGTTTGGT 462
QY 529 ATTCGAATCTGCTGCGGGTGTGCTGTGCTATGAGATGAGAGGAGCAAGAGCTAGG 588
Db 463 TTGAGAGATCTGGGCTGCTGGATGTTGCTCCGATACAAAGGCTGGGGCCGACTGAG 522
QY 589 TTTCTCGAAAGCCCTTCTGTGTATGATACCATTTGTTTCTTATCGCTTCAATAGCAGT 648
Db 523 TTTCCAGGAAGCCCTCTGTGATGATGACATCTTGTGTGATTTGCTGTGCGCAGTG 582
QY 649 GTTCTGCAAAAACAGGATTAATTTTGGCAGCTGTGCACTGCAAGATCTCCGTTTC 708
Db 583 GTTCTGTGGGAAACCAAGGACATTTCTGGCCACT---CCCTGGCAACCCCTGCGCTTC 639
QY 709 CTACAGATCTCTCCGATGGTGGCATGAGCAAGGAGGAGCACTTGGAAATTAAGTGGT 768
Db 640 CTGAGATCTCTGGGATCTGGGATGAGCCGAGAGGTGGCACTGGAAGCTTCTGAGG 699
QY 769 TCAATGGTTTGTCTACAGCAAGGAATTAATCACAGCTTGTATCATATGATTTTGGTT 828
Db 700 TCACCAATCTGTGCGCACAGCAAAAGACATCACAGGCTGTGATCATGCTTCTGACA 759
QY 829 CTATTTTGTGCTGCTTCTGCTATCTGATGAGGAAAGAGTGGC-----873
Db 760 CTGATCTTCTTCTATTTCTTGTCTACCTGTTGAGAAAGACCTCCAGAGTGGATGCA 819
QY 874 -----AATTAAGATTTTCTACATATGAGATGCTGCTGGTGGGACACA 918
Db 820 CAAGAGAGAGATGAAGAGAGATTGAGACTTACAGATGAGCCCTGTGGTGGGCTG 879
QY 919 ATTACATGACATATTTGGCTATGAGACAAACTCCCTTAATCTTGGCTGGGAAGTTG 978
Db 880 ATCACTGAGCCACCATTTGGCTATGAGACAAACCAACCAACGTTGGAGGCGCTG 939
QY 979 CTTTCTGAGGCTTGGCACTCTTGGCAATTTCTTCTTGGCACTTCTGCGGCAATTTCT 1038
Db 940 ATTGCGCCCACTTTCTTCTTAAATGGCTCTCTTTTGGCTTCTTCCAGCGGCAATCTG 999
QY 1039 GGCCTCAGGTTTGCATTAAAGTACAAAGACACCGCCAGAAACACTTTTGAGAAAGA 1098
Db 1000 GGGTCCGGGCTGGGCTCAAGGTGAGAGCAACACCGTCAAGAGCACTTTGAGAAAG 1059
QY 1099 AGGAGCCCACTGCGCACTCATTCAGTGTGTTGGCTAGTTAGCAGCACTGATGAGAA 1158
Db 1060 AGGAGCCCACTGCTGAGCTCATTCAGGCTCCGAGATATATGCTCAACCAACCAAC 1119
QY 1159 TCTGTTTCCATTG-----CAACCTGGAAGCCACACTTGAAGGCTTGAACACTG 1209
Db 1120 AGGATTTGACTGTGGGAGCATGAGATTTTATGATATAGTCGTCTTTTCTCTTCTTC 1179
QY 1210 AGCCCTACCAATFAGAGATTAAGGAGAGGAGTGGCCATGCTAGCCAGGGG 1269
Db 1180 AGGAAAGAACAGCTGAGGAGCATCCAGCAAAAGCTGGGTCTTTGGATGGGGTGGC 1239
QY 1270 CAGAGTATTAAGCCGACAGCTCTAGTGTGATGAGAGAGTCCCAAGCAACCAATC 1329
Db 1240 CTTTCTAATCTCTGTGTAGCAATTAATTAAGGAAGGATTTTACCCCTCTGATGTAGAT 1299
QY 1330 ACAGCCGAGGGGAGTCCCAACCAAGTGCAGAGAAGCTGAGACTTCAAGACGCAACCCG 1389

```

```

Db 1300 GCATATGAGAAAGATCTCTTCTAAAGAACCAAGCTGTGGCTTAAACATTAAGAGCT 1359
QY 1390 TTCGGGCGCTCGCTCGCCCTCAAAAGTTCTCAGCCAAACAGATGATAGCTGACACA 1449
Db 1360 TTCGCGACGGCTTCCCATGAAAGCCTTCTTCTGCGAGAGTTCGAGATGCCGGG 1419
QY 1450 GCCCTTGGCAGCATGATGATATATGATGAGAAAGATGCGAGTGTGATGATGAGCA 1509
Db 1420 ACAGGTGACCCCATGCG-----GGAAGACAGGGGCTATGGGAAGTCTCCCATCGAA 1473
QY 1510 GACCTCACCCACACACTTAAAACTGTCTTTCGACATACAGATATGAAATATGATATG 1569
Db 1474 GACATGATCCCAACCCGAGAGGCGCGCATCCGACCCGTCACAAATTTCAATTCGCTC 1533
QY 1570 GCAAAACGAGATTTAAGAAACATTAAGTCCATATGATGTAAGAGATGCTTGAACA 1629
Db 1534 TATTAATAAAATTAACAGAGACTTTGAGGCTTACGATGTAAGAGATGTGATGAGCAG 1593
QY 1630 TATTCGCTGTCATCGACATGTTGTTGATGATTAAGCCCTTCAACACGTTGAT 1689
Db 1594 TATTCGCGGGGATCTCGACATGCTTCCAGATTAAGTACCTTCAAGAGATTAAGAT 1653
QY 1690 CAATTTCT 1697
Db 1654 ATGATTTT 1661

RESULT 26
AAK26587
ID AAK26587 standard; DNA; 3287 BP.
XX
AC AAK26587;
XX
DE 16-JUN-1999 (first entry)
XX
KW Nucleotide sequence of human KCNQ2 (formerly known as KvL1).
XX
KW Human; KCNQ protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCNQ modulator;
KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 61..2676
FT FT /tag=a
XX
PN W09907832-A1.
XX
PD 18-FEB-1999.
XX
PE 26-JUN-1998; 98WO-US13276.
XX
PR 12-AUG-1997; 97US-0055599.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Blonar MA, Dworetzky S, Gribkoff VK, Levesque PC;
PI Little WA, Neubauer MG, Yang W;
XX
DR P-PSDB; AAY01529.
XX
WPI: 1999-190047/16.
XX
PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
XX
PS Claim 5; Fig 2; 64pp; English.
XX
CC The present sequence encodes human KCNQ2/KvL1. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium

```


CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.

XX Sequence 3287 BP; 587 A; 1062 C; 1083 G; 555 T; 0 other:

Query Match 15.5%; Score 428.4; DB 20; Length 3287;
 Best Local Similarity 64.8%; Pred. No. 2,5e-102;
 Matches 633; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

169 GGCCTGCTACTGCTGGGACCCGCGGCGACGCTGGTGGCGCGGCTGACG 228
 127 GGCCTGCTGGGCTGGACCCCGCGCGCGCTGACCCGCGGCGCGCTGATC 186
 229 GAGAGCGCGCGCGGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGG 288
 187 GCGGCGCTCGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
 289 ACGAGTACGCGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 247 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
 349 AAGCTGCTGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 307 AAGCTGCTGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 366
 409 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
 367 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
 469 TCAAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
 427 GAGGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 529 ATTGCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 487 GTCGCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 589 TTTGCTGCGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 547 TTTGCGCGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 649 GTTTCGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 607 CTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 709 CTGAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 667 CTGAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 769 TCAAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 727 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 829 CTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 787 CTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
 889 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
 847 ACCTAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 949 AAAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
 907 AAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
 1009 TCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 967 TCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026

QY 1069 CAACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1128
 DB 1027 CAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1086
 QY 1129 GTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
 DB 1087 GCGTGGAGATTTTACGC 1103

RESULT 27
 AAT85964
 ID AAT85964 standard; cDNA; 1182 BP.

XX AAT85964;
 XX 09-JAN-1998 (first entry)
 XX Human K+ channel gene coding sequence.
 DE Human; neuroblastoma; K+ channel; glioma; probe; diagnosis; detection;
 KM tumour; ds.

XX Homo sapiens.
 XX JP09191882-A.
 XX 29-JUL-1997.
 XX 16-JAN-1996; 96JP-0004726.
 XX 16-JAN-1996; 96JP-0004726.
 XX (NISH) JAPAN TOBACCO INC.

XX WPI; 1997-429182/40.
 XX P-PSDB; AAM14282.

PT DNA encoding new human K+ channel protein - useful for detecting
 PT glioma(s) and tumours
 PS Claim 3; Page 10-12; 14pp; Japanese.

XX This is the nucleotide sequence encoding a novel human K+ channel
 CC protein which is expressed on human glioma cells. The gene was isolated
 CC from a 3' directed cDNA library prepared from human neuroblastoma cell
 CC line CHP134. The screen isolated a clone designated GS008740 whose
 CC insert contained the coding sequence (presented here) and the 5' and 3'
 CC sequences of the gene (AAT85965-6 respectively). Expression of the gene
 CC was detected in neuroblastoma cell lines. Oligonucleotides derived from
 CC the sequence of the K+ channel gene can be used as probes for diagnosing
 CC human gliomas, and in the detection of new tumours.

XX Sequence 1182 BP; 201 A; 372 C; 364 G; 245 T; 0 other;

Query Match 15.3%; Score 425; DB 18; Length 1182;
 Best Local Similarity 64.7%; Pred. No. 1.1e-101;
 Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

QY 169 GGCCTGCTACTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
 DB 67 GGCCTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126
 QY 229 GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 288
 DB 127 GCGGCGCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
 QY 289 ACGAGTACCGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 DB 187 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
 QY 349 AAGTGTGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 DB 247 AAGTGTGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306

DB 241 GATGATTCAGTGGAGAACTCACCACCACTTAAATCTCATTCAGCATATAGATTT 300
 OY 1555 ATGAATTTTCATGTTGCCAAACGGAAGTTTAAAGAAACATTACGTCATATGATGTAATA 1614
 DB 301 ATGAATTTTCATGTTGCCAAACGGAAGTTTAAAGAAACATTACGTCATATGATGTAATA 360
 OY 1615 GATGTCATGAAACATATTTCTGCTGTCATCTGACATCTGTTGTGTAATAATTAA 1668
 DB 361 GATGTCATGAAACATATTTCTGCTGTCATCTGACATCTGTTGTGTAATAATTAA 414

RESULT 29
 AAH99526
 ID AAH99526 standard; cDNA; 2900 BP.
 XX
 AC AAH99526;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein encoding cDNA sequence SEQ ID NO:361.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiast; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
 KW antilegic; haemostatic; vulnery; antileuc; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antidiabetic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153455-A2.
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000MO-US35017.
 XX
 PR 23-DEC-1999; 9905-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 DR P-PSDB; AAM25585.
 XX
 PT 'Isolated human polynucleotides encoding polypeptides, useful for the
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX
 PS Claim 1; Page 467; 1217P; English.
 XX
 CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: anti-inflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiast;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianemic; antilegic; antileuc; osteopathic; eczema;
 CC antidiabetic; cyostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for

agonists or antagonists of a protein and for the treatment and diagnosis
 of disorders associated with the activity of a protein e.g. inflammation,
 rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 infections, autoimmunity, genetic diseases, haematopoietic disorders,
 anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 osteoporosis, severe combined immunodeficiency, eczema, allergic
 rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 Alzheimer's disease, Parkinson's disease, neurodegenerative and
 neurological disorders.

Sequence 2900 BP; 676 A; 795 C; 818 G; 611 T; 0 other;

Query Match 13.4%; Score 372; DB 22; Length 2900;
 Best Local Similarity 55.7%; Pred. No. 1.8e-87;
 Matches 955; Conservative 0; Mismatches 695; Indels 66; Gaps 10;

OY 39 CGCGGGCTCTGGTGAAGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCTTGG 98
 DB 16 CGCAGGGCGCGGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 75
 OY 99 CAGCGCATGAAAGATGTGGAGTCGGGCGG--GGCAGGGTGTGCTGACTCGGACCC 156
 DB 76 GCTAACCCAGCGGAGGGGACGGCGCGCGCGCGCGCGCGCGCGCGCGCG 135
 OY 157 GCCAGGGCGGAGCGCGCTGCTACTGCTGGGACCCCGCGCGCGCGCGCGCG 216
 DB 136 GCGCGCGGAGCGTGGAGCAATGACCTTGGCGCTGCGCGCGCGCGCGCGCG 195
 OY 217 GGTGCGCTGAGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276
 DB 196 ACCCTGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 255
 OY 277 CGGCTCTTACAGAGTACAGAGTGC-----GGCGCAAGCTCACTACCG 327
 DB 256 GGGCTCTGCGCAAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 315
 OY 328 CGGGTCAGAACTACCTGTACAAAGCTGCTGAGAGACCCCGCGCGCGCGCT 387
 DB 316 CGCATCAAACTTGTATCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCT 375
 OY 388 CAC-GCTTTCGTTTCTCTCTGT-CTTGGTGTCTGATTTGTCTAGT-GTTTCT 444
 DB 376 CACAGGCTGTGCTTCTCTGATGTCTGAGGCTGTGATCTGTCTGTCTGAC 435
 OY 445 ATCCCTGAGCACAATAATGCGCTCAAGTGCCTCTGATCTGAGATTCGATG 504
 DB 436 TTCAGAGATGATGAGCTGTCTCGGAGACTGCTTCTGTACGAGACATTTG 495
 OY 505 GTGCTTTGGTTTGAAGTTCATTCGAATCTGTGCGGGTGTCTGTTCGATAT 564
 DB 496 TTCATCTTTGAGCCGAGTTGCTTGAAGATCTGCGCTGCTGATGTGCTG 555
 OY 565 AGAGATGCGAAGAACTGAGGTTGCTGCGAAGCGCTCTGATATGATACAT 624
 DB 556 AAAGGCTGGGGCGCGCTGAGTGTGCGAAGAACTGCTGCTGATTTGACATCT 615
 OY 625 GTTCTATCCCTTCAATAGAGTGTGCTGCAAAACTCAAGGATATATTTTCC 684
 DB 616 GTCTGATTTGCTTGTGCGAGTGTGCTGGAAGCAAGCAAGCAATGTTCTG 675
 OY 685 TGTGCACTCAAGATCTCCGTTTCTTACAGATCTCGCGAGTGTGCGATGAG 744
 DB 676 T---CCCTGGAGCGCTGCGCTTCTGCAAGTCTGCGAGTGTGCGAGTGA 732
 OY 745 GGAGG---CACTGGAATTAATCTGCTGCTGATCTGCTGCAAGCAAGATTA 800
 DB 733 GAAAGTGGACCTGGAAGCTTCTGCGCTGCGCATCTGTGCGCAAGCAAGAT 792
 OY 801 CACAGCTTGTATAGATTTTGTCTTATTTTGTCTTCTTCTTCTTCTTCTT 860
 DB 793 CAGGCGCTGTATAGGTTTCTGACACTCATCTTCTTCTTCTTCTTCTTCTT 852

```

QY 861 GGAAGAGATGCC-----AATAAGATTCTAC 890
DB 853 TGAGAAAGACGCTCCAGAGATGATGCACAGAGAGAGATGAAGAGAGATTGAGAC 912
QY 891 ATATGACATGCTCTGCTGGTGGGACAAATTACATTGACAACTATTGGCTATGAGACAA 950
DB 913 CTATGACATGCTCTGCTGGTGGGACAAATTACATTGACAACTATTGGCTATGAGACAA 972
QY 951 AACTGCCCTAACTGGTGGGAAATGCTTCTGAGGCTTGGCACTCCTGGCATTTG 1010
DB 973 GACACCCAAAAGCTGGAAAGCGGCTGATGCTGCGGACCTTTTCTTAATTTGGCTCTC 1032
QY 1011 TTTCTTGGCACTTCTGCTGGGCACTTCTGCTGAGTTTGCATTAAATACAGAGACA 1070
DB 1033 CTTTCTTGGCACTTCTGCTGGGCACTTCTGCTGAGTTTGCATTAAATACAGAGACA 1092
QY 1071 ACACCGCAGAAACCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1130
DB 1093 ACACCGCAGAAACCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1152
QY 1131 TTGGCTGATGATGACAGCTGATGAGAAATCTGTTCCATTTG-----CAACCTGGAA 1181
DB 1153 CTGAGGATATATGCTACCAACCCCAACAGATGACCTGCTGGGCAATGAGATTTTA 1212
QY 1182 GCCCACTTGAAGGCTTGCACACCTGAGCCCTACCAATCAGAACTAAGTTTAAAGA 1241
DB 1213 TGAATCAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1272
QY 1242 GCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
DB 1273 AAAGCTGGCTCTCTTGGATGCTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1332
QY 1302 TGACAGAGAGTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1361
DB 1333 AAAGCTATTAACCTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1392
QY 1362 GACCTGAGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1421
DB 1393 GCGTGTGCTTAAACATAAAGAGCCGCTTCCGACGCGCTTCCGATGAAAGCCTACGC 1452
QY 1422 GCCAAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1481
DB 1453 TTCTGTGCAAGATTTCTAAAGATGCGGAGACAGGATGCGGAGGAA-----GACAG 1506
QY 1482 AGATGCGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1541
DB 1507 GGGCTATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
QY 1542 AGCTATCAGATTAATGAAATTTCTGTTGCAAAAGAGTTTAAGAAACATACGTC 1601
DB 1567 AGCGGACAGATTTCTAAATTTCTGCTCTATTAATAAATAATTAAGAGAGACTTGGGCG 1626
QY 1602 ATATGATGTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1661
DB 1627 TTAAGATGTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
QY 1662 AATTAAGAGCTTCAACACAGCTGTTGATCAATTTCT 1697
DB 1687 GATTAAGATCCTTCAACAGAGAAATAGATATGATTTT 1722

```

```

RESULT 30
AAS73267
ID AAS73267 standard; cDNA; 2911 BP.
XX AAS73267;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #9071.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
KW

```

```

XX Homo sapiens.
OS
XX WO2001/5067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001MO-US08631.
PE
XX 31-MAR-2000; 2000US-0540217.
PR
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG09080.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 9071; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcr_sequences.
XX
XX Sequence 2911 BP; 679 A; 795 C; 822 G; 615 T; 0 other;
XX
XX Query Match 13.4%; Score 372; DB 23; Length 2911;
XX Best Local Similarity 55.7%; Pred No. 1.8e-87;
XX Matches 955; Conservative 0; Mismatches 695; Indels 66; Gaps 10;
XX
QY 39 GCGCGGCTCTGCTGTAAGAGCGGCGCAAGCGGCGGCGGCGGCGGCGGCGGCTTGGG 98
DB 16 GCGAGGCGGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 75
QY 99 CAGGCGCATGAGATGATGAGTGGGCGG--GGCAGGCTGCTGCTGAATCTGGCAGCC 156
DB 76 GCTAACCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGAGAGAGCGGAAAGTGGGCTG 135
QY 157 GCCAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
DB 136 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 195
QY 217 GGTGGCTTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276
DB 196 ACCCTGCTGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 255
QY 277 CCGCTCTTAACAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 327
DB 256 GGGCTCTGCGCAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 315

```

```

Oy 328 GGGTGCAGACTACCTGTACAGCTGCTGGAGAGACCCCGGGCTGGGCTTCATCTAC 387
Db 316 GGCATCAAACTTGTATCTACGACGCCCTGGAGAGACCGGGGCTGGGCTGCTTAT 375
Oy 388 CAC-GCTTCTGTTTTCTCCCTGTG-TTGGGTTGCTGATTTTGTAGT-GTTTCTACC 444
Db 376 CACAGCGTGGTGTCTCAATGCTCTAGGGGTCTTGATTTGCTGCTGACACACA 435
Oy 445 ATCCCTGACACACAATAATGGCTCAAGTTGCTTGTGATCCTGGAGTTGCTGATGAT 504
Db 436 TTCAAGGATATGAGACTGCTCGGGAGACTGGCTTCTGTACTGAGACATTTGCTATT 495
Oy 505 GTGCTGTTGTTGGAGTTTCATATTCGATCTGCTGCTGGGTTGCTGCTGCTGAT 564
Db 496 TTCACTTTTGGAGCCGAGTTTCTTGAGGATCTGGGCTGCTGATGTTGCTGCTGAT 555
Oy 565 AGAGGATGGCAAGAGAGACTGAGTTGCTGCAAAAGCCCTTGTGTTATGATACAT 624
Db 556 AAAGCTGGGCGGGCGGACTGAAAGTTGCCAGAGAGCCCTGTCATGTTGACATCTTT 615
Oy 625 GTTCTTATGCTTCAATAGCAGTTGTTTGCAGAAAACCTAGGTAATTTTGGCCAG 684
Db 616 GTGCTGATGCTCTGTGCGAGTGTGCTGGGAAACCAAGGCAATGTTCTGGCCAGC 675
Oy 685 TCTGCACCTAGAGTCCGTTTCTCTACAGATCCTCGCATGCTGGCATGACCGAAG 744
Db 676 T---CCCTCGAAGCCCTGCTCTCTCAGATCTCGCATGCTGGCATGACCGGGA 732
Oy 745 GGAG-----CACTTGGAAATTAAGTGGTTCAGTTTANGCTCAGACAGAAATTAAT 800
Db 733 GAAGGTGGCACTGGAAAGCTTCTGGGGCTCAGCCATCTGTCCACAGCAAAAGCTCAT 792
Oy 801 CACAGCTGTGATAGATTTTGTGCTTATTTTCTGCTTCTGCTTCTGCTATCTGCT 860
Db 793 CAGGCTGTGATATCGTTTCTGACACATCATCTTCTTCTTCTGCTTCTGCTGCT 852
Oy 861 GGAAGAGATGCC-----AATTAAGATTTTCTAC 890
Db 853 TGAGAAAGAGCTCCACAGAGTGGATGACAGAGAGAGAGATGAAGAGAGATTTGAGAC 912
Oy 891 ATATGAGATGCTCTGCTGGGGGACAAATTAATGACAACTATTTGCTATGAGACAA 950
Db 913 CTATGAGATGCTCTGCTGGGGGACAAATTAATGACAACTATTTGCTATGAGACAA 972
Oy 951 AACTCCCTTAATGCTGGGAGAAATGCTTCTGACAGCTTGTGACACTCTGCTGCTGCT 1010
Db 973 GACACCCAAAACGTGGAGAGCGCTGATGCTGACCACTTTTCTTATTTGCTGCTGCT 1032
Oy 1011 TTTCTTGCACCTTCTGCGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
Db 1033 CTTTGTGCTTCTGACGGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Oy 1071 ACACCGGAGAAACATTTGAGAAAAGAGAACCCAGCTGCAACCTTCACTGCTGCT 1130
Db 1093 ACACCGGAGAAACATTTGAGAAAAGAGAACCCAGCTGCTGCTGCTGCTGCTGCTGCT 1152
Oy 1131 TTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
Db 1153 CTGGAGTATTAATCTACCAACCCCAACAGATTAACCTGCTGCTGCTGCTGCTGCTGCT 1212
Oy 1182 GCCACACTTGAAGCCCTGACACACCTGACACCTTACCAATGAAAGCTTAAGTAAG 1241
Db 1213 TGAATCACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1272
Oy 1242 GCGAGTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 1273 AAAGCTGGGCTCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Oy 1302 TGACAGGAGTCCCAAGCAGACATACACAGCCGAGGAGGAGCCCAAGCAAGTGGAG 1361
Db 1333 AAAGCTATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1392

```

```

Oy 1362 GAGCTGAGCTTCAACAGACCCAGCCGCTTCCGGCCCTGCTGCGCTCAAAAGTTCTCA 1421
Db 1393 GCGTCTTGGCTTAACCAATTAAGAGGCTTCCGACAGGCTTCCGATGAAGGCTTACGC 1452
Oy 1422 GCCAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGAT 1481
Db 1453 TTTCTGCGAGAGTCTGAAGATGCGGGAGAGTACCCCATGCGGAA-----GACAG 1506
Oy 1482 AGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1541
Db 1507 GGGCTATGAGGAATGCTTCCCATCAACAGATGATGATGATGATGATGATGATGATGAT 1566
Oy 1542 AGCTATCAAGATTAAGAAATTTATGATGATGATGATGATGATGATGATGATGATGAT 1601
Db 1567 AGCCGTCAAGATTTCAATTCCTGCTCTATATAAAAAAATTCAGAGAGACTTGAAGCC 1626
Oy 1602 ATATGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1661
Db 1627 TTACGATGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
Oy 1662 AATTAAGCTTCAACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1697
Db 1687 GATTAAGTACCTTCAACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1722

RESULT 31
AAS83921
ID AAS83921 standard; cDNA; 4154 BP.
AC AAS83921;
DX 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19725.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dermanac RT, Liu C, Tang YT;
XX
PI
XX
DR WPI: 2001-639362/73.
XX
DR P-PSDB: ABG19734.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID No 19725; 103pp; English.
XX
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical

```


KM	neuronal excitability; neurotransmitter release; KCNQ modulator;
KW	ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KX	age-associated memory loss; learning deficiency; motor neuron disease;
KY	epilepsy; stroke; ss.
OS	Rattus sp.
PN	MO9907832-A1.
PD	18-FEB-1999.
PF	26-JUN-1998; 98WO-US13276.
PR	12-AUG-1997; 97US-0055599.
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
PI	Bianar MA, Dworetzky S, Gribkoff VK, Levesque PC;
PI	Little WA, Neubauer MG, Yang W;
DR	WPI: 1999-190047/16.
XX	P-PsDB: AAY01531.
PT	New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT	neurotransmission and neuroprotection, used to treat, e.g. ataxia
XX	
PS	Disclosure: Fig 16; 64pp; English.
CC	The present sequence encodes rat KCNQ2/KvLRI. KCNQ proteins are
CC	nervous system-specific potassium channels. In neurons, potassium
CC	channels regulate neuronal excitability, action potential shape
CC	and firing pattern, and neurotransmitter release. KCNQ modulators
CC	may be used to treat disorders such as ataxia, myokymia, seizures,
CC	Alzheimer's disease, Parkinson's disease, age-associated memory
CC	loss, learning deficiencies, motor neuron diseases, epilepsy, and
CC	stroke.
XX	
SQ	Sequence 735 BP; 143 A; 191 C; 214 G; 187 T; 0 other;
Query Match	11.9%; Score 331; DB 20; Length 735;
Best Local Similarity	68.1%; Pred. No. 6e-77;
Matches 460; Conservative	0; Mismatches 215; Indels 0; Gaps 0
QY	477 CCTCTGATCGTGGATTCGTGATGATTGTCTCTTTGGAGTTCATTCGAAT 536
DB	
	30 CCTACATCMTGGAAATCGTAGCATCGTGATTCGGTGGTACTTGTGAGAAT 89
QY	537 CTGCTCTCGGGTCTCTGTCATATNAGATGAGCAAGAAGACTAGTTGCTCG 596
DB	
	90 CTGGGCTCAGGCCTGCTCGCGGATTCGAGGCTGGAGGCCCGGCTCAAGTTGCCAG 149
QY	597 AAAGCCCTTCGTGTATAGATACATTTGTTTCGCTTAATAGCAGTTGTTCTGC 656
DB	
	150 GAAGCATTCGTGTGATCGACATCATGCTGTGATTCGCTCATATGCTGTGCTGCTGC 209
QY	657 AAAAAGCTCAGGTAATATTTTTGCCAGCTCTCAGACTCAGAGTCTCCGTTTCTACAGAT 716
DB	
	210 TGCGTCCAGGCGCATGCTTTGCTACGCTCACCTTCGAGACTTCGGCTTCTTACAATA 269
QY	717 CCTCGGCAATGGGCGCATGAGCAGCAAGGGGAGAGCACTTGGAAATTCAGGGTCACTGGAT 776
DB	
	270 CTTACGAGATGATCCGTATGAGCCGAGGGGGTGGCACCTTGGAAAGCTTTGGGATCGGTAGT 329
QY	777 TTATGCTCACAGCAAGAAATTAATCACAGCTTGATACATAGATTTTGGTTCTTAATTTT 836
DB	
	330 CTAGCCTCACAGCAAGAGAGCTGGTAGCTCGTAGTATTTGGCTTCTCGCTCATTCCT 389
QY	837 TTTCGTTTCCCTGTCTATCTGTGTGAAAAGATGCCATTAAGAGTTTCTACATATGC 896
DB	
	390 GGCCCTCGTTTCTGGGTACTTGTGGCAGAAAAAGGGTGAAGATGACCACCTTGACACCTAACG 449
QY	897 AGATGCTCTCTGTGTGGGCGCAATTAATCAATTTGACACTAATGCTATGAGAGACAAAATCQC 956

Accession	Sequence	Position
Db	450 GGATGCACTCGTGGGGGTTGATACACCTGACAAACCATTTGGCTACGGGGGCAAGTACCC	509
Qy	957 CCTAATCTGGCTGGGAAGATTGCTTTTTCGACAGCTTTGCACTCCTTGGCATTTCTTTCTT	1016
Db	510 TCACACCTGTGAACCGGAGGCTGTTAGACAGCAGCTTTAACCTCATTTGGTGTCTAATTTT	569
Qy	1017 TGCACCTTCCTCCGCGCATTTCTGGCTCGAGTTTTCATTAAAGTACAAAGAACACCG	1076
Db	570 CGCTCTTCCTGCTGTGGCATTTTGGGATCCGGCTTTGGCCCTGAAGTCCAAAGACAGCATCG	629
Qy	1077 CCAGAAACACTTTGAGAAAGAGAACCCAGCTGCCAACTCATTTAGTGTGTTGGCG	1136
Db	630 GCAAAAACACTTTGAGAAACGCGGAAATCCGCGGACAGTCCATCCAGTGTGCTGGAG	689
Qy	1137 TAGTTACGAGCTGA	1151
Db	690 ATTCTATGCTACTAA	704

RESULT 33
 AAS73266
 ID AAS73266 standard; cDNA; 1320 BP.
 XX
 AC AAS73266;
 XX
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #9070.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX
 XX
 PI Drmanac RT, Liu C, Tang YT;
 DR WPL: 2001-639362/73.
 P-PSDB: ABE09079.
 XX
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS
 PS Claim 1; SEQ ID NO 9070; 103pp; English.
 XX
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

Db	1375	ATTTGGCGTATGAGACAGACACACCCAAAACGTTGGGAAGGCCGCTGTGATTTGCCGCACACTTT	1438
QY	994	GCACCTCCTTTGGCACTTTCTTTCTTTGGCACTTCTCTCCGCGCATTTCTTGGCTCAGTTTTGCA	1053
Db	1435	TCCTTAATTGCGCGTCTCTCTTTTGTGCTTTCCAGCGGGCATCTGGGGGTCCGGGCTGGCC	1494
QY	1054	TTAAAGTACAGAACAAACACCCGCGAAGAACACTTTGAGAAAAAGGAAGAACCCAGCTGCC	1113
Db	1495	CTCAAGGTGCAGAGCAACACCGTTCAGAGACACTTTGAGAAAAAGGAGAACCCAGCTGCT	1554
QY	1114	AACCTATTTCAG	1125
Db	1555	GAGCTCATTCAG	1566
RESULT 36			
AAS84027			
ID	AAS84027	standard; cDNA; 1566 BP.	
XX	AAS84027;		
AC			
XX			
DT	13-FEB-2002	(first entry)	
XX			
DE	DNA encoding novel human diagnostic protein #19831.		
XX			
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200175067-A2.		
XX			
PD	11-OCT-2001.		
XX			
XX	30-MAR-2001; 2001WO-US08631.		
PF	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Drmamac RT, Liu C, Tang YT;		
DR	WPI: 2001-639362/73.		
XX	P-PSDB; ABG19840.		
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			
PS	Claim 1; SEQ ID No 19831; 103pp; English.		
XX			
XX	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. AAS64197-AAS94564 represent novel human		
CC	diagnostic coding sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		

CC	at ftp.wipo.int/pub/published_pct_sequences.
xx	
SQ	Sequence 1566 BP;348 A; 473 C; 397 G; 348 T; 0 other;
	Query Match 11.1%; Score 307.6; DB 23; Length 1566;
	Best Local Similarity 64.4%; Pred. No. 1.3e-70;
	Matches 510; Conservative 0; Mismatches 249; Indels 33; Gaps 2
OY	364 CCCGGCGGCTGGGGCTTCATCTACCAAGCCTTTTGTCTTCTCTTGCTTGGTGTCTG 423
Db	778 CCCCTAGACC GGCCCCCGCCCCCGCCCGCACGCCGCTCTGTATTGCTCGGGGTCTTG 837
OY	424 ATTTTGCAGTGTTTTCTACCATCCCTGAGACACAAAATGGACCTCAAGTGGCTCTTG 483
Db	838 ATTCTGGCTGTCTGACACAACTTCAAGAGGTATGACACTGTCTCGGAGAAGCTGCTCTG 897
OY	484 ATCTGGAGTTCGTGATATTGTGCTCTTTGGTTGGAGTTCAATTCGAATCTGTCT 543
Db	898 TTACTGGAGACATTTGTGCTATTTCATCTTTGGAGCCGAGTTTCTTGAGAGATCTGGGCT 957
OY	544 GCGGGTGTCTGTGCGATATVAGAGATGGACAAGAAAGCTGAGTTTGTCTCCAAACCC 603
Db	958 GCTGGATGTTCCTGCGGATCAAAAGCTGTGCGGGGCGGAGTGAAGTTTGCAGGAACCC 1017
OY	604 TTCTGTATTATAGATPACCATTTGTTCTTAACGCTTCAATAGCACTTGTTCGAAAACT 663
Db	1018 CTGTGCATGTGGACATCTTTGTGCTGATGTGCTCTGTGCACATGGTGTCTGAGGAAC 1077
OY	664 CAGGGTATATTTTTGCCAGCTGTCCACTCABAAGCTCCGTTTCTACAGATCTCCG 723
Db	1078 CAAGGCAATGTTCTGGCCACT--CCCTGCAGAGCTCCGTTCTCTGCAGATCTCTCGC 1134
OY	724 ATGTGCGCATGGAACCGAAGGGAAGGACATTTGGAATTACTGGGTTCAGTGGTTATGCT 783
Db	1135 ATGCTGGGATGTGACCCGAGAGGTGGACACTGGAAGCTTCTGGGCTCAGCATCTGTGCG 1194
OY	784 CAAAGCAGGAATTAATCACAGCTTGTGACATAGAAATTTTGGTCTTAATTTTGTGCT 843
Db	1195 CAAAGCAAAGAACATCAACGCGCTGTGATCAATCGGTTTCTGACACTCACTCTTCTTCA 1254
OY	844 TTCTTGTCTATCTGGTGGAAAGAGATGCC----- 873
Db	1255 TTTCCTTGTCACTCGTGTGGAAGAAAGACTCCCAAGGTGATGACACAGAAGAGAGATG 1314
OY	874 AATAAAGATTTTCTACATATGCAAGATCTCTGTGTGGGACAAATTACATGACAAC 933
Db	1315 AAAGAGAGATTGAGACCTATGACAGATCCCTGTGTGGGCGTGTATCAACATCGGCAAC 1374
OY	934 ATTGGCTATGSAACAACAACTCCCCTAACTTGGCTGTGGGAAGATTGCTTCTGAGGCTTT 993
Db	1375 ATTGGCTATGSAACAACAAACCCAAAACGTGGGAAGCCGCTGATATCCCGCACCTTT 1434
OY	994 GCACCTCTTGGCACTTTCTTTCTTTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGA 1053
Db	1435 TCCTTAATTGGGCTCTCTTTTGGCCCTTCAGAGGGGCACTCTGGGGTCCGGGCTGGCC 1494
OY	1054 TTTAAAGTACAGAACACACCCGCAAGAACACTTTGAGAAAAAGAAACCAAGCTGCG 1113
Db	1495 CTCGAAGTGCAGAGAACACCGTCAAGAACACTTTGAGAAAAAGAAAGCAACCACTGCT 1554
OY	1114 AACCTTATTCAG 1125
Db	1555 GAAGCTCATTTCAAG 1566
RESULT 37	
ID	ABL28585 standard; DNA; 1280 BP.
XX	ABL28585;
XX	ABL28585;
CT	26-MAR-2002 (first entry)
XX	

DE Drosophila melanogaster genomic polynucleotide seq ID NO 37228.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 37228; 21bp + Sequence Listing: English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB157737-AB172072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 1280 BP; 288 A; 334 C; 341 G; 317 T; 0 other:

Query Match 10.3%; Score 285.4; DB 23; Length 1280;
 Best Local Similarity 60.0%; Pred. No. 8.8e-65;
 Matches 562; Conservative 0; Mismatches 346; Indels 29; Gaps 4;

QY 295 AGCCAGAGCTGCGGCGCAAGTACCGGCGGCTGCAACTACTGACAGCTG 354
 DB 97 AACCGGCGGACCGCGCGATGTCGCTACCGGCGGCTCGGCTTACAACTTC 156
 QY 355 CTGGAGAGACCGCGGCGCTG---GCGTTCATTCACACGCTTCTTCTCTCTGTC 411
 DB 157 CTGGAGAGCGCGGCGGCTGCAAGCTTCTTACCATTCGATGATTCCTGATGCTG 216
 QY 412 TTGTGTTGCTTGTATTTGTACGTTTTCACATCCCTGACACAAATTTGGCTCA 471
 DB 217 TTCACGTCGCTGGGCGCTCAGAGTGTTCACACATCAAGAGTACGAGAGAGCGCGTC 276
 QY 472 AGTTGCTCTTGTATCCGAGATTCGATGATGTCGCTTGTGTTGTTGAGTTCATTC 531
 DB 277 TACATCTGTGTCGACATGAGATCCTGATGTTATCTGATTCACATGAGATTGAGACT 336
 QY 532 CGATTCGATCTGCGGCTGCTGTTGTCGATATAGAGATGGAAGAGACTGAGGTTT 591
 DB 337 CGACTCTGGATCAGCGGCTGCGGCTCGGATACAGAGGATCCTGGCTGCAATGATTC 396
 QY 592 GCTCGAAGCCCTTCTGTATATAGATACATGTTCTTATCGCTTCAATAGCACTGTT 651
 DB 397 GTGAAGGACCATCTCTATATATAGATATTCACACATTTTACCTCAATGTAGTATTA 456
 QY 652 TCTGCAAAAACCTCAGGTAATTTTTCACAGCTGACACAGAGTCTCGTTTCCCA 711
 DB 457 GGAATGGGACCTCGGCGGCGAGTGTGCGCACGAGTGTTCATTCAGGCTCGGTTCTTT 516

QY 712 CAGATCCTCCGATGCTGGCAGATGACCGAAGGAGGAGCACTTGAATTAATCTAGGTTCA 771
 DB 517 CAGATCCTCCGATGCTGGCAGATGATTCGCGGCGGCGGCGCACTTGAAGCTGCTCGCTCG 576
 QY 772 GTGTTTATGCTACAG---CAAGGAATTAATCAGACCTTGTATAGATATTTTGGTT 828
 DB 577 GTTGTATAGCAGATATGAGACAGCAAGATGATCACAACATGATATAGGTTCTTAGT 636
 QY 828 CTTATTTTTCGCTTCTTCTGCTATCTGATGCTGGAAGAGATGCCAATAAGAGTTTCT 888
 DB 637 CTTATCTTTCATCATCTCTGCTGCTATATGTTGGAGAGAGCGTCAATGATTAATGAC 696
 QY 889 ACATATGACAGATGCTCTGCTGCTGAGCACAATTAATTAATGATGCTTATGAGAC 948
 DB 697 AATTTCGCCCAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 754
 QY 949 AAAACTCCCTTAACCTTGGCTGGGAGAGATGCTTCTGCAAGCTTTCATCTTGGCAAT 1008
 DB 755 ATGCTGCCCATCAGCTGCGAGGCAAGCTAATGCTCTGCTGCTGCTGCTGCTGCTGCTA 814
 QY 1009 TCTTCTTTCGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
 DB 815 TCTTCTTTCGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
 QY 1048 TTTGATTAAGTATACAGAACACACCGCCAGAACACTTTGAGAAAGAGAGACCA 1107
 DB 875 TTTGCTCTAGAGTGTGACAGCAGCAGCGGCGCAGACAGCATGATGCTCGCGCAGACCG 934
 QY 1108 GCTGCCAACCTCATTCAGTGTGTTGGCTGAGTTTACGACCTGATGAGAAATCTGTTCC 1167
 DB 935 GGGGCGACATCTCTATTCACAGGCGGCTGTGAGATGCTATGCGGCGCAGACATTCGTTATG 994
 QY 1168 ATTGCACTGGAAGCCACTTGAAGGCTTGCACA 1204
 DB 995 GTGCTACGTAACATTCACCGGCTGCGCTGCGCA 1031

RESULT 38
 AAF30824
 ID AAF30824 standard; DNA; 2028 BP.
 XX
 AC AAF30824;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Human KVLQ1 gene.
 XX
 KW KVLQ1 gene; Long QT syndrome; LQTS; cardiovascular disease;
 KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
 KW diagnosis; prognosis; therapy; drug screening; ds.
 OS Homo sapiens.
 XX
 XX Key
 FH location/Qualifiers
 FT replace(332,G)
 FT /*tag- a
 FT replace(478,A)
 FT /*tag- b
 FT mutation
 FT replace(521,A)
 FT /*tag- c
 FT replace(535,A)
 FT /*tag- d
 FT mutation
 FT replace(580,C)
 FT /*tag- e
 FT mutation
 FT replace(727,T)
 FT /*tag- f
 FT mutation
 FT /*tag- g
 FT replace(742,C)
 FT /*tag- h
 FT mutation
 FT /*tag- i
 FT replace(921,+1T)
 FT /*tag- j

FT	mutation	replace(928,A)	
FT	mutation	/*tag= j	
FT	mutation	replace(1046,G)	
FT	mutation	/*tag= k	
FT	mutation	replace(1066,T)	
FT	mutation	/*tag= l	
FT	mutation	replace(1097,A)	
FT	mutation	/*tag= m	
FT	mutation	replace(1172,T)	
FT	mutation	/*tag= n	
FT	mutation	replace(1343,G)	
FT	mutation	/*tag= o	
FT	mutation	replace(1588,T)	
FT	mutation	/*tag= p	
FT	mutation	replace(1697,T)	
FT	mutation	/*tag= q	
FT	mutation	replace(1747,T)	
FT	mutation	/*tag= r	
FT	mutation	replace(1781,A)	
FT	mutation	/*tag= s	
PN	WO200124681-A2.		
PD	12-APR-2001.		
XX			
XX	09-AUG-2000; 2000OWO-US21660.		
PR	09-AUG-1999; 99US-0147488.		
PR	17-MAR-2000; 2000OUS-0190057.		
XX			
PA	(UTAH) UNIV UTAH RES FOUND.		
XX			
PI	Keating MT, Splawski I;		
DR	WPI; 2001-290564/30.		
PT	P-PSDB; AAB82220.		
PT	New KVLQ1 and SCN5A genes, which contains alterations or mutations,		
PT	useful in diagnostic/prognostic or drug screening methods, particularly,		
PT	long QT syndrome -		
XX			
PS	Claim 1; Page 56-59; 76pp; English.		
XX			
CC	The present sequence is that of the human KVLQ1 gene. This gene		
CC	is implicated in Romano-Ward syndrome, the autosomal dominant form		
CC	of Long QT syndrome (LQTS), and in Jervell and Lange-Nielsen		
CC	syndrome, a form of LQTS associated with deafness, a phenotype		
CC	abnormality inherited in an autosomal recessive fashion. Novel		
CC	mutations have been identified in the gene using single strand		
CC	conformation polymorphism analysis. These are: A332G (altering		
CC	codon TAC to TGC, resulting in a Y111C mutation in the encoded		
CC	protein); G478A (GAG/AAG, E160K); G521A (CGC/CAC, R174H); G535A		
CC	(GGC/AGC, G179S); G580C (GGC/CCG, A194P); C727T (CGC/TGC, R243C);		
CC	T742C (TGG/CGG, W248R); T797C (CTG/CCG, L266P); G921-1T (GTG/GTGT,		
CC	alters reading frame leading to protein truncation); A922-2C;		
CC	G928A (GTC/ATC, V310I); C1046G (TGC/TGG, S349W); C1066T (CAG/TAG,		
CC	truncation after amino acid 355); G1097A (CGG/CAG, R366Q); C1172T		
CC	(ACC/ATC, T311I); C1343G (CGA/CGA, P488R); C1588T (CAG/TAG,		
CC	truncation after amino acid 529); C1697T (TCC/TTT, S566F); C1747T		
CC	(GGC/GGC, R583C); and G1781A (CGA/CAA, R594Q). Isolated DNA		
CC	sequences comprising 1 or more of these mutations are claimed.		
CC	Also claimed are nucleic acid probes that specifically hybridise		
CC	to a mutated KVLQ1 gene but not to the wild-type gene. These are		
CC	used in claimed methods: for detecting a mutation in the KVLQ1		
CC	gene; assessing risk of an individual for LQTS; and diagnosing a		
CC	mutation which causes LQTS. Assays may be performed using nucleic		
CC	acid microchip technology. Mutated KVLQ1 proteins (see		
CC	AA882221-38) are also used in a claimed diagnostic method, and in		
CC	a claimed method of screening for drugs useful in treating a		
CC	person having a mutation in the KVLQ1 gene.		
XX			
XX	Sequence 2028 BP; 367 A; 691 C; 612 G; 358 T; 0 other;		
XX			

Query Match	9.7%	Score 267.8	DB 22	Length 2028
Best Local Similarity	59.5%	Pred. No. 5e-60		
Matches 499; Conservative	0	Mismatches 322	Indels 18	Gaps 2

OY		33	GTCGAGACACTCCGTCTACACGTTGGTGGAGAGACC	CGGGGGTG---GGTTCATCTAC	387
Db		316	GTCACAGGGCCGCCTCTACAACTTCTCGAGCCTCC	ACACCGGCTGGAAATGCTTGTTTAC	375
OY		388	CACGCTTTCGTTTTCTCCTTGTCTTGGTGGTGGTA	TATTGTCAGTGTTCATCAATC	447
Db		376	CACATCCCGCTTCCTCATCGTCTGCTGCCATCTTC	AAGCGCTGTCTCACATC	435
OY		448	CTTAGAACACAAAATTGGCCCTCAAGTTGCCCTTAT	CCTGGAGTTTCGATCATGTCTC	507
Db		436	GAGCAGTATGCGCCCTGGCCACGGGAGACTCTTCT	TGTGATGAGATCGTCTGGTGTG	495
OY		508	GCTTTTGTTGGATTCATCATTTGAATCTGTCTGCG	GGTGGTCTTGTGCATATAGA	567
Db		496	TTCCTTGGAGCGAGTACGTGGTCCGCCCTCTGTG	CCCGCGCTCCGACACAATACGTG	555
OY		568	GGATGGCAGAGAACTAGAGTTTGCTCGAAGACCCT	TCTGTGTATAGATPACCATGTT	627
Db		556	GGGCTCTGGGGCGCGCTGGCTTTTCCCGGAAGCC	ATTTCCATCGACTCATCTGTG	615
OY		628	CTTATCGCTTCATAGCAGTTGTCTTGTGCAAAAA	ACTCAGGGATATATTTTGGCAGCT.	.687
Db		616	GTTGTGGCCCTCCATGTTGTCTCTCTGCGTGGGCT	CCAAGGGCAGGTTTGGCAGCTG	675
OY		688	GCACTCAGAAAGTCTCCGTTCCCTACAGATCCTCC	GCATGTCGCGATGACGGAAGGGA	747
Db		676	GCATCATGAGGGCAATCCGCTTCCTGCAAGATCC	TACAGCTACGCGCAGCGCAAGGA	735
OY		748	GGCAGTTGGAATAACTAGTGGTTACGTGGTTATF	AGCTCAGAGCAAGAAATATACAGCT	807
Db		736	GGCAGCTGGAGGCTCTGTGGCTCCGTGGTCTTCA	TCCACCGCAGGAGCTGATPACACC	795
OY		808	TGGTACATAGAAATTTTGGTTCTTATTTTTCGTC	TTTTCCTTGTCTATCTGTTGGAAG	867
Db		796	CTGTACATCGGCTTCTGTGGCCTCATCTTCTCTG	TACTTGTGTACCTGGCTGAGAG	855
OY		868	GATGCCAATPAAA-----GAGTTTCTACATPAG	CAGATGCTCTGTGGTG	912
Db		856	GAGCGGTGAAACGAGTACGGCCGGTGGAGTTTCC	GACGTACGCAATGGCTGTGGTG	915
OY		913	GGCACAATTACATTGACAACTATTGGCTATGAGA	CAAAACTCCCCTAACTTGGCTGGGA	972
Db		916	GGGGTGGTCAcAGTCAcCACCATCGGGCTATG	GGGGAAGAGTGCACAGCTGGGTGGG	975
OY		973	AGATTGCTTCTGcAGGCTTGTGCACTCCTTGGCA	TTTTCTTTTTCACATCTCTGCCGGC	1032
Db		976	AAGACCATCGCCTCTGTCTGTGTGTGTGGCACT	CTCTCTTTTTCGCTCCACGGGGG	1035
OY		1033	ATTCTTGGCTCAGGTTTGTGATTAAAGTACAAAG	AACAACACCGCCAGAAACACTTTGAG	1092
Db		1036	ATTCTTGGCTCGGGGTTTGGCCCTGAAGGTGAG	CAGAAGCAGAAGGCAAGCACTTCAAC	1095
OY		1093	AAAAGAAGAACCCAGCTGCCACACTATTTAGTGT	TTTGGCGTATGTTACGCACTGA	1151
Db		1096	CGGCAgATCCGGCGCGACGCTCACTATTCAGAC	CGCATGGAAGGTGCTATGCTGCCGA	1154
<hr/>					
RESULT 39					
ID	AAZ90669				
XX	AAZ90669 standard; cDNA; 3181 BP.				
XX	AAZ90669;				
XX	19-JUN-2000 (first entry)				
DE	Human KVLQTL protein encoding cDNA.				
KW	KVLQTL; KCNEL; long QT syndrome; LQT syndrome; mink protein;				


```

Db      718 GGCCTTGGGGGGCGGCTGCTTGGCCGGAAGCCCATTTCCATCATGACCTCATGCTG 777
Oy      628 CTTATTCCTTCAATAGCAGTGTGTTCTGCAAAAACATCAGGGTAATATTTTGGCAGCT 687
Db      778 GTCTGGCCCTCCATGATGCTGCTCTGCTGGGCTCCAAAGGGGAGTGTGTCACAGTGTG 837
Oy      688 GCACATGAAAGTCCCGCTTCTACAGATCCCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTG 747
Db      838 GCCATCAGGGGAGCTCCCTCTGCAATCTCTGAGATCTCTGAGATCTGAGATCTGAGAT 897
Oy      748 GGCACCTTGGAAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
Db      898 GGCACCTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
Oy      808 TGTGATCATGATTTTGTGCTTCTTATTTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 867
Db      958 CTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
Oy      868 GATGCAATTA-----GAGTTTCTCATATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 912
Db      1018 GACGCGGTAAGAGATCAGGCGGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 1077
Oy      913 GGCACAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 972
Db      1078 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
Oy      973 AGATGCTTCTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
Db      1138 AAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
Oy      1033 ATTCTTGGCTCAGTTTGCATTTAAAGATGATGATGATGATGATGATGATGATGATGATG 1092
Db      1198 ATTCTTGGCTCAGTTTGCATTTAAAGATGATGATGATGATGATGATGATGATGATG 1257
Oy      1093 AAAAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1151
Db      1258 CGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1316

RESULT 42
AAC89984
ID      AAC89984 standard; cDNA; 2734 BP.
AC      AAC89984;
XX      08-MAR-2001 (first entry)
XX      Mutant human KVLQT1 coding sequence #1.
XX      Human: KVLQT1; antiarrhythmic; cardiac; gene therapy;
XX      cardiac potassium channel; Jervell and Lange-Nielsen syndrome; JLN;
XX      chromosome 11p15.5; long QT syndrome; ss.
XX      Homo sapiens.
XX      OS
XX      US6150104-A.
XX      PN
XX      21-NOV-2000.
XX      PD
XX      17-AUG-1998; 98US-0135021.
XX      PF
XX      29-JUL-1998; 98US-0094477.
XX      PR      13-JUN-1997; 97US-0874655.
XX      XX
XX      PA      (UTAH ) UNIV UTAH RES FOUND.
XX      Keating MT, Splawski I;
XX      MPI; 2001-060013/07.
XX      DR      P-PSDB; AAB49499.
XX      PT      DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT      syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,

```

```

PT      or diagnosing or prognosing JLN -
XX      Claim 2; Columns 91-96; 58pp; English.
XX      CC      KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
XX      cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
XX      chromosome 11p15.5. The present sequence is a mutant KVLQT1 coding
XX      sequence. The mutant KVLQT1 coding sequence is useful in the diagnosis of
XX      long QT syndrome and in screening humans for the presence of KVLQT1 gene
XX      variants which cause JLN syndrome.
XX      SQ      Sequence 2734 BP; 551 A; 864 C; 809 G; 510 T; 0 other;
XX      Query Match      9.6%; Score 266.6; DB 22; Length 2734;
XX      Best Local Similarity 59.3%; Pred. No. 1.2e-59;
XX      Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

Oy      329 GGGTGCAGAACTACCTGTACACAGTGTGAGAGACCCCGCGCTG---GCGTTCATCT 385
Db      29 GCGGCCAGGGCGCGCTACAACTCTCGAGCGCTCCACCGCGTGAATGCTTCGTT 88
Oy      386 ACCACGCTTCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
Db      89 ACCACTTCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Oy      446 TCCCTGAGCACAAATTTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
Db      149 TCGAGAGATATGCGCGCTGCGACAGGGAGACTCTCTTGATGAGATGATGATGATGATG 208
Oy      506 TCGTCTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 565
Db      209 TGTCTTCTGCGAGGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 268
Oy      566 GAGATGAGCAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
Db      269 TGGGCTCTGAGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
Oy      626 TCTTATGCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 685
Db      329 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 388
Oy      686 CTGACATGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
Db      389 CGGCTCATGAGGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Oy      746 GAGGCACTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
Db      449 GAGGCACTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
Oy      806 CTTGATCATGAGATTTTGTGCTTATTTTGTGCTTATTTTGTGCTTATTTTGTGCTTATTT 865
Db      509 CCTGTACATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
Oy      866 AGGATGCCAATAA-----GAGTTTCTCATATGATGATGATGATGATGATGATGATG 910
Db      569 AGGACGCGGTGAAGAGATGAGGCGCGGTGGAAGTGGGAGCTGAGAGATGAGATGAGATG 628
Oy      911 GGGGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970
Db      629 GGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
Oy      971 GAGATGCTTCTGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1030
Db      689 GGAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
Oy      1031 GCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Db      749 GATTCCTTGGCTGCGGGGTTTCCCTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
Oy      1091 AGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150
Db      809 ACCGGAGATGCCGGGCGAGGCTCACTATTCAGACCGGATGAGAGGCTGATGCTGCGG 868

```


Key Location/Qualifiers
 CDS 88..1833
 /tag- a

MO9723598-A2.

03-JUL-1997.

20-DEC-1996: 96MO-US19756.

29-OCT-1996: 96US-0739383.

22-DEC-1995: 95US-0019014.

(UTAH) UNIV UTAH RES FOUND.

Curran ME, Keating MT, Sanguinetti MC;
 WPI: 1997-402190/37.
 P-PSDB: AAM30038.

Human mink and xenopus KVLQT1 coding sequences - used for assays for
 identifying drugs which can be used for preventing or treating long
 QT syndrome

Example 9: Page 76-79; 105pp; English.

This CDNA sequence includes a full-length coding sequence for human
 KVLQT1 (see AAM30038), a novel cardiac potassium channel protein.
 The sequence was assembled from partial clones isolated from human
 pancreatic and cardiac cDNA libraries. KVLQT1 was mapped to
 chromosome 1p15.5 making it a candidate for the long QT syndrome
 (LQT) gene. LQT is an inherited cardiac arrhythmia. One intragenic
 deletion and 10 different missense mutations which cause LQT have
 been identified in KVLQT1. The KVLQT1 gene product coassembles
 with human mink to form a cardiac IKs potassium channel.
 Coexpression of these 2 proteins in a host cell provides a means
 for screening for drugs useful in treating or preventing LQT. The
 products can also be used for studying mechanisms underlying common
 arrhythmias and for presymptomatic diagnosis of LQT. Transgenic
 animals expressing human mink and KVLQT1 can be used to test
 therapeutic agents against LQT.

Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 9 6%: Score 266.6; DB 18; Length 2821;
 Best Local Similarity 59.3%: Pred. No. 1.2e-59;
 Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

329 GGGTGCAGAACTACCTGTACACAGTGTGAGAGACCCCGCGCTGG--GCGTTCATCT 385
 116 GCGGCGAAGGGCGCGCTACACACTTCTGAGCGTCCACCGCTGGAATGCTTGGTT 175
 386 ACCACGCTTTGCTTTTCTCCCTGCTTGTGCTGCTGATTTTGTACGTTTTCACCA 445
 176 ACCACTTGCCTGCTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
 446 TCCCGACACACAAATATGGCTCAAGTTCCTTGAATCCGAGTTTGATGATG 505
 236 TCGACAGATATCCCGCCCTGCGCAGCGGAGACTCTCTTGTGATGAGATGCTGCTG 295
 506 TCGCTTTGGTTGGAGTTCATCATTCATGATCTGCTGCGGGTTCCTGTTGCGATATA 565
 296 TGTCTTGGGAGCGAGTACGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
 566 GAGGATGCGAAGAGCTGAGTTCGTGCTGCAAGCCCTCTCTGTTATGATACCATTTG 625
 356 TGGGCTCTGGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415
 626 TTTCTATCGCTTCATATGAGATGTTTCTGCAAAAATCTCAGGTATATTTTGCACAGT 685
 416 TGGTCTGGCTTCACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
 686 CTGCACTCAAGAAAGTCTCCCTTCTTACAGATCTCCGCAATGCTGCGCATGAGCCGAA 745

476 CGGCCATCAGGGGCGCATCCGCTTCTGCAAGTCCGTGAGATGCTACAGCTGACCGCAGG 535
 746 GAGGACCTTGGAATATCTAGGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 805
 536 GAGGACCTTGGAATATCTAGGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 595
 806 CTGGTACATATGATTTTGGTCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 865
 596 CCTGTACATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
 866 AGGATGCAATATA-----GAGTTTCTACATATGAGATCTCTGCT 910
 656 AGGACCGGCTGCAAGATCAGCGCGCTGAGATTCGCGCAGCTACGAGATGCGTGTGT 715
 911 GGGGCAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970
 716 GGGGGGTGTCACAGTACACCATGCGCTATGAGGACAGAGTCCGACAGCTGAGTGTG 775
 971 GAAGATTGCTTTCTGACAGCTTTGACCTCTTGCATTTCTTTCTTGTGCACTTCTGCG 1030
 1031 GCATTTCTGCTCAGGTTTTCATTAAGTACAGAACACACACCGCCAGAACACTTGTG 1090
 836 GGAATCTTGGCTCGGGGTTTCCCTGAGGTGACAGACAGACAGAGACAGACTTCA 895
 1091 AGAAAGAGAGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCTGATTACGCAAGCTG 1150
 896 ACCGGCAGATCCCGCGGCGACAGCTCATTGATTCAGACCGCATGGAGTGTATGCTGCG 955

1151 A 1151
 956 A 956

RESULT 45
 ABN96861
 ID ABN96861 standard; DNA: 2821 BP.
 AC ABN96861;
 13-AUG-2002 (first entry)
 Gene #3359 used to diagnose liver cancer.
 DE Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX Homo sapiens.
 XX W0200229103-A2.
 XX 11-APR-2002.
 XX 02-OCT-2001; 2001WO-US30589.
 XX 02-OCT-2000; 2000US-237054P.
 XX (GENE-) GENE LOGIC INC.
 XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI: 2002-426119/45.
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample
 PS Claim 1; SEQ ID NO 3359; 298bp; English.

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumor in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotrophic, and
CC cytoskeletal activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 9.6%; Score 266.6; DB 24; Length 2821;

Best Local Similarity 59.3%; Pred. No. 1.2e-59;

Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

QY 329 GGGTCAGAACATCTGATGCTGAGAGACCCCGGGCTGG---GGCTCATCT 385
DB 116 GCGGCGCAGGCGCGCTTACAACTTCTCGAGCCGCCACCGGCGGAATGCTTGT 175
QY 386 ACCACGCTTCTGTTCTCTCTGTTGCTGATTTGTCAGTGTCTTACCA 445
DB 176 ACCACTTCGCGCTCTCTCATCGTCTGCTGCTATCTTACGCGTGTCTCACC 235
QY 446 TCCCTGAGCACAAATATGCGCTCAAGTTGCTTCTGATCTGAGATCTGATGATG 505
DB 236 TCGAGCATATGCGCGCTGCGCACGGGAGCTCTTGTGATGAGATGCTGCTGG 295
QY 506 TCGCTCTTGGTTGAGTTCAATTCGATCTGCGGGGCTGCTGTCATATA 565
DB 296 TGTCTTCGGAGCAGAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
QY 566 GAGATGCGCAGAGAGTACGAGTTGCTGCAAAAGCCCTTCTGTTATATACATG 625
DB 356 TGGGCTCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
QY 626 TTTCTATCGCTTCAATAGCAGTTGTTCTGCAAAAACACAGGTAATTTTGGCAGT 685
DB 416 TGTGCTGCGCTCATAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
QY 686 CTGCACTCAAGAGTCTCGTTCTCTACAGATCTCCGATGATGAGATGCTACACG 745
DB 476 GCGCCATCAAGGCGATCCGCTCTGAGATCTGAGATGCTACACGCTGACGCG 535
QY 746 GAGGCACTGGAATTTCTGGGTTGATGCTACACAGCAAGAAATTAATACAG 805
DB 536 GAGGCACTGGAATTTCTGGGTTGATGCTACACAGCAAGAAATTAATACCA 595
QY 806 CTGTGATACATAGATTTTGTCTTATTTTGTCTGCTGCTGCTGCTGCTGCTG 865
DB 596 CCTGTACATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
QY 866 AGGATGCCAATAA-----GAGTTTCTACATATGAGATGCTGCTGCTG 910
DB 656 AGGATGCCAATAA-----GAGTTTCTACATATGAGATGCTGCTGCTGCTG 715
QY 911 GGGGCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 970
DB 716 GGGGCGGTGCTACAGTACACCATGATGATGATGATGATGATGATGATGATGATG 775
QY 971 GAAGATTTGCTTCTGAGGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
DB 776 GGAAGACATGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
QY 1031 GATTTCTTGGCTCAGTTTGCATTAAGATCAAGAAACACCGGCAAAACCTTTG 1090
DB 836 GATTTCTTGGCTCAGTTTGCATTAAGATCAAGAAACACCGGCAAAACCTTTCA 895

QY 1091 AGAAAGACGACACCGACCTGCAACCTTCACTGTTGCGGTACTACGACGTC 1150
DB 896 ACCGGCAGATCCCGGCGGACGCTCATCATTCACAGCCGATGAGGTGCTGTCGG 955
QY 1151 A 1151
DB 956 A 956

RESULT 46

AAC89914

ID AAC89914 standard; cDNA; 3182 BP.

XX AAC89914;

DT 08-MAR-2001 (first entry)

DE Mutant human KVLQT1 coding sequence #2.

XX

XX

KW Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;

KW cardiac potassium channel; Jervell and Lange-Nielsen syndrome; JLN;

KW chromosome 11p15.5; Long QT syndrome; ss.

OS Homo sapiens.

PN US6150104-A.

PD 21-NOV-2000.

XX 17-AUG-1998; 98US-0135021.

PR 29-JUL-1998; 98US-0094477.

PR 13-JUN-1997; 97US-0874655.

XX (UTAH) UNIV UTAH RES FOUND.

PA Keating MT, Splawski I;

PI WPI: 2001-060013/07.

DR P-PSDB; AAB49495.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Sequence 3182 BP; 581 A; 1073 C; 969 G; 559 T; 0 other;

Query Match 9.3%; Score 258.4; DB 22; Length 3182;

Best Local Similarity 59.5%; Pred. No. 1.9e-57;

Matches 500; Conservative 0; Mismatches 321; Indels 19; Gaps 3;

QY 331 GTGCAAACTACCTGACACAGTGTGAGAGACCCCGGGCTGG---GGCTCATCTAC 387
DB 478 GTCCAGGGGCGGCTGTACAACTTCTCGAGCGTCCACCGGCTGGAATGCTTCTTAC 537
QY 388 CACGCTTTCGTTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 447
DB 538 CACTTCGCGCTTCT 597
QY 448 CCGAGCACACAAATTTGCGCTCAAGTTGCTTGTGATCTGAGTTCGATGATGTC 507
DB 598 GAGCAGTATGCGCGCTGCGCACGGGAGACTCTTCTGATGAGATGCTGCTGCTGCTG 657

OY		508	GTCCTTGGATTGAGATCATCATATTCGCAGATCCGTGCGGGTTGGCTTGTCGATA-7AG	566
Db		658	TTCCTCGGACGGAGTACTGCTGCCGCTCTGTGTCGCCGCGTCCGACGCAAGTACGTG	717
OY		567	AGGATGGCMAAGGAAGACTAGAGTTTTGTCGAAAAGCCCTTGCTGTATTATAGATCAATTGT	626
Db		718	GGCCTCTGGGGGGGGCTGCCTTGTCCCGGAAGCCCATTTTCATCATATGACCCTCATGCT	777
OY		627	TCTATGCGCTTCANTAGAGATTGTTTCTGCAAAAAAAGTCAAGGGTAATATTTTGGCCAGTC	686
Db		778	GGTGTGGCCCTCCATGCTGTGCTCTGGCTGGGCTCCAAAGGGGCAAGTCTTGGCCAGTTC	837
OY		687	TGCACCTAGAAGTCTCCGTTTTCTCTACAGATCCCTCCGACATGCTGCGCATGGAGCGGAAGGG	746
Db		838	GGCCATCAGGGGGCATCCGCTTCCTGTCAGATCCTGTAGGATGTACAACGTGACCGCGCAGG	897
OY		747	AGGCACCTTGGAAATTACTGGGTTCACTAGTGGTTATAGTCTCACACAGGAATTAATCACAC	806
Db		898	AGGCACCCGGAGGGCTCCGGGGCTCCGTGGTCTTCATCCACCGCCAGAGCTGATTAACAC	957
OY		807	TTGGTACATPAGATTTTGGTCTCTATTATTTTTCGCTTCTCTGTTACTGATCTGGTGGAAA	866
Db		958	CCTGTACATCGGCTTCCTGGGCTCATCTTCCTCTGTAATTTGTGTACTGGCTGAGAA	1012
OY		867	GGATGCCAATAA-----GATTTTCTACATATGCAATGCTCTCTGGTG	911
Db		1018	GGAGCGGGGTGAACGATCAGCGCGCGGTGGAGTTTGGCAGACTTACGCAAGTGGCTGTGGTG	1077
OY		912	GGGCACTATTACATATGACACATPATTTGGGCTATGAGAGACAACACCCCCTAACCTGGCGGG	971
Db		1078	GGGGGTGGTCAACAGTACACCCATCGGCTATATGGGACAAAGGTGCCCCAGACGTGGGTGG	1133
OY		972	AAGATTGCTTCTGTGCAAGGCTTTGCACTCCCTGGCATTTCTTTCTTTGCACTTCCGCGG	1033
Db		1138	GAAAGACATWGGCCTCGCTCTGTGTCTTTGSCATCTCTCTCTTTGGCGCTCCAGCGGG	1199
OY		1032	CATCTTGGCTCAGGTTTTGCACTTAAAGTACAGAAGAACACCGCCAGAGAACTTTGA	1099
Db		1198	GATTTTGGCTCGGGGTTGGCCCTGAAGGTGCGCAGAAAGCAAGGAGGAGAACACTTCAA	1255
OY		1092	GAAAAGAAAGAACCCAGCTGCCCCAACCTCATTTCACTAGTGTGTTGGCGTATGTTACGACGTGA	1155
Db		1258	CCGGAGATCCCGGGGGGAGCGCTCACTCATTTGAGACCGCATGGAGGTATGATGTCGGA	1315
<hr/>				
RESULT 47				
AAK94798				
ID	AAK94798	standard;	cDNA; 3335 BP.	
XX AC	AAK94798;			
XX DT	06-NOV-2001	(first entry)		
XX DE	Human full-length cDNA, SEQ ID NO: 3918.			
XX KW	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.			
XX OS	Homo sapiens.			
XX PN	EPI130094-A2.			
XX PD	05-SEP-2001.			
XX PF	07-JUL-2000; 2000EP-0114089.			
XX PR	08-JUL-1999; 99JP-0194486.			
XX PR	11-JAN-2000; 2000JP-0118774.			
XX PA	02-MAY-2000; 2000JP-0183765.			
XX PI	(HELT-) HELIX RES INST.			
	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,			
	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;			

```

Db      686 TGGCAGCTCCACAAATGCCCACCTCCCAAGCAGCAGGAGGTGGGTGAGGCGACACACC 745
QY      1346 CCACCAAGTGGAGAGAGCTGGAGCTTCAACACCAACCCGCTTCCGCGCTGCTGC 1405
Db      746 CCACCAAGTGGAGAGAGCTGGAGCTTCAACACCAACCCGCTTCCGCGCTGCTGCA 805
QY      1406 GCGTCCAAAAGTCTCAGCCAAAACAGTGTAGATGCTGACACAGCCGCTTGGCAGCTGATG 1465
Db      806 GACTC-----AAACCCCGCAGCTCTGCTGAGATGCCC--CCTGAGAGG 847
QY      1466 ATGTATATGATGAAAAAGATGCCAGTGTGATGTATCATGAGAGACCTCACCACACAC 1525
Db      848 AAGTAGCAGAGAGAGAGAGAGCTACAGTGTGAGCTCAGCGTGGAGAGACATCATGCTGCTG 907
QY      1526 TTAAGACGTCTATGAGTATCAGATATGAAATTTCTATGTTGCAAAAGCAAGTTTA 1585
Db      908 TGAAGACAGTCTATGCGCTCTCATCAGATGATTCCTCAAGTTCTGTTGCGCCAAAAGAAATTC 967
QY      1586 AGGAACATTAAGTCCATATGATGATGTAAGATGTCAATATTTCTGCTGATC 1645
Db      968 AGGAGACACTGGAGACGTAAGACGTAAGAGACTCATTTGAGCACTCAGCAGCCACC 1027
QY      1646 TGGACATTTTGTGTGATTAAGCCTTCAAAACACGCTGTGATCAAAATTTCTTGGAAAG 1705
Db      1028 TGGACATGCTGGCGCGATCAAGAGAGCTCAAACTGGGTGGACAAATTTGTGGTGGG 1087
QY      1706 GGC---AAATCATCATGATAGAGAGAGCCGAGAGAAATTAACAGCAAGACATGAGACA 1762
Db      1088 GCGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
QY      1763 CAGACGATCTAGTATGCTGCTGGTGGTGTGCAAGGTTGAAAAACAGAGTACAGTCAATG 1822
Db      1148 TGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1267
QY      1823 AATCAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1882
Db      1208 AGCAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1261
QY      1883 CAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1942
Db      1262 CCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
QY      1943 ATCAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1987
Db      1322 ACCACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1366

```

RESULT 48

```

ID      AAK92009 standard; cDNA: 798 BP.
XX      AAK92009;
XX      AC
XX      DT      06-NOV-2001 (first entry)
XX      XX
XX      DE      Human cDNA 5'-end sequence, SEQ ID NO: 469.
XX      KW      Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX      OS      Homo sapiens.
XX      PN      EP1130094-A2.
XX      PD      05-SEP-2001.
XX      PF      07-JUL-2000; 2000EP-0114089.
XX      PR      08-JUL-1999; 99JP-0194486.
XX      PR      11-JAN-2000; 2000JP-0118774.
XX      PR      02-MAY-2000; 2000JP-0183765.
XX      PA      (HELI-) HELIX RES INST.

```

```

XX      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX      WPI; 2001-524255/58.
XX
PT      830 Primers useful for synthesizing full length cDNA clones and their
PT      use in genetic manipulation -
XX
PS      Claim 2: SEQ ID NO 469; 1380bp + sequence listing; English.
XX
CC      The invention relates to primers for synthesizing full length cDNA
CC      clones. 830 cDNA molecules encoding a human protein have been
CC      isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC      molecules have been determined. Primers for synthesizing the full length
CC      cDNA are useful for clarifying the function of the protein encoded by
CC      the cDNA. The full length clones were obtained by construction of full
CC      length enriched cDNA libraries that were synthesised by the oligo-capping
CC      method. The primers enable the production of the full length cDNA easily
CC      without any special methods. The present sequence is the nucleotide
CC      sequence of the 5'-end of a cDNA provided in the invention.
CC      Note: The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ      Sequence 798 BP; 153 A; 274 C; 222 G; 146 T; 3 other:

```

```

Query Match      7.58; Score 208.4; DB 22; Length 798;
Best Local Similarity 71.2%; Pred. No. 1.5e-44;
Matches 275; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

```

```

QY      791 AGCAATTAATACAGCTGCTGATAGATTTTGTCTATTTTGTCTGCTGCTG 850
Db      26 AGAGCTGATACACCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 85
QY      851 TCTATCTGCTGGAAGAGATGCCAATTAAGATTTTCTATATATGATGATGCTGCTG 910
Db      86 TCTACTGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 145
QY      911 GGGGACAAATTAATGATGACATGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
Db      146 GGGGAGAGATTAATGATGACATGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 205
QY      971 GAAGATGCTTCTGAGAGCTTGTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
Db      206 GAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
QY      1031 GCATCTTGGCTCAGGTTTGCATTAAAGTACAGAGACACCGCCAGAGAACTTTG 1090
Db      266 GCATCTTGGCTCAGGTTTGCATTAAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY      1091 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150
Db      326 AGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385
QY      1151 ATGAGAAATCTGTTTCCATTTGCAAC 1176
Db      386 ATATGAGCGGCGCTACCTGACAGCC 411

```

RESULT 49

```

ID      AAK93662 standard; cDNA: 798 BP.
XX      AAK93662;
XX      AC
XX      DT      06-NOV-2001 (first entry)
XX      XX
XX      DE      Human cDNA clone representative sequence, SEQ ID NO: 2122.
XX      KW      Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX      OS      Homo sapiens.

```



```

Db      858  GTCACGGC---AGAACTCAGAAAGCAAGCCTCCCCGGAGAGACATTGTGATGACAA 914
QY      1482  AGCATGCCAGTGTATGTATCAGTGAAGACCTCACCCACCACTTAAACTGTATTG 1541
Db      915  GAGCTGCCCTCGCGAGTTGTGACCGAGACCTGACCCCGGCTCAGAGTCAGACATCAG 974
QY      1542  AGCTATCAGAAATTAATTTGATTTGCAAAACGGAAGTTTAAAGAAACATTACCTCC 1601
Db      975  AGCCGTGTGTGTATGATGCGGTCTGTGTCAGGAGGAAATTCAGAGAGAGCTGCGGCC 1034
QY      1602  ATATGATGTAAAGATGTATTGAACAATATTTCTGCTGTGATCTGAGACATGTTGTAG 1661
Db      1035  CTACGACGTGATGAGATCAGACAGTACTCAGCGGCGACCTGAGACATGCTGCCG 1094
QY      1662  AATTAAAGCCTTCA 1676
Db      1095  AATTAAAGCCTTCA 1109

```

Search completed: June 19, 2003, 08:13:53
 Job time : 641 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 04:49:01 ; Search time 6932 Seconds
(without alignments)

11637.764 Million cell updates/sec

Title: us-09-825-147-1

Perfect score: 2772
Sequence: 1 atgccccgcacacacgcgcgg.....ctcatgtcaactgaataa 2772

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_hgco_hum: *
40: em_hgco_mus: *
41: em_hgco_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2772	100.0	2772	6	AX268474	AX268474 Sequence
2	2772	100.0	3111	6	AX268476	AX268476 Sequence
3	2723.8	98.3	3074	6	AX253254	AX253254 Sequence
4	2723.8	98.3	3074	6	AX456864	AX456864 Sequence
5	2723.8	98.3	3074	6	AF249278	AF249278 Homo sapi
6	2630	94.9	3137	6	AX056817	AX056817 Sequence
7	2630	94.9	3137	6	AF202977	AF202977 Homo sapi
8	2625.2	94.7	2694	6	AX322509	AX322509 Sequence
9	2510.8	90.6	2832	6	AF263835	AF263835 Homo sapi
10	2159.8	77.9	3108	10	AF263836	AF263836 Mus muscu
11	965	34.8	1691	9	HSAT272519	AJ272519 Homo sapi
12	965	34.8	120846	9	AL365232	AL365232 Human DNA
13	769.2	27.7	162123	2	AC115920	AC115920 Mus muscu
14	755	27.2	179192	2	AC095904	AC095904 Rattus no
15	498.6	18.0	548	6	AX318576	AX318576 Sequence
16	498.6	18.0	548	6	AX318764	AX318764 Sequence
17	492	17.7	2335	6	AX032994	AX032994 Sequence
18	492	17.7	2335	6	AX456863	AX456863 Sequence
19	492	17.7	2335	9	AF105202	AF105202 Homo sapi
20	488.4	17.6	2827	10	AB000497	AB000497 Mus muscu
21	475.6	17.2	2750	6	AX456861	AX456861 Sequence
22	475.6	17.2	2750	9	AF110020	AF110020 Homo sapi
23	474.8	17.1	2899	10	AB000496	AB000496 Mus muscu
24	472.2	17.0	7420	9	AF074247	AF074247 Homo sapi
25	451.4	16.3	3195	9	AF087453	AF087453 Rattus no
26	448.4	16.2	4165	10	AF087453	A94975 Sequence 2
27	447	16.1	2565	6	A94975	AF087454 Rattus no
28	440.4	15.9	5927	10	AF087454	AB000496 Mus muscu
29	437.2	15.8	2935	10	AB000494	Y15065 Homo sapien
30	436.6	15.8	3029	6	A94974	AF074247 Homo sapi
31	433.2	15.6	2622	10	AY118171	AF087453 Rattus no
32	433	15.6	2920	10	AB000495	A94974 Sequence 1
33	432.4	15.6	2382	10	AB000498	AY118171 Mus muscu
34	431.4	15.6	2764	10	AB000499	AB000495 Mus muscu
35	429.4	15.5	1425	9	D82346	AB000499 Mus muscu
36	429.4	15.5	1425	9	D82346	A94977 Sequence 4
37	429	15.5	3232	9	AF033348	D82346 Homo sapien
38	427.8	15.4	2613	10	AF490773	AF033348 Homo sapi
39	427	15.4	2766	10	AF091247	AF490773 Mus muscu
40	425.4	15.3	2755	9	AF033347	AF091247 Rattus no
41	425	15.3	1182	6	E13516	AF033347 Homo sapi
42	425	15.3	1314	9	BC000699	E13516 Human mRNA
43	424.6	15.3	1818	10	AB000500	BC000699 Homo sapi
44	424.6	15.3	2014	10	AB000501	AB000500 Mus muscu
45	419.4	15.1	1689	10	AB000503	AB000501 Mus muscu
46	418.2	15.1	1227	10	AB000502	AB000503 Mus muscu
47	411.8	14.9	2671	4	AF325548	AB000502 Mus muscu
48	396.8	14.3	3005	6	AX456862	AF325548 Bos tauru
49	389.6	14.1	3005	6	AX456862	AX456862 Human DNA
50	365.6	13.2	2247	10	AB000504	AX456862 Sequence
51	342.4	12.4	248862	2	AC091215	AB000504 Mus muscu
52	339	12.2	215256	2	AC125433	AC091215 Rattus no
53	339	12.2	267605	2	AC125433	AC125433 Mus muscu
54	339	12.2	331447	2	AC127359	AC125433 Mus muscu
55	295.6	10.7	1372	5	XL071076	AC127359 Mus muscu
56	293	9.9	293	9	HSAT272506	U71076 Xenopus lae
57	273.6	9.9	3183	5	SAC232714	AJ272506 Homo sapi
58	272.4	9.8	158119	2	AC095944	AJ272506 Homo sapi
59	269.4	9.7	3129	2	AF000571	AC095944 Rattus no
60	267.8	9.7	2028	6	AR183726	AF000571 Homo sapi
61	267.8	9.7	3181	6	AR119240	AR183726 Sequence
62	267.8	9.7	3181	6	AR164692	AR119240 Sequence
63	266.6	9.6	2734	6	AR119313	AR164692 Sequence
64	266.6	9.6	2821	6	AX410712	AR119313 Sequence
65	266.6	9.6	2821	9	HS089364	AX410712 Sequence
						U89364 Homo sapien

Pred. No. is the number of results predicted by chance to have a

OY	421	TTGATTTTGTAGTGTCTTTTCTACCAATCCCTGAGCACACAAATTTGGCCCTCAGTTGCCCTC	480
OY	421	TTGATTTTGTAGTGTCTTTTCTACCAATCCCTGAGCACACAAATTTGGCCCTCAGTTGCCCTC	480
OY	421	TTGATTTTGTAGTGTCTTTTCTACCAATCCCTGAGCACACAAATTTGGCCCTCAGTTGCCCTC	480
OY	481	TTGATCTCTGGAGTTCGTATGATGATTTCTGCTTTGGTTTGGATTCATCATTTGAAATCTGG	540
OY	481	TTGATCTCTGGAGTTCGTATGATGATTTCTGCTTTGGTTTGGATTCATCATTTGAAATCTGG	540
OY	481	TTGATCTCTGGAGTTCGTATGATGATTTCTGCTTTGGTTTGGATTCATCATTTGAAATCTGG	540
OY	541	TCCTGGGCTTGTCTGTTGTGATATATAGAGATGGCAAGAACTGAGTTTGTCTCGAAAG	600
OY	541	TCCTGGGCTTGTCTGTTGTGATATATAGAGATGGCAAGAACTGAGTTTGTCTCGAAAG	600
OY	541	TCCTGGGCTTGTCTGTTGTGATATATAGAGATGGCAAGAACTGAGTTTGTCTCGAAAG	600
OY	601	CCCTTCTCTGTATATGATATACCATTTCTTATTCGCTTCAATATGCACTTTCTTCTCGAAA	660
OY	601	CCCTTCTCTGTATATGATATACCATTTCTTATTCGCTTCAATATGCACTTTCTTCTCGAAA	660
OY	601	CCCTTCTCTGTATATGATATACCATTTCTTATTCGCTTCAATATGCACTTTCTTCTCGAAA	660
OY	661	ACTCAGGGTAATATTTTTGGCCAGCTCTGACACAGAAAGCTCCGTTTCTTACAGATCTCAC	720
OY	661	ACTCAGGGTAATATTTTTGGCCAGCTCTGACACAGAAAGCTCCGTTTCTTACAGATCTCAC	720
OY	661	ACTCAGGGTAATATTTTTGGCCAGCTCTGACACAGAAAGCTCCGTTTCTTACAGATCTCAC	720
OY	721	CGCATGTGTGCATATGAGACCGAAGGGGAGGCACTTGGAAATTAAGTGGTTTCAGTGGTTTAT	780
OY	721	CGCATGTGTGCATATGAGACCGAAGGGGAGGCACTTGGAAATTAAGTGGTTTCAGTGGTTTAT	780
OY	721	CGCATGTGTGCATATGAGACCGAAGGGGAGGCACTTGGAAATTAAGTGGTTTCAGTGGTTTAT	780
OY	781	GCTCAGACAGAAAGAAATTAATCAGACTTGTGTATATAGAAATTTTGGTCTTATATTTTTCG	840
OY	781	GCTCAGACAGAAAGAAATTAATCAGACTTGTGTATATAGAAATTTTGGTCTTATATTTTTCG	840
OY	781	GCTCAGACAGAAAGAAATTAATCAGACTTGTGTATATAGAAATTTTGGTCTTATATTTTTCG	840
OY	841	TCCTTCCCTTGTATCTGTGTGGAAAAAGATGGCAATTAAGAGTTTTCATCATATATGAGAT	900
OY	841	TCCTTCCCTTGTATCTGTGTGGAAAAAGATGGCAATTAAGAGTTTTCATCATATATGAGAT	900
OY	841	TCCTTCCCTTGTATCTGTGTGGAAAAAGATGGCAATTAAGAGTTTTCATCATATATGAGAT	900
OY	901	GCTCTCTGTGTGGGGGCAATTAACATTTGACAACTATTTGGCTATGAGACACAAACTCCCTTA	960
OY	901	GCTCTCTGTGTGGGGGCAATTAACATTTGACAACTATTTGGCTATGAGACACAAACTCCCTTA	960
OY	901	GCTCTCTGTGTGGGGGCAATTAACATTTGACAACTATTTGGCTATGAGACACAAACTCCCTTA	960
OY	961	ACTTGGCTGTGGAAAGATCTCTTCTCAGAGCTTTGACACTCTTGGCATTTTCTTCTTTCGA	1020
OY	961	ACTTGGCTGTGGAAAGATCTCTTCTCAGAGCTTTGACACTCTTGGCATTTTCTTCTTTCGA	1020
OY	961	ACTTGGCTGTGGAAAGATCTCTTCTCAGAGCTTTGACACTCTTGGCATTTTCTTCTTTCGA	1020
OY	1021	CTTCTGTGCGGCAATCTTGGGCTCAGAGTTTTCGATTTAAAGTATCAAGAACACACCGCCAG	1080
OY	1021	CTTCTGTGCGGCAATCTTGGGCTCAGAGTTTTCGATTTAAAGTATCAAGAACACACCGCCAG	1080
OY	1021	CTTCTGTGCGGCAATCTTGGGCTCAGAGTTTTCGATTTAAAGTATCAAGAACACACCGCCAG	1080
OY	1081	AAACACTTTTGAGAAAAAGAAAGAACCCAGCTGCCAACTCATTCAGTGTCTTTTGGCCCTAGT	1140
OY	1081	AAACACTTTTGAGAAAAAGAAAGAACCCAGCTGCCAACTCATTCAGTGTCTTTTGGCCCTAGT	1140
OY	1081	AAACACTTTTGAGAAAAAGAAAGAACCCAGCTGCCAACTCATTCAGTGTCTTTTGGCCCTAGT	1140
OY	1141	TACGCAAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAGGCCACCTTGAAGGCCCTTG	1200
OY	1141	TACGCAAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAGGCCACCTTGAAGGCCCTTG	1200
OY	1141	TACGCAAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAGGCCACCTTGAAGGCCCTTG	1200
OY	1201	CACACTCTGAGCCCTTACCAATCAGAAAGCTAACTTTTAAAGACGAGTGTGGCAATGGCTTAGC	1260
OY	1201	CACACTCTGAGCCCTTACCAATCAGAAAGCTAACTTTTAAAGACGAGTGTGGCAATGGCTTAGC	1260
OY	1201	CACACTCTGAGCCCTTACCAATCAGAAAGCTAACTTTTAAAGACGAGTGTGGCAATGGCTTAGC	1260
OY	1261	CCCAAGGGGCGCAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGTACAGAGAGTCCCAAGC	1320
OY	1261	CCCAAGGGGCGCAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGTACAGAGAGTCCCAAGC	1320
OY	1261	CCCAAGGGGCGCAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGTACAGAGAGTCCCAAGC	1320
OY	1321	ACCGCATCTACAGCCGAGGGGAGTCCCAACCAAGTGTCAAGAGGCTGTGAGCTTCAACGAGC	1380
OY	1321	ACCGCATCTACAGCCGAGGGGAGTCCCAACCAAGTGTCAAGAGGCTGTGAGCTTCAACGAGC	1380
OY	1321	ACCGCATCTACAGCCGAGGGGAGTCCCAACCAAGTGTCAAGAGGCTGTGAGCTTCAACGAGC	1380
OY	1381	CGAACCCGCTTCCGGGCGCTGCTGGGCGCTCAAAAGTTCTACACCCAAACACAGATGATGAT	1440
OY	1381	CGAACCCGCTTCCGGGCGCTGCTGGGCGCTCAAAAGTTCTACACCCAAACACAGATGATGAT	1440
OY	1381	CGAACCCGCTTCCGGGCGCTGCTGGGCGCTCAAAAGTTCTACACCCAAACACAGATGATGAT	1440
OY	1441	GCTGACACAGCCCTTGGCAGCTGATGATATATATGATGAAAGAGATGCCAGTGTGATGAT	1500
OY	1441	GCTGACACAGCCCTTGGCAGCTGATGATATATATGATGAAAGAGATGCCAGTGTGATGAT	1500
OY	1441	GCTGACACAGCCCTTGGCAGCTGATGATATATATGATGAAAGAGATGCCAGTGTGATGAT	1500
OY	1501	TCATGTGAAAGACCTTACCCCACTTAAACTGTATTCAGAGCTATTCAGAAATTAATGA	1560

Db	1501	TCAGTGGAGAGCTTCACCCCACTTTAAACTGTCAATTCAGACTATCCAGATTATGAAA	1560
QY	1561	TTTCATGTTGCAAAACGGAGTTTAAAGAAACATTTACGTCCATATGATGTAAAAAGATGTC	1620
Db	1561	TTTCATGTTGCAAAACGGAGTTTAAAGAAACATTTACGTCCATATGATGTAAAAAGATGTC	1620
QY	1621	ATTGAAACATATTCTGCTGCTGTCATCTGACATGTTTGCTAGATTTAAAGCCTTCAACA	1680
Db	1621	ATTGAAACATATTCTGCTGCTGTCATCTGACATGTTTGCTAGATTTAAAGCCTTCAACA	1680
QY	1661	CGTGTGATTCAAATTTCTTGSGAAAAGGGCAATTCATCAGATTAAGAAAGGCGAGAGAA	1740
Db	1661	CGTGTGATTCAAATTTCTTGSGAAAAGGGCAATTCATCAGATTAAGAAAGGCGAGAGAA	1740
QY	1741	ATAACAGAGAAACATGAGACCAACAGACGATCTCAGTATGTCGCGGTGGGTCAAGGTT	1800
Db	1741	ATAACAGAGAAACATGAGACCAACAGACGATCTCAGTATGTCGCGGTGGGTCAAGGTT	1800
QY	1801	GA AAAACAGGTACAGTCCATAGAAATCCAGCTGAGCTGCTACTAGACATCTATCAACAG	1860
Db	1801	GA AAAACAGGTACAGTCCATAGAAATCCAGCTGAGCTGCTACTAGACATCTATCAACAG	1860
QY	1861	GTCCTTGSGAAAGGCTGCTGCTCCAGCCCTCGCTTTGGCTTCAATTCACATCCACCTTTT	1920
Db	1861	GTCCTTGSGAAAGGCTGCTGCTCCAGCCCTCGCTTTGGCTTCAATTCACATCCACCTTTT	1920
QY	1921	GAATGTGAACAGACATCTGACTATTCAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTC	1980
Db	1921	GAATGTGAACAGACATCTGACTATTCAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTC	1980
QY	1981	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTGCAG	2040
Db	1981	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTGCAG	2040
QY	2041	TTTCATTTGAGAGCCAAATGAGTTTCAAGTGGCCAGACTTTTCAAGGCTTAAAGCCTTACTATG	2100
Db	2041	TTTCATTTGAGAGCCAAATGAGTTTCAAGTGGCCAGACTTTTCAAGGCTTAAAGCCTTACTATG	2100
QY	2101	CACAGTCAAGACACACAGGTGGCCAAATTAGTCAAAAGCGATGGCTCAGCTAGTGGCAGCCACC	2160
Db	2101	CACAGTCAAGACACACAGGTGGCCAAATTAGTCAAAAGCGATGGCTCAGCTAGTGGCAGCCACC	2160
QY	2161	AACACCATTTGCAAAACCAATTAATTAAGGCGACCCCAAGCCGAGAGCCCAACAATTTACAG	2220
Db	2161	AACACCATTTGCAAAACCAATTAATTAAGGCGACCCCAAGCCGAGAGCCCAACAATTTACAG	2220
QY	2221	ATCCGACCTCCTCTCCAGCCATCAAGCATCTGCCAGAGCCAGAAACTCTGCACCCCTAAC	2280
Db	2221	ATCCGACCTCCTCTCCAGCCATCAAGCATCTGCCAGAGCCAGAAACTCTGCACCCCTAAC	2280
QY	2281	CGTGAGGCTTACAGGAAGCATTTCTAGCTCACACCTTCGCTTTGCTCCAGAGAA	2340
Db	2281	CGTGAGGCTTACAGGAAGCATTTCTAGCTCACACCTTCGCTTTGCTCCAGAGAA	2340
QY	2341	AATGTTCAAGTTGCACTCAATTCACCAAGGACCGTTCTATGAGGAAAAAGCTTTGAC	2400
Db	2341	AATGTTCAAGTTGCACTCAATTCACCAAGGACCGTTCTATGAGGAAAAAGCTTTGAC	2400
QY	2401	ATGGAGAGAGAACTCTGTTGCTGTCTGTCCCATGGTGGCGAAGGACTTTGGGCAAACTC	2460
Db	2401	ATGGAGAGAGAACTCTGTTGCTGTCTGTCCCATGGTGGCGAAGGACTTTGGGCAAACTC	2460
QY	2461	TTGCTGTGCAAAACCTGATCAGGTCGACGAGGAACATGATATACACTTTCAAGGAGT	2520
Db	2461	TTGCTGTGCAAAACCTGATCAGGTCGACGAGGAACATGATATACACTTTCAAGGAGT	2520
QY	2521	GAGTCAAGTGGCTCCAGAGGCCACAAATTTTAAACCCCAATGGAGGGAATCCAAATTG	2580
Db	2521	GAGTCAAGTGGCTCCAGAGGCCACAAATTTTAAACCCCAATGGAGGGAATCCAAATTG	2580
QY	2581	TTTATTACTGATGAAGAGGTGGTCCGAGAGACAGACAGACACTTTTGAATGCCGA	2640
Db	2581	TTTATTACTGATGAAGAGGTGGTCCGAGAGACAGACAGACACTTTTGAATGCCGA	2640

Db 2581 TTATACGTATGAAGAGTGGGTCCCGAAGACAGACAGACACTTTTGATCCGCA 2640
QY 2641 CCGCAGCTCCGACGAGAACTGCTTTGCATCAGACTCTTAAGAGCTGAAGGTACGA 2700
Db 2641 CCGCAGCTCCGACGAGAACTGCTTTGCATCAGACTCTTAAGAGCTGAAGGTACGA 2700
QY 2701 TCATCTCAGACATTTTGAAGCAGAGAAAGTACAGATCCCTCAGCTTGCCATATTC 2760
Db 2701 TCATCTCAGACATTTTGAAGCAGAGAAAGTACAGATCCCTCAGCTTGCCATATTC 2760
QY 2761 AACGTGAATAA 2772
Db 2761 AACGTGAATAA 2772

RESULT 2
AX268476 3111 bp DNA linear PAT 29-OCT-2001
LOCUS AX268476
DEFINITION Sequence 3 from Patent WO0175108.
ACCESSION AX268476
VERSION AX268476.1 GI:16541653
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu,Y., Klieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 3 11-OCT-2001;
FEATURES
source 1. 3111
/organism="Homo sapiens"
BASE COUNT 814 a 771 c 789 g 737 t
ORIGIN
Query Match 100.0%; Score 2772; DB 6; Length 3111;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGCCACACGCGGGAGAGAGAGGCGCGCGCGGCTCTGCTGTAAGAGC 60
Db 60 ATGCCCGCCACACGCGGGAGAGAGAGGCGCGCGCGGCTCTGCTGTAAGAGC 119
QY 61 GGGCCAGCGGG 120
Db 120 GGGCCAGCGGG 179
QY 121 TCGGCGCGGGGAGGCTGCTGTAACCTGCGCAGCGCGCAGGGGGCGACGCTGCTACTG 180
Db 180 TCGGCGCGGGGAGGCTGCTGTAACCTGCGCAGCGCGCAGGGGGCGACGCTGCTACTG 239
QY 181 CTGGGCAACCGCGCGCCACGCTCGTGGTGGCGGGCGGGTGGCTGAGGAGAGCGCGCG 240
Db 240 CTGGGCAACCGCGCGCCACGCTCGTGGTGGCGGGCGGGTGGCTGAGGAGAGCGCGCG 299
QY 241 GGCAGACAGGG 300
Db 300 GGCAGACAGGG 359
QY 301 AGTGCAGCGGCAAGTCAAGTACGCGGGGTGACAGACTACCTGTACAGAGTGTGGAG 360
Db 360 AGTGCAGCGGCAAGTCAAGTACGCGGGGTGACAGACTACCTGTACAGAGTGTGGAG 419
QY 361 AGACCCCGCGGCTGGCGCTTATCTACACAGCTTTGCTTTCTCTGCTTTGGTTGC 420
Db 420 AGACCCCGCGGCTGGCGCTTATCTACACAGCTTTGCTTTCTCTGCTTTGGTTGC 479
QY 421 TTGATTTTGTAGTGTTTTCTACATCCCTGAGACACAAATTTGGCCTCAAGTTGCTC 480
Db 421 TTGATTTTGTAGTGTTTTCTACATCCCTGAGACACAAATTTGGCCTCAAGTTGCTC 480

Db 480 TTGATTTTGTAGTGTTTTCTACATCCCTGAGACACAAATTTGGCCTCAAGTTGCTC 539
QY 481 TTGATTTTGTAGTGTTTTCTACATCCCTGAGACACAAATTTGGCCTCAAGTTGCTC 540
Db 540 TTGATTTTGTAGTGTTTTCTACATCCCTGAGACACAAATTTGGCCTCAAGTTGCTC 599
QY 541 TCGCGGGGTGCTGTTGCGATATAGAGATGGCAGAGAGACAGAGTTTGCCTGAAG 600
Db 600 TCGCGGGGTGCTGTTGCGATATAGAGATGGCAGAGAGACAGAGTTTGCCTGAAG 659
QY 601 CCCTTCTGTATTAGATACCATTTGCTTATTCGCTTCAATAGCAGTTGTTCTGCAAAA 660
Db 660 CCCTTCTGTATTAGATACCATTTGCTTATTCGCTTCAATAGCAGTTGTTCTGCAAAA 719
QY 661 ACTCAGGGTAATATTTTTCAGCTGCGACTGCAAGAGTCCGTTCTCTACAGATCCGC 720
Db 720 ACTCAGGGTAATATTTTTCAGCTGCGACTGCAAGAGTCCGTTCTCTACAGATCCGC 779
QY 721 CGCATGGTGGCATATGACCGCAAGGGGAGGCGACTTGAATTAAGTGGTTCAAGTGGTTAT 780
Db 780 CGCATGGTGGCATATGACCGCAAGGGGAGGCGACTTGAATTAAGTGGTTCAAGTGGTTAT 839
QY 781 GCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTCTTATTTTTCG 840
Db 840 GCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTCTTATTTTTCG 899
QY 841 TCTTCTCTGTCTATCTGCTGGTGAAGAAAGATGCCAATAGATTTTCTACATATGCAGAT 900
Db 900 TCTTCTCTGTCTATCTGCTGGTGAAGAAAGATGCCAATAGATTTTCTACATATGCAGAT 959
QY 901 GCTCTCTGTGGGGCAATTTACATTTGACAACTATTTGGCTATGAGACAAAACCTCCCTTA 960
Db 960 GCTCTCTGTGGGGCAATTTACATTTGACAACTATTTGGCTATGAGACAAAACCTCCCTTA 1019
QY 961 ACTTGGCTGGGAAGATTTGCTTTGCGAGGCTTTCGACATCTTGGCATTTTCTTTTGA 1020
Db 1020 ACTTGGCTGGGAAGATTTGCTTTGCGAGGCTTTCGACATCTTGGCATTTTCTTTTGA 1079
QY 1021 CTTCCTGCGCGCAATTTCTGCTCAGGTTTTCATTTAAAGATGACAAACACACCGCCAG 1080
Db 1080 CTTCCTGCGCGCAATTTCTGCTCAGGTTTTCATTTAAAGATGACAAACACACCGCCAG 1139
QY 1081 AAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAATCATTCAGTGTGTTGGCGTAGT 1140
Db 1140 AAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAATCATTCAGTGTGTTGGCGTAGT 1199
QY 1141 TACGAGCTGATGAGAAATGTTTCCATTGCAACCTGGAAGCCACACTTTGAAGCCCTTG 1200
Db 1200 TACGAGCTGATGAGAAATGTTTCCATTGCAACCTGGAAGCCACACTTTGAAGCCCTTG 1259
QY 1201 CACACCTGACGCTTACCATGAGAACTAAGTTTAAAGAGCGAGTCCGATGGCTTAGC 1260
Db 1260 CACACCTGACGCTTACCATGAGAACTAAGTTTAAAGAGCGAGTCCGATGGCTTAGC 1319
QY 1261 CCCAGGGGCGAGATATTAAGAGCCGCAAGCCCTCAGTAGGTGAAGAGGTTCCCAAGC 1320
Db 1320 CCCAGGGGCGAGATATTAAGAGCCGCAAGCCCTCAGTAGGTGAAGAGGTTCCCAAGC 1379
QY 1321 ACCGACATACAGCCGAGGAGCACTCCACCAAGATGAGAGAGCTGAGCTTCAACAGC 1380
Db 1380 ACCGACATACAGCCGAGGAGCACTCCACCAAGATGAGAGAGCTGAGCTTCAACAGC 1439
QY 1381 CGAACCCTGCTCCGGGCTGCTGCGGCTGCAAAAAGTTCTCGCCAAAACAGTGTATGAT 1440
Db 1440 CGAACCCTGCTCCGGGCTGCTGCGGCTGCAAAAAGTTCTCGCCAAAACAGTGTATGAT 1499
QY 1441 GCTGACACAGCCCTTGGACATGATGATATGATGAAAAAGATGACAGTGTATGAT 1500
Db 1500 GCTGACACAGCCCTTGGACATGATGATATGATGAAAAAGATGACAGTGTATGAT 1559
QY 1501 TCAATGGAAGAGCTCACCCACACACTTAAACATGCTCATTTGAGAGTATCAGAAATATGAAA 1560
Db 1560 TCAATGGAAGAGCTCACCCACACACTTAAACATGCTCATTTGAGAGTATCAGAAATATGAAA 1619

Oy	1561	TTTCATCTGTGCAAAACCGAAGCTTTAAGAAACATATTCGTCATATCATGTAAAGATGTC	1620
Db	1620	TTTTCATCTGTGCAAAACCGAAGCTTTAAGAAACATATTCGTCATATCATGTAAAGATGTC	1679
Oy	1621	ATTGAAACAATATCTGCTGGTCATCTGGACATGTGTGGTAATTAACACCTTCAACA	1680
Db	1680	ATTGAAACAATATCTGCTGGTCATCTGGACATGTGTGGTAATTAACACCTTCAACA	1739
Oy	1681	CGTGTGATCAAAATTTCTTGAAAAAGGCAAAATCAATCAGATPAAGAGCCGAGAGAA	1740
Db	1740	CGTGTGATCAAAATTTCTTGAAAAAGGCAAAATCAATCAGATPAAGAGCCGAGAGAA	1799
Oy	1741	ATAACACGAGAACTGAGACACAGACAGATCTGATTCGTCGGTGGGTGGTCAAGGTT	1800
Db	1800	ATAACACGAGAACTGAGACACAGACAGATCTGATTCGTCGGTGGGTGGTCAAGGTT	1859
Oy	1801	GAAAAACAGGTACAGTCCATAGAATCCAAAGCTGGACTGCTACTAGACATCTATCAACAG	1860
Db	1860	GAAAAACAGGTACAGTCCATAGAATCCAAAGCTGGACTGCTACTAGACATCTATCAACAG	1919
Oy	1861	GTCCTTGGAAGGCTGTGGCTCGAGCCCTGGCTTGGCTTCATTCGAGATCCACCTTT	1920
Db	1920	GTCCTTGGAAGGCTGTGGCTCGAGCCCTGGCTTGGCTTCATTCGAGATCCACCTTT	1979
Oy	1921	GAATGTGAACAGACATCTGACTATCAAAAGCCGTGTGATAGCAAAAGATCTTTCGGGTTC	1980
Db	1980	GAATGTGAACAGACATCTGACTATCAAAAGCCGTGTGATAGCAAAAGATCTTTCGGGTTC	2039
Oy	1991	GCACAAAAAGTGGCTGTTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTCTCAG	2040
Db	2040	GCACAAAAAGTGGCTGTTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTCTCAG	2099
Oy	2041	TTTCATTTGAGCGCCAAATGAGTTGATGAGCCAGACTTCTACGGCTTAGCCCTACTATG	2100
Db	2100	TTTCATTTGAGCGCCAAATGAGTTGATGAGCCAGACTTCTACGGCTTAGCCCTACTATG	2159
Oy	2101	CACAGTCAGACACAGAGTGGCCAAATTAATGTCATAAGCGATGGCTCAGCAGTGGCCACC	2160
Db	2160	CACAGTCAGACACAGAGTGGCCAAATTAATGTCATAAGCGATGGCTCAGCAGTGGCCACC	2219
Oy	2161	AACACCAATTGCAAAACCAATTAATTAATGAGCCACCCAGCAGAGAGCCCAACCACTTTACAG	2220
Db	2220	AACACCAATTGCAAAACCAATTAATTAATGAGCCACCCAGCAGAGAGCCCAACCACTTTACAG	2279
Oy	2221	ATCCCACTCTCTCCAGCCATCAAGCATCTGGCCAGGCCAGAACTCTGACACCTTAAC	2280
Db	2280	ATCCCACTCTCTCCAGCCATCAAGCATCTGGCCAGGCCAGAAACCTCTGACACCTTAAC	2339
Oy	2281	CCTGAGGCTTACAGGAAGCATTTCTGAGCTCACACACCTGCTGTTCCTCAAGGAA	2340
Db	2340	CCTGAGGCTTACAGGAAGCATTTCTGAGCTCACACACCTGCTGTTCCTCAAGGAA	2399
Oy	2341	AATGTTCAAGTGTGACAGTCAAAATCTCACCAAGGACCGTTTATGAGAGAAAAAGCTTTGAC	2400
Db	2400	AATGTTCAAGTGTGACAGTCAAAATCTCACCAAGGACCGTTTATGAGAGAAAAAGCTTTGAC	2459
Oy	2401	ATGGAGAGAGAAATCTGTTGTCTGTCTGTCCATGGTGGCCGAAGGACTTGGCAATCT	2460
Db	2460	ATGGAGAGAGAAATCTGTTGTCTGTCTGTCCATGGTGGCCGAAGGACTTGGCAAAATCT	2519
Oy	2461	TTGTGTGTGCAAAAACCTGATCAGGTGCGACGACAGAACTGAAATPAACAATTTCAAGGAGT	2520
Db	2520	TTGTGTGTGCAAAAACCTGATCAGGTGCGACGACGAGAACTGAAATPAACAATTTCAAGGAGT	2579
Oy	2521	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTACCCCAATGAGGGAATCCAAATTG	2580
Db	2580	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTACCCCAATGAGGGAATCCAAATTG	2639
Oy	2581	TTTATTAACGATGAAGAGGTGGGTGTCGGAAGAGACAGAGACACTTTTGATGAGCCGA	2640
Db	2640	TTTATTAACGATGAAGAGGTGGGTGTCGGAAGAGACAGAGACACTTTTGATGAGCCGA	2699

QY	2641	CCGACAGCTGCGACAGGAAAGCTGCTTTGGATCAACACTCTTAAGSACTGGAAGGTACAGA	2700
Db	2700	CCGACAGCTGCGACAGGAAAGCTGCTTTGGATCAACACTCTTAAGSACTGGAAGGTACAGA	2759
QY	2701	TCATCTCAGACACTTTGTGAAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCATCATGTC	2760
Db	2760	TCATCTCAGACACTTTGTGAAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCATCATGTC	2819
QY	2761	AAACTGAAATATA 2772	
Db	2820	AAACTGAAATATA 2831	
RESULT 3			
LOCUS	AX253254	3074 bp	DNA
DEFINITION	Sequence 1 from Patent WO0170811.		Linear
ACCESSION	AX253254		
VERSION	AX253254.1	GI:16073802	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 3074)		
JOURNAL	Leiche,C., Scherer,C., Seeböhm,G., Busch,A. and Stelmeyer,K. Potassium channel protein kcnq5, a target for diseases of central nervous system and cardiovascular system Patent: WO 0170811-A 1 27-SEP-2001;		
FEATURES	Aventis Pharma Deutschland GmbH (DE)		
source	Location/Qualifiers 1..3074 /organism="Homo sapiens" /db_xref="taxon:9606"		
BASE COUNT	788 a 784 c 789 g 713 t		
ORIGIN			
Query Match	98.3%; Score 2723.8; DB 6; Length 3074;		
Best Local Similarity	98.8%; Pred. No. 0;		
Matches 2765; Conservative	0; Mismatches 7; Indels 27; Gaps 1;		
QY	1	ATGCCCGCCACACACGCGGAGAGAGAGAGGCGCGCCGCGGCTGTGGGTGAAGAC	60
Db	110	ATGCCCGCCACACACGCGGAGAGAGAGAGGCGCGCGGCTGTGGGTGAAGAC	169
QY	61	GGCGGAGGCGCGCGCGCGCGCGCGCGCGCTTGGGACGGCATGAAGATGTGGAG	120
Db	170	GGCGGAGGCGCGCGCGCGCGCGCGCGCTTGGGACGGCATGAAGATGTGGAG	229
QY	121	TGCGGCGCGGCGAGGAGGTGCTGTGAACCTCGGACGCGGACAGGGGCGAGCGGCTGTACTG	180
Db	230	TGCGGCGCGGCGAGGAGGTGCTGTGAACCTCGGACGCGGACAGGGGCGAGCGGCTGTACTG	289
QY	181	CTGGGACACCGCGGCGGACACGCTGCGGTGGCGCGCGCGGTGGCTTANAGGAGAGCCCGG	240
Db	290	CTGGGACACCGCGGCGGACACGCTTGTGTGGCGCGCGCGGTGGCTTANAGGAGAGCCCGG	349
QY	241	GGCAAGACAGGGGGGCCCGGATGAGCCCTGGCTGGGGAAGCGCCTCTTACACAGAGTACGAG	300
Db	350	GGCAAGACAGGGGGGCCCGGATGAGCCCTGGCTGGGGAAGCGCCTCTTACACAGAGTACGAG	409
QY	301	AGCTGCGCGCGGACAGCTCAAGTACCGGCGGGTGCGAAGACTACCTGTACACGCTGCTGAG	360
Db	410	AGCTGCGCGCGGACAGCTCAAGTACCGGCGGGTGCGAAGACTACCTGTACACGCTGCTGAG	469
QY	361	AAACCCCGGCGGTGGCGGTATCATACACGCTTTCCTTTCCTGCTGTGCTTGGTGGC	420
Db	470	AAACCCCGGCGGTGGCGGTTCATCAACACGCTTTCCTTTCCTGCTGTGCTTGGTGGC	529
QY	421	TTCATTTTTCAGTGTCTTTCACATCCCTGAGACACAAAAATTGGCTCAAGTTGCTC	480
Db	530	TTCATTTTTCAGTGTCTTTCACATCCCTGAGACACAAAAATTGGCTCAAGTTGCTC	589

QY 481 TTGATCTGAGAGTCTGATGATGTTGCTGTTGGTTGGATTCATTCGAAATCGG 540
| | | | |
Db 590 TTGATCTGAGAGTCTGATGATGTTGCTGTTGGTTGGATTCATTCGAAATCGG 649
| | | | |
QY 541 TCTGGGGGTGCTGTTGTCGATATAGAGATGGCAAGAGACGTGAGTTGCTGGAAG 600
| | | | |
Db 650 TCTGGGGGTGCTGTTGTCGATATAGAGATGGCAAGAGACGTGAGTTGCTGGAAG 709
| | | | |
QY 601 CCCCTCTGTTATATAGATACCATTTGTTATGCTTCAATAGACGTTGCTGCAAAA 660
| | | | |
Db 710 CCCCTCTGTTATATAGATACCATTTGTTATGCTTCAATAGACGTTGCTGCAAAA 769
| | | | |
QY 661 ACTCAGGTAATATTTTCCACGCTGCTGCACTCAGAAATCTCCGTTCCACAGATCCCTC 720
| | | | |
Db 770 ACTCAGGTAATATTTTCCACGCTGCTGCACTCAGAAATCTCCGTTCCACAGATCCCTC 829
| | | | |
QY 721 CGCATGTCGATGACCGAAGGGGAGAGACATTTGGAATTTACTGGGTTGCTGTTAT 780
| | | | |
Db 830 CGCATGTCGATGACCGAAGGGGAGAGACATTTGGAATTTACTGGGTTGCTGTTAT 889
| | | | |
QY 781 GCTCAGCAGCAAGCAATTAATCAGACGTTGTTACATAGATTTTGGTTCTTATTTTTCG 840
| | | | |
Db 890 GCTCAGCAGCAAGCAATTAATCAGACGTTGTTACATAGATTTTGGTTCTTATTTTTCG 949
| | | | |
QY 841 TCTTTCCTTGTATCTGTCGTAAGAAAGATGCCAATTAAGAGTTTCTACATATGACAT 900
| | | | |
Db 950 TCTTTCCTTGTATCTGTCGTAAGAAAGATGCCAATTAAGAGTTTCTACATATGACAT 1009
| | | | |
QY 901 GCTCTCTGTGGGGCAATTAATGACATTAATGCTATGCTATGAGACAAACCTCCCTA 960
| | | | |
Db 1010 GCTCTCTGTGGGGCAATTAATGACATTAATGCTATGCTATGAGACAAACCTCCCTA 1069
| | | | |
QY 961 ACTTGGCTGGGAAGATTTGCTTCTGACGCTTTGCACTCCCTGGCATTTCTTTTGA 1020
| | | | |
Db 1070 ACTTGGCTGGGAAGATTTGCTTCTGACGCTTTGCACTCCCTGGCATTTCTTTTGA 1129
| | | | |
QY 1021 CTCTCTGCGGCGATCTTGGCTGACAGTTTTCATTAAGTACAGAACACCGCCGAG 1080
| | | | |
Db 1130 CTCTCTGCGGCGATCTTGGCTGACAGTTTTCATTAAGTACAGAACACCGCCGAG 1189
| | | | |
QY 1081 AATCAGCTTGAAGAAAGAAAGAACCCAGCTGCCACCTCATAGTGTGTTGGCGTAGT 1140
| | | | |
Db 1190 AATCAGCTTGAAGAAAGAAAGAACCCAGCTGCCACCTCATAGTGTGTTGGCGTAGT 1249
| | | | |
QY 1141 TACGACGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCCAGACTTGAAGGCTTG 1200
| | | | |
Db 1250 TACGACGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCCAGACTTGAAGGCTTG 1309
| | | | |
QY 1201 CACACCTGACAGCCCTACCAA-----TCGAAGCTTAAGT 1233
| | | | |
Db 1310 CACACCTGACAGCCCTACCAAAGAAAGAAAGAAAGCAAGCAAGTCAAGAGCTTAAGT 1369
| | | | |
QY 1234 TTTTAAGAGGAGTGGCAGTGGCTAGCCCGAGGGGCGAGATTTTAAGAGCCGACAGGCC 1293
| | | | |
Db 1370 TTTTAAGAGGAGTGGCAGTGGCTAGCCCGAGGGGCGAGATTTTAAGAGCCGACAGGCC 1429
| | | | |
QY 1294 TCACTAGCTGACAGAGAGTCCCAAGCAACGACATTCACAGCCGAGGCGACTCCACCAA 1353
| | | | |
Db 1430 TCACTAGCTGACAGAGAGTCCCAAGCAACGACATTCACAGCCGAGGCGACTCCACCAA 1489
| | | | |
QY 1354 GTGAGAGAGAGCTGGAGCTTCAAGCAAGCAAGCCGCTTCCGCGCTCGCCCTCAAA 1413
| | | | |
Db 1490 GTGAGAGAGAGCTGGAGCTTCAAGCAAGCAAGCCGCTTCCGCGCTCGCCCTCAAA 1549
| | | | |
QY 1414 AGTTCTCAGCCAAAACAGATAGATGCTGACAGCCCTTGGCAGCTGATGATATAT 1473
| | | | |
Db 1550 AGTTCTCAGCCAAAACAGATAGATGCTGACAGCCCTTGGCAGCTGATGATATAT 1609
| | | | |
QY 1474 GATGAAAAAGAGATCCAGTGTGATGATCAGTGAAGACCTCACCCACACTTAAACT 1533
| | | | |
Db 1610 GATGAAAAAGAGATCCAGTGTGATGATCAGTGAAGACCTCACCCACACTTAAACT 1669
| | | | |
QY 1534 GTCATTGAGACTATCAGAAATATGAAATTTTCATGTTGCAAAAGCAAGTTTAAGAAACA 1593
| | | | |

Db 1670 GTCAATTGAGCTATCAGAAATATATGAATTTCTGTTGCAAAAGCAAGTTTAAGAAACA 1729
| | | | |
QY 1594 TTACGTCATATGATGTAAGAAAGATGTCATTGAACAATATTTGCTGTCATCTGACATG 1653
| | | | |
Db 1730 TTACGTCATATGATGTAAGAAAGATGTCATTGAACAATATTTGCTGTCATCTGACATG 1789
| | | | |
QY 1654 TTGCTGTAATTTAAACCCCTTCAAAACAGCTGTGATCAATTTCTTGGAAAAGGCAATC 1713
| | | | |
Db 1790 TTGCTGTAATTTAAACCCCTTCAAAACAGCTGTGATCAATTTCTTGGAAAAGGCAATC 1849
| | | | |
QY 1714 ACATCAGATTAAGAAAGACCCGAGAGAAATTAACAGAGAAATGACAGCCAGACATCTC 1773
| | | | |
Db 1850 ACATCAGATTAAGAAAGACCCGAGAGAAATTAACAGAGAAATGACAGCCAGACATCTC 1909
| | | | |
QY 1774 AGTATGCTCGGTGGGTGTCAGGTGTAAGTGAAGAAACAGTATCAGTCCATGAATCCAAGCTG 1833
| | | | |
Db 1910 AGTATGCTCGGTGGGTGTCAGGTGTAAGTGAAGAAACAGTATCAGTCCATGAATCCAAGCTG 1969
| | | | |
QY 1834 GACTGCTACTATAGCATCTATCAACAGGTCCTTGGAAAGGCTCTGCTCAGCCCTCGCT 1893
| | | | |
Db 1970 GACTGCTACTATAGCATCTATCAACAGGTCCTTGGAAAGGCTCTGCTCAGCCCTCGCT 2029
| | | | |
QY 1894 TTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATGACTATCAAAAGCCCT 1953
| | | | |
Db 2030 TTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATGACTATCAAAAGCCCT 2089
| | | | |
QY 1954 GTGATAGCAAAATCTTTTGGGTTCCGACAAACAGTGCCTGTTATCCAGATCACT 2013
| | | | |
Db 2090 GTGATAGCAAAATCTTTTGGGTTCCGACAAACAGTGCCTGTTATCCAGATCACT 2149
| | | | |
QY 2014 AGTCCAAACATCTCGAGAGGCTCGACATTCATTCGAGCCCAATGATTCAGTCCAG 2073
| | | | |
Db 2150 AGTCCAAACATCTCGAGAGGCTCGACATTCATTCGAGCCCAATGATTCAGTCCAG 2209
| | | | |
QY 2074 ACTTTTACGCGCTTAGCCCTACTATGACAGTGCAGAGCAACAGAGTGCATTAATGTCAA 2133
| | | | |
Db 2210 ACTTTTACGCGCTTAGCCCTACTATGACAGTGCAGAGCAACAGAGTGCATTAATGTCAA 2269
| | | | |
QY 2134 AGCGATGGCTCAGCATGTGGGAGCCACCAACACCTTGCACAAACCAATTAATAGCCACCC 2193
| | | | |
Db 2270 AGCGATGGCTCAGCATGTGGGAGCCACCAACACCTTGCACAAACCAATTAATAGCCACCC 2329
| | | | |
QY 2194 AAGCCAGAGCCCAACCAATTTACAGATCCCACTCTCTCCAGCCATCAAGATCTG 2253
| | | | |
Db 2330 AAGCCAGAGCCCAACCAATTTACAGATCCCACTCTCTCCAGCCATCAAGATCTG 2389
| | | | |
QY 2254 CCCAGGCCAAGAACTCTGCAACCTTAACCTGACAGGCTTACAGAAAGCAATTTGACGCTC 2313
| | | | |
Db 2390 CCCAGGCCAAGAACTCTGCAACCTTAACCTGACAGGCTTACAGAAAGCAATTTGACGCTC 2449
| | | | |
QY 2314 ACCACCTGCTTGTTCCTCCCAAGGAAATGTTCAAGTGCACAGTCAAACTCAACCAAG 2373
| | | | |
Db 2450 ACCACCTGCTTGTTCCTCCCAAGGAAATGTTCAAGTGCACAGTCAAACTCAACCAAG 2509
| | | | |
QY 2374 GACCGTTCTATGAGGAAAAAGCTTTGACATGGAGGAGAAACTGTTGTCTGTGTCCTC 2433
| | | | |
Db 2510 GACCGTTCTATGAGGAAAAAGCTTTGACATGGAGGAGAAACTGTTGTCTGTGTCCTC 2569
| | | | |
QY 2434 ATGTGCGGAGAGACTTGGGCAAAATCTTGTCTGTGCAAAACCTGATCAGGTGACGAG 2493
| | | | |
Db 2570 ATGTGCGGAGAGACTTGGGCAAAATCTTGTCTGTGCAAAACCTGATCAGGTGACGAG 2629
| | | | |
QY 2494 GAATGAAATATCACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGAGGACGACCAAGATTTT 2553
| | | | |
Db 2630 GAATGAAATATCACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGAGGACGACCAAGATTTT 2689
| | | | |
QY 2554 TAACCCAAATGAGGGAATCCAAATGTTTATTAATGATTAAGAGGTGGGTCGCGAAGAG 2613
| | | | |
Db 2690 TAACCCAAATGAGGGAATCCAAATGTTTATTAATGATTAAGAGGTGGGTCGCGAAGAG 2749
| | | | |
QY 2614 ACAGAGACAGACATTTTGTATGTCGCGACGACGACGAGGAAAGCTGCTTTCATCA 2673
| | | | |

Db 2750 ACAGAGACAGACATTTTATGCGCCGACCCGACCTGCGCAGGAGAGCTGCTTTCATCA 2809
 QY 2674 GACTCTTAAGAGACTGGAAGTCCAGCATATCTCAAGCACTTTGTAAGCAGAGAACT 2733
 Db 2810 GACTCTTAAGAGACTGGAAGTCCAGCATATCTCAAGCACTTTGTAAGCAGAGAACT 2869
 QY 2734 ACAGATGCTTCAAGCTTGGCTCATGTCACAACTGAATTA 2772
 Db 2870 ACAGATGCTTCAAGCTTGGCTCATGTCACAACTGAATTA 2908

RESULT 4
 AX456864
 LOCUS AX456864 3074 bp DNA linear PAT 06-JUL-2002
 DEFINITION Sequence 5 from Patent WO0232960.
 ACCESSION AX456864
 VERSION AX456864.1 GI:21715731
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 Argenti, T.M. and Sheldon, J.H.
 Methods of selecting compounds for modulation of bladder function
 Patent: WO 0232960-A 5 25-APR-2002;
 Wyeth (US)

FEATURES
 source 1.3074
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 788 a 784 c 789 g 713 t
 ORIGIN

Query Match 98.3%; Score 2723.8; DB 6; Length 3074;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 2765; Conservative 0; Mismatches 7; Indels 27; Gaps 1;

QY 1 ATGCCCCGCCACACCGCGGAGAGAGAGGCGCGCGCGCGCTTGGGTGAAGAC 60
 Db 110 ATGCCCCGCCACACCGCGGAGAGAGAGGCGCGCGCGCGCTTGGGTGAAGAC 169
 QY 61 GGGCGAGCGCGCGCGCGCGCGCGCGCGCGCTTGGGACGCGCATGAAGATGGAG 120
 Db 170 GGGCGAGCGCGCGCGCGCGCGCGCGCGCGCTTGGGACGCGCATGAAGATGGAG 229
 QY 121 TCGGGCGGGGCGAGGCTGCTGAACCTCGGACCGCGCAGGGGCGAGCGCTGCTACTG 180
 Db 230 TCGGGCGGGGCGAGGCTGCTGAACCTCGGACCGCGCAGGGGCGAGCGCTGCTACTG 289
 QY 181 CTGGGACCGCGCGCGCGCGCGCGCGCGCGCTGAGGAGAGAGAGAGAGAGAGAG 240
 Db 290 CTGGGACCGCGCGCGCGCGCGCGCGCGCGCTGAGGAGAGAGAGAGAGAGAGAG 349
 QY 241 GGCAG 300
 Db 350 GGCAG 409
 QY 301 AGCTGCGGCGCAACGTCAGTACCGCGGCGGTGCAAGTACCTGTACAGCTGCTGAG 360
 Db 410 AGCTGCGGCGCAACGTCAGTACCGCGGCGGTGCAAGTACCTGTACAGCTGCTGAG 469
 QY 361 AGAGCCCGCGCGCGCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCT 420
 Db 470 AGAGCCCGCGCGCGCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCT 529
 QY 421 TTGATTTTGTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480
 Db 530 TTGATTTTGTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 589
 QY 481 TTGATCTGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 590 TTGATCTGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649

QY 541 TCTGGGGGTGCTGTTGCTGATATAGAGATGGCAAGAGAGAGAGAGAGAGAGAGAGAG 600
 Db 650 TCTGGGGGTGCTGTTGCTGATATAGAGATGGCAAGAGAGAGAGAGAGAGAGAGAGAG 709
 QY 601 CCTTCTGTGTTATGATACCATTTGCTTATGCTTCAATAGACAGTGTGTTCTGCAAAA 660
 Db 710 CCTTCTGTGTTATGATACCATTTGCTTATGCTTCAATAGACAGTGTGTTCTGCAAAA 769
 QY 661 ACTCAGGGTAAATTTTCCACAGTGTGACATCAGAAAGTCTCGTTCCTACAGATCTCT 720
 Db 770 ACTCAGGGTAAATTTTCCACAGTGTGACATCAGAAAGTCTCGTTCCTACAGATCTCT 829
 QY 721 GCGATGTCGCGATGGACCGAAGGGGAGGACACTTGGAAAATTAAGTGGTTCAGTGTAT 780
 Db 830 GCGATGTCGCGATGGACCGAAGGGGAGGACACTTGGAAAATTAAGTGGTTCAGTGTAT 889
 QY 781 GCTCAGCAGAGAAATTAATCAGAGCTGTGTACATAGATTTTGGTCTTATTTTTCG 840
 Db 890 GCTCAGCAGAGAAATTAATCAGAGCTGTGTACATAGATTTTGGTCTTATTTTTCG 949
 QY 841 TCTTCTCTGTCTATCTGTGTGGAAGAGATGCCAATTAAGTGTCTACATATGAGAT 900
 Db 950 TCTTCTCTGTCTATCTGTGTGGAAGAGATGCCAATTAAGTGTCTACATATGAGAT 1009
 QY 901 GCTCCTGTGTTGGGCGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
 Db 1010 GCTCCTGTGTTGGGCGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1069
 QY 961 ACTTGGCTGGAGAAATTTGCTTGTGAGGCTTTGACCTCTTGGCATTTCTTTTTCGA 1020
 Db 1070 ACTTGGCTGGAGAAATTTGCTTGTGAGGCTTTGACCTCTTGGCATTTCTTTTTCGA 1129
 QY 1021 CTTCCTGCGCGCATTTCTGTGCTGAGTTTGTGCAATTAAGTGTGCTTGTGCTGAG 1080
 Db 1130 CTTCCTGCGCGCATTTCTGTGCTGAGTTTGTGCAATTAAGTGTGCTTGTGCTGAG 1139
 QY 1081 AAACACTTGTGAGAAAG 1140
 Db 1190 AAACACTTGTGAGAAAG 1249
 QY 1141 TACGAGCTGTATGAGAAATTTGCTTGTGCAATTAAGTGTGCTTGTGCTGAG 1200
 Db 1250 TACGAGCTGTATGAGAAATTTGCTTGTGCAATTAAGTGTGCTTGTGCTGAG 1309
 QY 1201 CACACTGTGAGCCCTTCCAA-----TCAGAGCTAAGT 1233
 Db 1310 CACACTGTGAGCCCTTCCAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
 QY 1234 TTTAAGAGAGAGATGCGATGCTAGCCCGAGGGGCGAGATTAAGAGGCGCAAGCC 1293
 Db 1370 TTTAAGAGAGAGATGCGATGCTAGCCCGAGGGGCGAGATTAAGAGGCGCAAGCC 1429
 QY 1294 TCAGTAGGTGACAG 1353
 Db 1430 TCAGTAGGTGACAG 1489
 QY 1354 GTGCAAG 1413
 Db 1490 GTGCAAG 1549
 QY 1414 AGTTCTCAGCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1473
 Db 1550 AGTTCTCAGCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
 QY 1474 GATGAAAAAG 1533
 Db 1610 GATGAAAAAG 1669
 QY 1534 GTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1593
 Db 1670 GTCATTCGAGCTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1729

Db	110	ATGCCCCGCCACCCAGCCGGAGAGAGAGGGCGCCGCCGCCCGGGGCTCTGGGTGAAGAGC	169
QY	61	GGCCGAGCGCGCGCGCGCGCGCGCGCTTGGGCAGCGGCATGAAATCTGAG	120
Db	170	GGCGCAGCGCGCGCGCGCGCGCGCGCTTGGGCGAGCGCATGAAATGTGGAG	229
QY	121	TCGGGCGCGGCGAAGGTCGTCTGAACTCGGGCAGCGCCGAGGGGCGAGCGCTGCTACMG	180
Db	230	TCGGGCGCGGCGAAGGTCGTCTGAACTCGGGCAGCGCCGAGGGGCGAGCGCTGCTACMG	289
QY	181	CTGGGCAACCCGCGCGCGCACGCTCGGGTGGGGGGCGGTGGCTCGAGGAGAGCCGCCG	240
Db	290	CTGGGCAACCCGCGCGCGCACGCTTGGTGGGGGGCGGTGGCTCGAGGAGAGCCGCCG	349
QY	241	GGCAAGCAGGGGGCCCGGATGAGCTCTGCTGGGGAAGCCGCTCTTACACAGTAGCCAG	300
Db	350	GGCAAGCAGGGGGCCCGGATGAGCTCTGCTGGGGAAGCCGCTCTTACACAGTAGCCAG	409
QY	301	AGCTGCGCGCGCAACGTCAAGTACCGCGCGGGTGCAGAACTCCTGTACAGCTGCTGAG	360
Db	410	AGCTGCGCGCGCAACGTCAAGTACCGCGGGTGCAGAACTCCTGTACAGCTGCTGAG	469
QY	361	AGACCCCGCGCGCGGCTCATCTACACAGCTTTCGTTTTCTCTGCTCTTGGTTC	420
Db	470	AGACCCCGCGCGCGGCTCATCTACACAGCTTTCGTTTTCTCTGCTCTTGGTTC	529
QY	421	TTGATTTTGTCAATGTTTTTACACATCCGTAGAGACACAAATGGCCCAAGTGGCC	480
Db	530	TTGATTTTGTCAATGTTTTTACACATCCGTAGAGACACAAATGGCCCAAGTGGCC	589
QY	481	TTGATCCTGAGTTCGTATGATTTGTGCTCTTGGTTGGAGTTTCATCATTCGAATCTGG	540
Db	590	TTGATCCTGAGTTCGTATGATTTGTGCTCTTGGTTGGAGTTTCATCATTCGAATCTGG	649
QY	541	TCGCGGGGTGCTGTTTCCGATATAGAGAGTGCAGAAAGTCAAGTTCCTGTGAAAG	600
Db	650	TCGCGGGGTGCTGTTTCCGATATAGAGAGTGCAGAAAGTCAAGTTCCTGTGAAAG	709
QY	601	CCCTTCTGTATATAGATACCATTTGTTCTTATGCTTCAATAGCAGTTGTTCTGCAAA	660
Db	710	CCCTTCTGTATATAGATACCATTTGTTCTTATGCTTCAATAGCAGTTGTTCTGCAAA	769
QY	661	ACTCAGGGTAATATTTTTGCCAGCTCTGCACTCAGAAGTCTCCGTTTCTACAGATCTTC	720
Db	770	ACTCAGGGTAATATTTTTGCCAGCTCTGCACTCAGAAAGTCTCCGTTTCTACAGATCTTC	829
QY	721	CGATGGTGGCAGTGAAGCCGAAAGGGAGAGCACTTGAATTTACTGGGTCAGAGGTTTAT	780
Db	830	CGATGGTGGCAGTGAAGCCGAAAGGGAGAGCACTTGAATTTACTGGGTCAGAGGTTTAT	889
QY	781	GCTCAGCAGCAAGAAATTAATCAGACGCTTGGTACATAGATTTTTGGTCTATATTTTTCG	840
Db	890	GCTCAGCAGCAAGAAATTAATCAGACGCTTGGTACATAGATTTTTGGTCTATATTTTTCG	949
QY	841	TCCTTCTGTCTATCTGCTGGTGAAGAAAGATGGCAATTAAGAGTTTCTCATATGGAGAT	900
Db	950	TCCTTCTGTCTATCTGCTGGTGAAGAAAGATGGCAATTAAGAGTTTCTCATATGGAGAT	1009
QY	901	GCCTCTGCTGGGCGCACAAATTAATGAACATTAATTTGGCTATGAGACAAAACTCCCTTA	960
Db	1010	GCCTCTGCTGGGCGCACAAATTAATGAACATTAATTTGGCTATGAGACAAAACTCCCTTA	1069
QY	961	ACTTGGCTGGGAAGATTCTTTCGACAGGCTTTCGACCTCTTGGCATTTCTTCTTTGCA	1020
Db	1070	ACTTGGCTGGGAAGATTCTTTCGACAGGCTTTCGACCTCTTGGCATTTCTTCTTTGCA	1129
QY	1021	CTTCTGTGCGGCAATTTCTGGCTCAGGTTTTCGATTAAAGTACAAACAAACCCGCGAG	1080
Db	1130	CTTCTGTGCGGCAATTTCTGGCTCAGGTTTTCGATTAAAGTACAAACAAACCCGCGAG	1189
QY	1081	AAACACTTTGAGAAAGAAGAACCCAGCTGCGCAACCTCATTCAGTGTGTTTGGCGTAGT	1140

Db	1190	MAACACTTTGAGAAAAGAAAGAACCCAGCGCCACCTCATTCAGTGTGTGGCGTAGT	1249
OY	1141	TAGCGACGTGATGAGAAATCTGTTTCATTGCAACTGGAAGCCACACTTGAAGGCGCTTG	1200
Db	1250	TAGCAGACTGATGAGAAATCTGTTTCATTGCAACTGGAAGCCACACTTGAAGGCGCTTG	1309
OY	1201	CACACCGTCGAGCCCTACCA-----TCGAAAGCTATAGT	1233
Db	1310	CACACCGTCGAGCCCTACCA-----TCGAAAGCTATAGT	1369
OY	1234	TTTAAAGGAGGAGGTGCGCATGGCTAGGCCCGAGGGCCAGATATTAAAGCGACAAAGCC	1293
Db	1370	TTTAAAGGAGGAGGTGCGCATGGCTAGGCCCGAGGGCCAGATATTAAAGCGACAAAGCC	1429
OY	1294	TCAGTAGTGACAGAGAGAGCTCCCAAGACCGACATCATCAGCCGAGGGCAGTCCGACCAAA	1353
Db	1430	TCAGTAGTGACAGAGAGAGCTCCCAAGACCGACATCATCAGCCGAGGGCAGTCCGACCAAA	1489
OY	1354	GTGCGAAGAGAGCTGGAGCTTCACAGCAGCAACCCGCTTCGCGCCCTCGCTGCGCTCAAA	1413
Db	1490	GTGCGAAGAGAGCTGGAGCTTCACAGCAGCAACCCGCTTCGCGCCCTCGCTGCGCTCAAA	1549
OY	1414	AGTTCTCAGCCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1473
Db	1550	AGTTCTCAGCCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1609
OY	1474	GATGAAAAAGAGTCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1533
Db	1610	GATGAAAAAGAGTCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1669
OY	1534	GTCATTCGAGCTATCAGATATTATGAATTTTCATGTTCCAAACAGGAAGTTTAAAGGAACA	1593
Db	1670	GTCATTCGAGCTATCAGATATTATGAATTTTCATGTTCCAAACAGGAAGTTTAAAGGAACA	1729
OY	1594	TTAGCTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1653
Db	1730	TTAGCTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1789
OY	1654	TTGTTGATGAATTTAAAGCCTTCAAAACAGCTGTTGATCAAAATCTTGGAAAAAGGCAATC	1713
Db	1790	TTGTTGATGAATTTAAAGCCTTCAAAACAGCTGTTGATCAAAATCTTGGAAAAAGGCAATC	1849
OY	1714	ACATGAGATGAAGAAAGAGCCGAGAGAAAAATACACAGAACATGTGAGACACAGAGATCTC	1773
Db	1850	ACATGAGATGAAGAAAGAGCCGAGAGAAAAATACACAGAACATGTGAGACACAGAGATCTC	1909
OY	1774	AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGTACGTCGATGATGATGATGATGATGATGAT	1833
Db	1910	AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGTACGTCGATGATGATGATGATGATGATGAT	1969
OY	1834	GACTGCTCTATGAGATCATCATCAACAGGTCCTGGGAAAGGCTCGGCTCGAGCCTGCTGCT	1893
Db	1970	GACTGCTCTATGAGATCATCATCAACAGGTCCTGGGAAAGGCTCGGCTCGAGCCTGCTGCT	2029
OY	1894	TTGGGCTTATTTCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCT	1953
Db	2030	TTGGGCTTATTTCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCT	2089
OY	1954	GTGAGATGACAAAGATCTTTCGGGTCCGACAAAAACAAGTGGCTGTTATCCAGATCAACT	2013
Db	2090	GTGAGATGACAAAGATCTTTCGGGTCCGACAAAAACAAGTGGCTGTTATCCAGATCAACT	2149
OY	2014	AGTGCACATCTCGAGAGGCTCGAGAGTTCATCTGAGCCCAAAATGAGTTGAGTGCAG	2073
Db	2150	AGTGCACATCTCGAGAGGCTCGAGAGTTCATCTGAGCCCAAAATGAGTTGAGTGCAG	2209
OY	2074	ACTTTCTACGGCTTAAGCCTTAATGCAAGTCAAGCAACAGAGTGCAGTCAAGTCAAGTCAAGTCAAG	2133
Db	2210	ACTTTCTACGGCTTAAGCCTTAATGCAAGTCAAGCAACAGAGTGCAGTCAAGTCAAGTCAAGTCAAG	2269
OY	2134	AGGATGAGTCTGAGAGTGGCAGCCACCAACAGCATTTGCAAAACCAATTAATATAGGCAACC	2193
Db	2270	AGGATGAGTCTGAGAGTGGCAGCCACCAACAGCATTTGCAAAACCAATTAATATAGGCAACC	2329

QY 2194 AAGCCAGACCCCAACAATTATACAGATCCACCTCTCCACGACATCAAGCATCTG 2253
 DB 2330 AAGCCAGACCCCAACAATTATACAGATCCACCTCTCCACGACATCAAGCATCTG 2389
 QY 2234 CCCAGGCCAAGAACTCTGCACCTTAACCTGCAGGCTTACAGAAAGCATTTCTGACGTC 2313
 DB 2390 CCCAGGCCAAGAACTCTGCACCTTAACCTGCAGGCTTACAGAAAGCATTTCTGACGTC 2449
 QY 2314 ACCACCTGCTTGTGGCCCTCAAGGAAATGTTACAGTTGACAGTCAATCTCACCAG 2373
 DB 2450 ACCACCTGCTTGTGGCCCTCAAGGAAATGTTACAGTTGACAGTCAATCTCACCAG 2509
 QY 2374 GACGCTCTATGAGAAAAAGCTTTGACATGAGGAGAAACTCTGTCTGTCTGCTCC 2433
 DB 2510 GACGCTCTATGAGAAAAAGCTTTGACATGAGGAGAAACTCTGTCTGTCTGCTCC 2569
 QY 2434 ATGGGCGGAGGAGCTTGGGCAATCTTGTCTGTCTGCAAAACCTGATCAGTCCAGCAG 2493
 DB 2570 ATGGGCGGAGGAGCTTGGGCAATCTTGTCTGTCTGCAAAACCTGATCAGTCCAGCAG 2629
 QY 2494 GAACGTAATATACAACTTTCAGAGGAGTCAAGTCAAGTCCAGAGGAGCCCAAGATTTT 2553
 DB 2630 GAACGTAATATACAACTTTCAGAGGAGTCAAGTCAAGTCCAGAGGAGCCCAAGATTTT 2689
 QY 2554 TACCCCAATATGAGGAGTCCAAATTTTATTAATGATGAGAGTGGTCCCGAAGAG 2613
 DB 2690 TACCCCAATATGAGGAGTCCAAATTTTATTAATGATGAGAGTGGTCCCGAAGAG 2749
 QY 2614 ACAGACAGACACTTTTATGAGGAGGAGTCAAGTCCAGAGGAGGAGTCCCTTTGATCA 2673
 DB 2750 ACAGACAGACACTTTTATGAGGAGGAGTCAAGTCCAGAGGAGGAGTCCCTTTGATCA 2809
 QY 2674 GACTCTTAAAGGAGTCAAGGAGTCAAGTCAATCTCAGAGGAGTCAAGGAGGAGTCA 2733
 DB 2810 GACTCTTAAAGGAGTCAAGGAGTCAAGTCAATCTCAGAGGAGTCAAGGAGGAGTCA 2869
 QY 2734 ACAGTGGCTTCACTTCTCTCATCTCAAACTGAAATTA 2772
 DB 2870 ACAGTGGCTTCACTTCTCTCATCTCAAACTGAAATTA 2908
 RESULT 6
 AX056817 3137 bp DNA linear PAT 17-JAN-2001
 LOCUS Sequence 1 from Patent W00077035.
 ACCESSION AX056817
 VERSION AX056817-1 GI:12309758
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 JOURNAL
 TITLE Novel potassium channels and genes encoding these potassium
 channels
 REFERENCE Patent: WO 0077035-A 1 21-DEC-2000;
 NEUROSEARCH A/S (DK)
 FEATURES
 source Location/Qualifiers
 1..3137
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..2694
 /note="unnamed protein product"
 /protein_id="Cac22381.1"
 /db_xref="GI:12309758"
 /translation="MKDVGSGRGRLVLLNSAARGDGLLGLTRATLGGGGGGRRESR
 RKQGRMSLIGKPLSYTSQSCRNVKTRVONYLNVLEPRGAFITHAFFLLV
 RPKRLSVSTIPEHTRKSLASCLLIEFVMIIVFGLFETLRISAGCCRRRGQGRLL
 RPKRFVIVITVLIAVSAKQGNIFATSALESLFLILNRVRRRGRTK
 LLGSSVVAHSHKELITAMVIGFVLIFSSFLVYLVKDNKEFTYADALMWGTTLLT

QY 106 ATGAAGATGAGAGTGGGCGGCGGAGGAGTGGTCTGTAACCTGCGGAGCCGCGGAGGCG 165
 DB 1 ATGAAGATGAGAGTGGGCGGCGGAGGAGTGGTCTGTAACCTGCGGAGCCGCGGAGGCG 60
 QY 166 GACGCGCTGCTACTGCTGGGACCCGCGGCGCAAGCTCGGTGGCGGCGGCGGCTGCT 225
 DB 61 GACGCGCTGCTACTGCTGGGACCCGCGGCGCAAGCTCGGTGGCGGCGGCGGCTGCT 120
 QY 226 AGGAGAGCCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
 DB 121 AGGAGAGCCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 QY 286 TACACGATGAGCAGAGCTGCGGCGGCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 345
 DB 181 TACACGATGAGCAGAGCTGCGGCGGCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 240
 QY 346 TACACGATGAGCAGAGCTGCGGCGGCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 405
 DB 241 TACACGATGAGCAGAGCTGCGGCGGCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 300
 QY 406 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
 DB 301 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 466 GCTTCAAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
 DB 361 GCTTCAAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 526 ATCATTCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
 DB 421 ATCATTCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 586 AGGTTGCTGCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
 DB 481 AGGTTGCTGCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 646 GTTGTGCTGCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
 DB 541 GTTGTGCTGCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 706 TTCTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
 DB 601 TTCTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 766 GGTTCAGTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
 DB 661 GGTTCAGTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 826 GTTCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
 DB 721 GTTCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 886 TCTACATGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945
 DB 781 TCTACATGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

REFERENCE 2 (bases 1 to 3137)
 AUTHORS Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and
 Jentsch, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistraase
 85, Hamburg 20246, Germany
 FEATURES
 source 1..3137
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="brain"
 gene 1..3137
 /gene="KCNQ5"
 1..2694
 /gene="KCNQ5"
 /note="splice variant I"
 /codon_start=1
 /product="potassium voltage-gated channel, KQT-like
 subfamily, member 5"
 /protein_id="AA069797.1"
 /db_xref="GI:7798696"
 /translation="MKDVEGRGVILNSAARGDILLGTRATLGGGGLRER
 RGGQARMILIGKPLSTSSOSCRNRYRQNTLYNLERPRAFTHAFVLLV
 FGLILSVETIPHTKLASCLILEVMIVFGLFTIRLSAGCCCRKRGQGL
 RFARKPCVIDTIVLASIAVSAKTQNIETASLRFLQILMVRDRGCTWK
 LLSVYVHSELITAMVIGFLVLFSSFLVLEKDKNESTYADALMWGTILTLT
 LGVDKPLTWLGRILSAGFALLGISFALPGILSGFALVQEGHROKHFEKRRP
 AANLIOCVMRSYADEKRSVJATMKPHLKALHCSPTKEGEGASSOSFEERYM
 ASRPGSIRKSROASVGRSPSTDTAAGSPKVKOKSMGFNRPTRRSPILRLKSQPK
 PVIDADPALGTDVYDEKCCGCCDVSEDLTPPLKTVIRIRIMKEHVARKEETLRP
 YDKVDIEQYSAGHLDMLCRILKSLQTRVDQILKGQITVSDKSRKELTAHEHTDLS
 MLKRVAVKEROVQIESKLDCLDLIDYQVLRGSAALASLQILPFECEQSDVS
 PVSQKDLDSGASONGCLSRSTASRGLQILTPNESACFTALSPMHSGATQV
 IOSDGSVAVATINTANOINTAPKPAATTTQIPLPLAIKLHPRETLHPNAGLOE
 SIDVTTCVLVASKEVNOVAOSNLTKRDMRSFMDGSLVCPVPRDICKSLISVO
 NLIRFTELNIOLSGSESSGSGSODEPKPKRRESKLTITDEVGPEPETETDTPDAPO
 PAHEAPASLSLRGRSSOSICKAGESTDLSLPHVKKL"
 BASE COUNT 865 a 749 c 745 g 778 t
 ORIGIN
 Query Match 94.9%; Score 2630; DB 9; Length 3137;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

Db 421 ATCATTCGATCTGCTGCGGGTGGCTGTGTGATATAGAGTGGCAAGGAGACTG 480
 QY 586 AGGTTTGCAGAAAGCCCTTCTGTATATAGATACCATTTGTTTATGCTTCAATACGA 645
 Db 481 AGGTTTGCAGAAAGCCCTTCTGTATATAGATACCATTTGTTTATGCTTCAATACGA 540
 QY 646 GTTGTTCGCAAAAACTCAGGGTAATATTTTGGCCACGTCGTGCACAGAGTCCTCGT 705
 Db 541 GTTGTTCGCAAAAACTCAGGGTAATATTTTGGCCACGTCGTGCACAGAGTCCTCGT 600
 QY 706 TTCCTACAGATCCTCCGATGGTGGCAGTACCGAAGGGGAGGACCTTGGAAATTAAGT 765
 Db 601 TTCCTACAGATCCTCCGATGGTGGCAGTACCGAAGGGGAGGACCTTGGAAATTAAGT 660
 QY 766 GGTTCAGTGGTTTATGCTCAGACCAAGAAATTAATACAGCTTGTACATAGATTTTGTG 825
 Db 661 GGTTCAGTGGTTTATGCTCAGACCAAGAAATTAATACAGCTTGTACATAGATTTTGTG 720
 QY 826 GTTCTATTTTTCGCTTCCCTTCTGTCTATCTGTGTGAAAAAGATGCCAATTAAGACTTT 885
 Db 721 GTTCTATTTTTCGCTTCCCTTCTGTCTATCTGTGTGAAAAAGATGCCAATTAAGACTTT 780
 QY 886 TCTACATATGACAGATGCTCTGTGTGGGACCAATTACATTGACACATTTGGCTATGGA 945
 Db 781 TCTACATATGACAGATGCTCTGTGTGGGACCAATTACATTGACACATTTGGCTATGGA 840
 QY 946 GACAAATCCTCCCTTAACCTTGCTGGGAGATTCCTTTCGACAGGCTTTCACACTCTTGGC 1005
 Db 841 GACAAATCCTCCCTTAACCTTGCTGGGAGATTCCTTTCGACAGGCTTTCACACTCTTGGC 900
 QY 1006 AATTTTCTTTCGCACTTCTCGCGGCAATTCCTTGGCTTGGCTTATTAAGTACAA 1065
 Db 901 AATTTTCTTTCGCACTTCTCGCGGCAATTCCTTGGCTTGGCTTATTAAGTACAA 960
 QY 1066 GAACACACACCGGCAAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTATTCAG 1125
 Db 961 GAACACACACCGGCAAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTATTCAG 1020
 QY 1126 TGTGTTGGCGTAGTACGACCTGATGAGAAATCTGTTCCATTGCACTTGAACCA 1185
 Db 1021 TGTGTTGGCGTAGTACGACCTGATGAGAAATCTGTTCCATTGCACTTGAACCA 1080
 QY 1186 CACTTGAAGGCTTCACACACTGCGACCCCTACCA----- 1220
 Db 1081 CACTTGAAGGCTTCACACACTGCGACCCCTACCA----- 1140
 QY 1221 --TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATGCTTAGCCCAAGGGGCAAGATATT 1278
 Db 1141 AGTCAGAAAGCTAAGTTTAAAGAGCGAGTGGCATGCTTAGCCCAAGGGGCAAGATATT 1200
 QY 1279 AAGAGCCGACAAAGCTCAGTAGTGAAGAGAGTGGCCCAAGCAAGCAATCAAGCCGAG 1338
 Db 1201 AAGAGCCGACAAAGCTCAGTAGTGAAGAGAGTGGCCCAAGCAAGCAATCAAGCCGAG 1260
 QY 1339 GGCAGTCCACCAAGAGTGCAGAAAGCTGGAGCTTCAAGACCGAAGCCGCTTCGAGCC 1398
 Db 1261 GGCAGTCCACCAAGAGTGCAGAAAGCTGGAGCTTCAAGACCGAAGCCGCTTCGAGCC 1320
 QY 1399 TCGCTGGGCGTCAAAAGTTCTCAGCCAAACCAAGATAGATGATGCTACACAGCCCTTGGC 1458
 Db 1321 TCGCTGGGCGTCAAAAGTTCTCAGCCAAACCAAGATAGATGATGCTACACAGCCCTTGGC 1380
 QY 1459 ACTGATGATGATATGATGAGAAAAGAGTCCAGTGTGATGATGATGAGAAAGCTCAGC 1518
 Db 1381 ACTGATGATGATATGATGAGAAAAGAGTCCAGTGTGATGATGATGAGAAAGCTCAGC 1440
 QY 1519 CCACCACTTAACCTGTCATTCGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1578
 Db 1441 CCACCACTTAACCTGTCATTCGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAACGG 1500
 QY 1579 AAGTTTAAAGAAATTAACCTGTCATTCGAGCTATCAGAAATTAAGAAATTCATGTTGCT 1638

Db	1501	AAGTTTAAGGAACAATTACGTCCTATGATGATGTAAACATGTCATTGAACAATATCTCGCT	1560
Qy	1639	GGTCATCTGGACATGTTGTGTAGATTAAAGCCTTCAACACGCTGTTGATCAAAATCTT	1698
Db	1561	GGTCATCTGGACATGTTGTGTAGATTAAAGCCTTCAACACGCTGTTGATCAAAATCTT	1620
Qy	1699	GGAAAGGGCAATACATCATCAGATTAACAAAGCCGAGAGAAAATTAACAGCAAACTAGAG	1758
Db	1621	GGAAAGGGCAATACATCATCAGATTAACAAAGCCGAGAGAAAATTAACAGCAAACTAGAG	1680
Qy	1759	ACCACAGACGATCTCAGTATGCTGCTGGGTGTCGAAGGTTGGAAAACAGGTCACTGC	1818
Db	1681	ACCACAGACGATCTCAGTATGCTGCTGGGTGTCGAAGGTTGGAAAACAGGTCACTGC	1740
Qy	1819	ATAGAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1878
Db	1741	ATAGAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1800
Qy	1879	GGCTCAGCCCTCGGCTTTGGCTTCACTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1938
Db	1801	GGCTCAGCCCTCGGCTTTGGCTTCACTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1860
Qy	1939	GACATATCAAAAGCCCTGTGGATAGAGAAAGATTTTCGGGTTCCGACAAACAGTGGCTGC	1998
Db	1861	GACATATCAAAAGCCCTGTGGATAGAGAAAGATTTTCGGGTTCCGACAAACAGTGGCTGC	1920
Qy	1999	TTATTCAGATCACTAGTGGCCACATCTCGAGAGCCCTGCAGTTCACTTCTGACGCCAAAT	2058
Db	1921	TTATTCAGATCACTAGTGGCCACATCTCGAGAGCCCTGCAGTTCACTTCTGACGCCAAAT	1980
Qy	2059	GAGTTCAAGTGGCCAGACTTTCTACGGGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2118
Db	1981	GAGTTCAAGTGGCCAGACTTTCTACGGGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2040
Qy	2119	GTGCCAATTAATYCAAGAGCGATGCTCTACAGAGTGGCAGACCAACACACTTGCACAAACAA	2178
Db	2041	GTGCCAATTAATYCAAGAGCGATGCTCTACAGAGTGGCAGACCAACACACTTGCACAAACAA	2100
Qy	2179	ATAAATACGGGACCCCAAGCCAGACGCCCAACAACCTTTACAGATCCCACTCTCTCCCA	2238
Db	2101	ATAAATACGGGACCCCAAGCCAGACGCCCAACAACCTTTACAGATCCCACTCTCTCCCA	2160
Qy	2239	GCATTCAGACATCTGCCCCAGGCCAGAAAACCTTGCACCCCTACCGCTTACAGGAA	2298
Db	2161	GCATTCAGACATCTGCCCCAGGCCAGAAAACCTTGCACCCCTACCGCTTACAGGAA	2220
Qy	2299	AGCATTTCTGACGTCACACACCTGCTGTTGGCCGCAAGAAATGTTACAGGTTGCACAG	2358
Db	2221	AGCATTTCTGACGTCACACACCTGCTGTTGGCCGCAAGAAATGTTACAGGTTGCACAG	2280
Qy	2359	TCAAAATCTCACCAAGGACCGTTCTATATAGAGAAAGCTTTGCATGAGGAGAGAAACTCTG	2418
Db	2281	TCAAAATCTCACCAAGGACCGTTCTATATAGAGAAAGCTTTGCATGAGGAGAGAAACTCTG	2340
Qy	2419	TTGTCTGTCTGTCCCATGCTGCGAAGGACTTGGGCAAACTTGTCTGTGCAAAACCTG	2478
Db	2341	TTGTCTGTCTGTCCCATGCTGCGAAGGACTTGGGCAAACTTGTCTGTGCAAAACCTG	2400
Qy	2479	ATTCAGGTCGACCGAGGAACTGAATATATCAACTTTCAGGAGTAGTCAAGTGGCTCCAGA	2538
Db	2401	ATTCAGGTCGACCGAGGAACTGAATATATCAACTTTCAGGAGTAGTCAAGTGGCTCCAGA	2460
Qy	2539	GGCAGGCCAAGATTTTATACCCCAATATGAGGAGATCCAAATGTTTATTAAGTGAAGAGAG	2598
Db	2461	GGCAGGCCAAGATTTTATACCCCAATATGAGGAGATCCAAATGTTTATTAAGTGAAGAGAG	2520
Qy	2599	GTGGGTCCCGAAGACAGACAGACACTTTTGATGCGCAGCCGACGCTCCAGAGGAA	2658
Db	2521	GTGGGTCCCGAAGACAGACAGACACTTTTGATGCGCAGCCGACGCTCCAGAGGAA	2580
Qy	2659	GCTGCTTTTGATACAGACTCTCTTAAGACTGGAAGGTCACGATATATCTCAGAGCAATTTGT	2718
Db	2581	GCTGCTTTTGATACAGACTCTCTTAAGACTGGAAGGTCACGATATATCTCAGAGCAATTTGT	2640

[illegible]

QY	706	TTCTCAACAGATCCCTCCGATGGTGGCATATGACCCGAAGGGAGGACCTTTGGAAATTACTG	765
Db	601	TTCTTCACAGATCCCTCCGATGGTGGCATATGACCCGAAGGGAGGACCTTTGGAAATTACTG	660
QY	766	GGTTCAAGTGGTTTATGCTACAGCAAGAATAATATACAGCTGGATGACATAGATTATTTG	825
Db	661	GGTTCAAGTGGTTTATGCTACAGCAAGAATAATATACAGCTGGATGACATAGATTATTTG	720
QY	826	GTTCTTAATTTTTTGTCTTCCCTTGTCTATCTGTGTGAAAAGGATGCCAATAAGACTTT	885
Db	721	GTTCTTAATTTTTTGTCTTCCCTTGTCTATCTGTGTGAAAAGGATGCCAATAAGACTTT	780
QY	886	TTTACATATGCAAGATGCTCTCTGGTGGGGGACAAATTAATCAATGTGCAACTATTTGGTATAGA	945
Db	781	TTTACATATGCAAGATGCTCTCTGGTGGGGGACAAATTAATCAATGTGCAACTATTTGGTATAGA	840
QY	946	GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTTTGCAAGGCTTGGCACTCCCTTGGC	1005
Db	841	GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTTTGCAAGGCTTGGCACTCCCTTGGC	900
QY	1006	ATTTCCTTCTTTCGTGCACTTCCTGCGGCATCTTGGCTCAGGTTTGCATTTAAAAGTACAA	1065
Db	901	ATTTCCTTCTTTCGTGCACTTCCTGCGGCATCTTGGCTCAGGTTTGCATTTAAAAGTACAA	960
QY	1066	GAACAACACGCGGCGAANAACATTGTGAGAAAAGAAAGAACCCGACGCTGCCAACCTCATTCAG	1125
Db	961	GAACAACACGCGGCGAANAACATTGTGAGAAAAGAAAGAACCCGACGCTGCCAACCTCATTCAG	1020
QY	1126	TGTGTTTGGCGTAGTTACGCAAGCTGATAGAATGTGTTCCATTGCAACCTGGAAAGCCA	1185
Db	1021	TGTGTTTGGCGTAGTTACGCAAGCTGATAGAATGTGTTCCATTGCAACCTGGAAAGCCA	1080
QY	1186	CACTTGAAGGCTTTCACACCTGCAAGCCCTTACCA-----1220	1220
Db	1081	CACTTGAAGGCTTTCACACCTGCAAGCCCTTACCAAGAAAGAACAAAGGGAAGCATCAAGC	1140
QY	1221	--TCAGAAAGTAAAGTTTAAAGAGGAGTGGCCATGGCTAGAGCCGACGGGGCCAGAGATT	1278
Db	1141	AGTCAGAAAGTAAAGTTTAAAGAGGAGTGGCCATGGCTAGAGCCGACGGGGCCAGAGATT	1200
QY	1279	AAGAGCGGACAAGCCTCAGTAGTGATGACAGAGAGTCCCCCAAGCACCGACATCACAGCCGAG	1338
Db	1201	AAGAGCGGACAAGCCTCAGTAGTGATGACAGAGAGTCCCCCAAGCACCGACATCACAGCCGAG	1260
QY	1339	GGGAGTCCCAACAAAGTGCAGAAAGCTGTGAGAGCTTTCMAAGACCGAAACCCGCTTCCGGCC	1398
Db	1261	GGGAGTCCCAACAAAGTGCAGAAAGCTGTGAGAGCTTTCMAAGACCGAAACCCGCTTCCGGCC	1320
QY	1399	TGCGTCCGCGCTCAAAAAGTTTTCACAGCAAAACAGATGATGATGCTGACACAGCCCTTGGC	1458
Db	1321	TGCGTCCGCGCTCAAAAAGTTTTCACAGCAAAACAGATGATGATGCTGACACAGCCCTTGGC	1380
QY	1459	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTGATGTATCACTGGAAGACCTTACC	1518
Db	1381	ACTGATGATGTATATGATGAAAAAGATGCCAGTGTGATGTATCACTGGAAGACCTTACC	1440
QY	1519	CCACCACTTAAAACTGTCATTCGAGCTATCAGAAATTATGAATTTTATGTGCAAAACGG	1578
Db	1441	CCACCACTTAAAACTGTCATTCGAGCTATCAGAAATTATGAATTTTATGTGCAAAACGG	1500
QY	1579	AAGTTTAAGGAACATTAACGTCATATATATGTAAGAAAGTGTATGAACAAATFTTCGT	1638
Db	1501	AAGTTTAAGGAACATTAACGTCATATATATGTAAGAAAGTGTATGAACAAATFTTCGT	1560
QY	1639	GGTCATCTGACATGTTGTGTAGATTAAAAAGCCTTCAAAACAGCTGTTGATCAAAATCTT	1698
Db	1561	GGTCATCTGACATGTTGTGTAGATTAAAAAGCCTTCAAAACAGCTGTTGATCAAAATCTT	1620
QY	1699	GGAAAAGGGCAATCACATCAGATTAAGAAAGCCGAGAGAAAATTAACAGCAGACATGAG	1758
Db	1621	GGAAAAGGGCAATCACATCAGATTAAGAAAGCCGAGAGAAAATTAACAGCAGACATGAG	1680

LOCUS	AP263835	2832 bp	mRNA	linear	PRI 01-JUN-2000
DEFINITION	Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,				
Db	1759	ACCAACACAGATTCACAGATGCTGGTGGGGGAGTCACAGTTGAAACACAGTACATCC	1818		
Db	1681	ACCAACACAGATTCACAGATGCTGGTGGGGGAGTCACAGTTGAAACACAGTACATCC	1740		
QY	1819	ATAGAAATCCAGACTGAGTGGCTACATGACATCTATCAACAGGTCCCTCGGAAAGGCTCT	1878		
Db	1741	ATAGAGTCCAAAGCTGAGTGGCTACATGACATCTATCAACAGGTCCCTCGGAAAGGCTCT	1800		
QY	1879	GCCTCACGCTCGCTTGGCTTCATTCCAGATCCACCTTTTGAATGTAAACAGACATCT	1938		
Db	1801	GCCTCACGCTCGCTTGGCTTCATTCCAGATCCACCTTTTGAATGTAAACAGACATCT	1860		
QY	1939	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGCACAAAACAGTGGCTG	1998		
Db	1861	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGCACAAAACAGTGGCTG	1920		
QY	1999	TATATCCAGATCACTAGTGGCCACATCTTCAGAGAGGCTGCAGTTCAATCTTGACGCCAAT	2058		
Db	1921	TATATCCAGATCACTAGTGGCCACATCTTCAGAGAGGCTGCAGTTCAATCTTGACGCCAAT	1980		
QY	2059	GAGTTGAGTGGCCAGACTTTTACGCGGTTTACGCCCTACTATGAGACAGTCAAGAACACAG	2118		
Db	1981	GAGTTGAGTGGCCAGACTTTTACGCGGTTTACGCCCTACTATGAGACAGTCAAGAACACAG	2040		
QY	2119	GTGCAATATATGTCAAAGGAGATGGCTCAGACAGTGGACGCCAACCAACCATTTGCAACCAA	2178		
Db	2041	GTGCAATATATGTCAAAGGAGATGGCTCAGACAGTGGACGCCAACCAACCATTTGCAACCAA	2100		
QY	2179	ATTAATATCGGACCCCAAGCCAGCCAGCCCAACAACTTTACAGATGCCACCTCCTCTCCCA	2238		
Db	2101	ATTAATATCGGACCCCAAGCCAGCCAGCCCAACAACTTTACAGATGCCACCTCCTCTCCCA	2160		
QY	2239	GCCATCAAGCATCTGCCAGGCCACAGAAACTCTGCACCTTAACCCCTCAGGCTTACAGAA	2298		
Db	2161	GCCATCAAGCATCTGCCAGGCCACAGAAACTCTGCACCTTAACCCCTCAGGCTTACAGAA	2220		
QY	2299	AGCATTTCTGACGTCACCACTGCTTGTGGCTCCAGAGAAATATGTTACAGTTTGACAG	2358		
Db	2221	AGCATTTCTGACGTCACCACTGCTTGTGGCTCCAGAGAAATATGTTACAGTTTGACAG	2280		
QY	2359	TCAAAATCTACCAAGAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAGAAACTCTG	2418		
Db	2281	TCAAAATCTACCAAGAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAGAAACTCTG	2340		
QY	2419	TTGTCTGTCTGTCCCATGTGTGCCAGAGACTTTGGGCAAACTCTTGTCTGTGCAAAACTGT	2478		
Db	2341	TTGTCTGTCTGTCCCATGTGTGCCAGAGACTTTGGGCAAACTCTTGTCTGTGCAAAACTGT	2400		
QY	2479	ATCAGGTGCGACCGAGGAACGAAATATATACACTTTCAGGAGAGTGAAGTGGCTCCAGA	2538		
Db	2401	ATCAGGTGCGACCGAGGAACGAAATATATACACTTTCAGGAGAGTGAAGTGGCTCCAGA	2460		
QY	2539	GCGAGCCAGAAATTTTAAACCCCAATATGAGGGAATCCAAATTTGTTAACTGATGAAGAG	2598		
Db	2461	GCGAGCCAGAAATTTTAAACCCCAATATGAGGGAATCCAAATTTGTTAACTGATGAAGAG	2520		
QY	2599	GTTGGTCCCGAAGACAGACAGACAGACACTTTTGAATGCCGACCCGACAGCTGCCAGGGAA	2658		
Db	2521	GTTGGTCCCGAAGACAGACAGACAGACACTTTTGAATGCCGACCCGACAGCTGCCAGGGAA	2580		
QY	2659	GCTGCCCTTTCATAGACTCTCTAAAGAGCTGGAAGGTACAGATCATCTCAGACATTTGT	2718		
Db	2581	GCTGCCCTTTCATAGACTCTCTAAAGAGCTGGAAGGTACAGATCATCTCAGACATTTGT	2640		
QY	2719	AAGGACGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA	2772		
Db	2641	AAGGACGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA	2694		

partial cds.
 AF263835
 AF263835.1 GI:8132996

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
 1 (bases 1 to 2832)
 Kniazeva, M. and Han, M.
 A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders
 Unpublished
 2 (bases 1 to 2832)
 Kniazeva, M. and Han, M.
 Direct Submission
 Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

FEATURES
 source
 1. 2832
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q: D6S280"
 /tissue_type="brain; retina"
 <1. 2832
 /gene="KCNQ5"
 <1. 2586
 /gene="KCNQ5"
 /note="member of the KCNQ family"
 /codon_start=1
 /product="voltage-gated potassium channel KCNQ5"
 /protein_id="AA073446.1"
 /db_xref="GI:8132997"
 /translation="GGGLRESRRKQKGRMSLLKPLSYTSQSCRNVKRYRVQNTL
 YNLEPRGMFVHFAVEFLVFGCLISVSTIPEHTKLASSCLLIEFWAVVGL
 EFLIRISAGCCFRRGWRGRRLRFRKPCVVIDLVLASIVVAKTQGNIFASAL
 RSLRFQILRRVMDRRCQTKLIGSVYVASKELITWYIGFVLIFESFVLVYER
 DANKESTYDALMGMGTTTLTIGDGKDTPLMGLISAGFALIGISFPAIDGILG
 SGPLAKVQEOHRKHFEKRRNPANLLOCVRSYVADKESVSIATWPKPLKHLHNSP
 TKRQGRASSSQKLSFEKVRMASPRGOSISRQASVGDNRSPSTDIAGSPKLYOK
 SMSNDRTREFRSLRKLSSOPKVIDADTALGTDVDEKGCQCDVSEDLPEPLKTV
 IRAIRIKFHVAKRKFETLRPYDKVIEQVSAGHLMCLIKSLQTRVDILGQO
 ITSDKSRKETIAHEFTDLSMLGRVYKVEKOVOSIESKLDLIDYQVLRKGSAS
 ALALASFOIPFECEOTSQVOSPVDSKLSGSAONSGLSRSTSNISGILPILTPN
 EFSQOTYALSPYHMSQATQYPISSDSSAYVATNTIANQITAPRAPATLQIPEP
 LPAIKHLPREPTLHPNPAQLESISDVATCLVASKENOVAVOASNPKDRSMKSPDMG
 GETLISVCPMVKDKLGSLSVONLIRSTEELNIQLSGSSGSRGRDQFPMWRBSKL
 FTIDEEVGPETETFDPAPOPARAAFAFASDSLRTGRSSOSISICKAGESTDALSLP
 HVKRLK"

BASE COUNT 783 a 685 c 663 g 701 t

ORIGIN

Query Match 90.6%; Score 2510.8; DB 9; Length 2832;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 2552; Conservative 0; Mismatches 7; Indels 27; Gaps 1;

QY 214 GCGGTGCGCTGAGGAGAGCGCGGGGCAAGAGCGGGCGCGATGAGCGCTGGGG 273
 |||||||
 DB 1 GCGGTGCGCTGAGGAGAGCGCGGGGCAAGAGCGGGCGCGATGAGCGCTGGGG 60
 |||||||

QY 274 AAGCGCTCTCTTACAGAGTAGCCAGAGCTCCGGCGCAAGCTCAAGTACCGCGGGT 333
 |||||||
 DB 61 AAGCGCTCTCTTACAGAGTAGCCAGAGCTCCGGCGCAAGCTCAAGTACCGCGGGT 120
 |||||||

QY 334 CAGAACTACCTGTACAGAGTGTGAGAGAGACCCCGCGCTGGCGCTTACACAGCT 393
 |||||||
 DB 121 CAGAACTACCTGTACAGAGTGTGAGAGAGACCCCGCGCTGGCGCTTACACAGCT 180
 |||||||

QY 394 TTCGTTTTCCTCTGCTTTGCTGCTGATTTTGTACAGTGTCTTACCATCCCTGAG 453
 |||||||
 DB 181 TTCGTTTTCCTCTGCTTTTGTGCTTGTGATTTTGTACAGTGTCTTACCATCCCTGAG 240
 |||||||

QY 454 CACACAAAATGGCCCTCAAGTGCCTCTTGATCCTGGAGTCTGTGATGATGTCGCTTT 513
 |||||||
 DB 241 CACACAAAATGGCCCTCAAGTGCCTCTTGATCCTGGAGTCTGTGATGATGTCGCTTT 300
 |||||||

QY 514 GGTTCGAGTTCATTCATTCGAATCTGGTCTGCGGGTGTGCTGTGCAATATAGAGGATG 573
 |||||||
 DB 301 GGTTCGAGTTCATTCATTCGAATCTGGTCTGCGGGTGTGCTGTGCAATATAGAGGATG 360
 |||||||

QY 574 CAGGAAGACTGGAGTGTGCTGCAAAAGCCCTGCTGTATAGATACATGTTCTTATC 633
 |||||||
 DB 361 CAGGAAGACTGGAGTGTGCTGCAAAAGCCCTGCTGTATAGATACATGTTCTTATC 420
 |||||||

QY 634 GCTTCATATACAGTGTGTTTGTGCAAAAACCTCAGGGTAATATTTTCCACGCTGCAC 693
 |||||||
 DB 421 GCTTCATATACAGTGTGTTTGTGCAAAAACCTCAGGGTAATATTTTCCACGCTGCAC 480
 |||||||

QY 694 AGAAGTCTCCGTTTCTTACAGATCTCCGATGCTGCGCATGACACCAAGGGAGGAC 753
 |||||||
 DB 481 AGAAGTCTCCGTTTCTTACAGATCTCCGATGCTGCGCATGACACCAAGGGAGGAC 540
 |||||||

QY 754 TGGAAATTTACTGGGTTGAGTGTATGCTCAGCAAGAAATTAATCAGCTGTGATC 813
 |||||||
 DB 541 TGGAAATTTACTGGGTTGAGTGTATGCTCAGCAAGAAATTAATCAGCTGTGATC 600
 |||||||

QY 814 ATAGATTTTGTGCTTATTTTGTGCTTCTGCTGTCTATCTGTGCGAAAGAGATGCC 873
 |||||||
 DB 601 ATAGATTTTGTGCTTATTTTGTGCTTCTGCTGTCTATCTGTGCGAAAGAGATGCC 660
 |||||||

QY 874 AATTAAGATTTTCTATATATGCAATGCAATGCTCTGCGGAGCAATTAATGCACT 933
 |||||||
 DB 661 AATTAAGATTTTCTATATATGCAATGCAATGCTCTGCGGAGCAATTAATGCACT 720
 |||||||

QY 934 ATTGGCATGAGACAAACACCTCCCTAACTTGGTGGGAAATGCTTTCTGACAGCTTT 993
 |||||||
 DB 721 ATTGGCATGAGACAAACACCTCCCTAACTTGGTGGGAAATGCTTTCTGACAGCTTT 780
 |||||||

QY 994 GCACTCTTGGCATTTCTTCTTGTGCACTTCTGCGGCAATCTTGGCTCAGTTTGA 1053
 |||||||
 DB 781 GCACTCTTGGCATTTCTTCTTGTGCACTTCTGCGGCAATCTTGGCTCAGTTTGA 840
 |||||||

QY 1054 TTTAAAGTTACAAAGAACACCCGCGAGAAACCTTGAAAGAGAACACCCAGCTGCC 1113
 |||||||
 DB 841 TTTAAAGTTACAAAGAACACCCGCGAGAAACCTTGAAAGAGAACACCCAGCTGCC 900
 |||||||

QY 1114 AACCTCATAGTGTGTTGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1173
 |||||||
 DB 901 AACCTCATAGTGTGTTGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 960
 |||||||

QY 1174 ACCTGGAAGCCACACTTGAAGGCTTGCACACCTGACACCTTACCA----- 1220
 |||||||
 DB 961 ACCTGGAAGCCACACTTGAAGGCTTGCACACCTGACACCTTACCA----- 1020
 |||||||

QY 1221 -----TCGAAAGCTAAGTTTAAAGAGGAGAGGCGGATGAGTGGCCAGG 1266
 |||||||
 DB 1021 GAAAGCTAAGCTAAGTTTAAAGAGGAGAGGCGGATGAGTGGCCAGG 1080
 |||||||

QY 1267 GCGCAGATATTAAGAGGCGCAAGCCTCAGTAGGTGAGAGAGGTGCCCAAGCAGCAG 1326
 |||||||
 DB 1081 GCGCAGATATTAAGAGGCGCAAGCCTCAGTAGGTGAGAGAGGTGCCCAAGCAGCAG 1140
 |||||||

QY 1327 ATCAGACCGAGGCGAGCTGCCACCAAAATGAGAGAGTGGAGTTCAGACGGAAC 1386
 |||||||
 DB 1141 ATCAGACCGAGGCGAGCTGCCACCAAAATGAGAGAGTGGAGTTCAGACGGAAC 1200
 |||||||

QY 1387 CGCTTCGCGCCCTGCTGCTGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGAC 1446
 |||||||
 DB 1201 CGCTTCGCGCCCTGCTGCTGCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGAC 1260
 |||||||

QY 1447 ACAGCCCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1506
 |||||||
 DB 1261 ACAGCCCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 |||||||

QY 1507 GAAGACCTACCCCAACCACTTAAACCTGTCATTCAGAGTATGAGAAATTTTCA 1566
 |||||||

Db 1321 GAAGACCTCACCACCACTTAAAGTGTATGAGTATGAGATTTGAAATTTCAAT 1380
 QY 1567 GTTGCAAAAGGAGGTTTAAAGAAACATTACGTCCATATGATGTAAAGATGTCATTTGA 1626
 Db 1381 GTTGCAAAAGGAGGTTTAAAGAAACATTACGTCCATATGATGTAAAGATGTCATTTGA 1440
 QY 1627 CAATATTTCTGTGTGTCATCTGTGACATGTTGTTAGATTTAAAGCCTTCAACACGTGT 1686
 Db 1441 CAATATTTCTGTGTGTCATCTGTGACATGTTGTTAGATTTAAAGCCTTCAACACGTGT 1500
 QY 1687 GATCAATTTCTGTGAAAAAGGCAATATCATATGATTAAGAAAGCCGAGAGAAATTTACA 1746
 Db 1501 GATCAATTTCTGTGAAAAAGGCAATATCATATGATTAAGAAAGCCGAGAGAAATTTACA 1560
 QY 1747 GCAGAACATGAGACACAGACGATCTCATGATGCTGGGCTGGGTTGCAAGTTGAAAAA 1806
 Db 1561 GCAGAACATGAGACACAGACGATCTCATGATGCTGGGCTGGGTTGCAAGTTGAAAAA 1620
 QY 1807 CAGGTACAGTCCATAGAAATCCAAAGCTGACCTGCTACTAGACATCTATCAACAGTCTCT 1866
 Db 1621 CAGGTACAGTCCATAGAAATCCAAAGCTGACCTGCTACTAGACATCTATCAACAGTCTCT 1680
 QY 1867 CGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTTCATTCAGATCCACCTTTTGAATGT 1926
 Db 1681 CGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTTCATTCAGATCCACCTTTTGAATGT 1740
 QY 1927 GAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAA 1986
 Db 1741 GAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAA 1800
 QY 1987 AACAGTGGCTGCTTATTCAGATCAATAGTCCAAATCTCTGAGAGGCTGAGATTCATT 2046
 Db 1801 AACAGTGGCTGCTTATTCAGATCAATAGTCCAAATCTCTGAGAGGCTGAGATTCATT 1860
 QY 2047 CTGACGCCCAATAGTATCAGTGGCCAGACTTCTACGGGCTTAGGCCCTACTATGCAACT 2106
 Db 1861 CTGACGCCCAATAGTATCAGTGGCCAGACTTCTACGGGCTTAGGCCCTACTATGCAACT 1920
 QY 2107 CAAGCAACACAGGTGCCAATTTAGTCAAAAGCATGGCTCAGCAGTGGCAGCCCAACAC 2166
 Db 1921 CAAGCAACACAGGTGCCAATTTAGTCAAAAGCATGGCTCAGCAGTGGCAGCCCAACAC 1980
 QY 2167 ATTGCAACCAATTAATATAGGCGACCAAGCCAGCAGCCCAACAATTTACAGATCCA 2226
 Db 1981 ATTGCAACCAATTAATATAGGCGACCAAGCCAGCAGCCCAACAATTTACAGATCCA 2040
 QY 2227 CCTCTCTCTCCACCATCAAGCATCTGCCAGCCAGAAACCTCTACCCCTTAACCTTGA 2286
 Db 2041 CCTCTCTCTCCACCATCAAGCATCTGCCAGCCAGAAACCTCTACCCCTTAACCTTGA 2100
 QY 2287 GCGTTACAGAAAGCATTTCTGACGTACCAACCTGCTTGTGCTCCAGAGAAATGTT 2346
 Db 2101 GCGTTACAGAAAGCATTTCTGACGTACCAACCTGCTTGTGCTCCAGAGAAATGTT 2160
 QY 2347 CAGGTTGCAAGTCAATCTCACCAAGACCGTCTATGAGAAAAAGCTTTGACATGGCA 2406
 Db 2161 CAGGTTGCAAGTCAATCTCACCAAGACCGTCTATGAGAAAAAGCTTTGACATGGCA 2220
 QY 2407 GGAGAAACCTGTGTGTCTGTCTCTCCATGATGGCGAAGGACTTGGCAAAATCTTTGCT 2466
 Db 2221 GGAGAAACCTGTGTGTCTGTCTCTCCATGATGGCGAAGGACTTGGCAAAATCTTTGCT 2280
 QY 2467 GTTGCAAAACCTGTATGAGTGCAGCCGAGAACTGATATACAACTTTCAAGGAGTGA 2526
 Db 2281 GTTGCAAAACCTGTATGAGTGCAGCCGAGAACTGATATACAACTTTCAAGGAGTGA 2340
 QY 2527 AGTGGTCCAGAGGCGCAAGATTTTACCCTCAATGAGAGGAAATCCAAATTTGTTATA 2586
 Db 2341 AGTGGTCCAGAGGCGCGCAAGATTTTACCCTCAATGAGAGGAAATCCAAATTTGTTATA 2400
 QY 2587 ACTGATGAAGAGGTGGTCCCGAAGAGACACACTTTGATGGCGGACCGGAG 2646
 Db 2400 ACTGATGAAGAGGTGGTCCCGAAGAGACACACTTTGATGGCGGACCGGAG 2646

Db 2401 ACTGATGAAGAGGTGGTCCCGAAGAGACAGACACACTTTTGAATGGCGGACCGAG 2460
 QY 2647 CCTGCCAGGAAAGCTGCTTTGTCATCAGACTCTCTAAGAACTGAGATCAGATCATCT 2706
 Db 2461 CCTGCCAGGAAAGCTGCTTTGTCATCAGACTCTCTAAGAACTGAGATCAGATCATCT 2520
 QY 2707 CAGACATTTTGAAGGACAGAGAAATACAGATGCCCTCAGCTTGCCTCATGTCAAACTG 2766
 Db 2521 CAGACATTTTGAAGGACAGAGAAATACAGATGCCCTCAGCTTGCCTCATGTCAAACTG 2580
 QY 2767 AAATTA 2772
 Db 2581 AAATTA 2586
 RESULT 10
 AF263836
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3108)
 Kniazeva, M. and Han, M.
 A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders
 Unpublished
 2 (bases 1 to 3108)
 Kniazeva, M. and Han, M.
 Direct Submission
 Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA
 location/Qualifiers
 1. 3108
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /sex="male"
 /tissue_type="Brain"
 /dev_stage="9-11 weeks"
 <1. 3108
 /gene="Kcnq5"
 <1. 2638
 /gene="Kcnq5"
 /note="similar to the Homo sapiens voltage-gated potassium
 channel KCNQ5; member of the KCNQ family"
 /codon_start=2
 /product="voltage-gated potassium channel KCNQ5"
 /protein_18="AAF73447.1"
 /db_xref="GI:813299"
 /translation="GDDLLLTTRAALGGGGGRLRESRKGQANSLKGLSTYS
 SOSCRNMYKRVONYLVLEPRGMGFVYAFVLLVFGCLILSFVTPHTKLA
 SSCILIEFVWIVGELFIRIMAGCCCRKMGGRIRFRKPCVLDITVLSI
 AVASAKQNEFATSAISRLRIOLIRMRDRGCTGLLSVYAHSEKLTNTI
 GFYLISSPLVLYEKANKREFSTYBALNMGTITLTITGDKTPLTWGLSLAG
 FALGISFFALXAGISGFEALKVOEHQKHFEKRRNPAANLIDCVMSYVADERSY
 SIATWPKHLAKLHFCSPKRBQGEASSQKLSFKRVRMASSPQGISKRSASVGR
 SPSTDIAGSGPTVOKSMFNDRTFRPSLKLSSQPEVIDADALIDIVYDKG
 COCVSEVDELTPLEKTVIRAIRIMKEFHAKRFEKRLRPDYKDVTEOYSAHGLDMC
 RIKSLQIRVDDIILKGQWTSRKSSREKLTAEHEETDDPSMLARVYVEQVDSIEKL
 DCLIDIQVILKRSASALTLASROIPEPEECQTDYOSPVSKIDLSGSAAQNGCLTR
 SASANISRGLOFILTPENEQAOTFALSPHMSQATQVPMSONDGSVYATNNIAQI
 SAAPKPAAPPTLIQIPPLSAIKHLRPEPLSNPGLQESIDVTICLVASKESTYFA
 QSNLTIDRSILRSKSFDMGEGELLVAPVMPKIDGLKLSYONLIRSTELMLQFSGSSS
 GRSQSDQFVPMKRSKLEITDEYGAETEDTDPGTPPPAGEAFAFSSDSLTRGRSS
 SONICKRGDSIDSLSPHKLN"
 BASE COUNT 830 a 779 c 748 g 743 t 8 others
 ORIGIN

Query Match 77.9%; Score 2159, 8; DB 10; Length 3108;
 Best Local Similarity 89.18; Pred No. 0;
 Matches 2351; Conservative 0; Mismatches 260; Indels 27; Gaps 1;

162 GGGGAGAGGCGCTGCTACTGCTGGGACCCGGCGGCAACGCTGGTGGCGGCGGCTGG 221
 1. GGGGAGAGGCGCTGCTACTGCTGGGACCCGGCGGCGGCTGGGAGAGGCGGCGG 60
 222 CCGAGAGAGAGCGCGCGGCGGCAACGAGGGGCGCGGATGAGCTGCTGGGAGCGCT 281
 61 CTTGAGAGAGAGCGCGCGGCGGCAACGAGGGGCGCGGATGAGCTGCTGGGAGAGCGCT 120
 282 CTTTACAGAGAGAGCGGAGCTGCGGCGGCAACGAGCTGCGGCGGCGGATGAGCTGCTGG 341
 121 CTTCTACAGAGAGAGCGGAGCTGCGGCGGCAACGAGCTGCGGCGGCGGATGAGCTGCTGG 180
 342 CTTTACAGAGAGAGCGGAGAGAGCGGCGGCGGCGGCTGCTACCTACCGAGCTTCTGTTT 401
 181 TCTGTACAGAGAGAGCGGAGAGAGCGGCGGCGGCGGCTGCTACCTACCGAGCTTCTGTTT 240
 402 TCT 461
 241 TCT 300
 462 ATTGAG 521
 301 ATTGAG 360
 522 GTTCATCATTCGAG 581
 361 GTTCATCATTCGAG 420
 582 ACTGAG 641
 421 ACTGAG 480
 642 AGCAG 701
 481 AGCAG 540
 702 CCGTTCATTCGAG 761
 541 CCGTTCATTCGAG 600
 762 ACTGAG 821
 601 GCTGAG 660
 822 TTTGAG 881
 661 TTTGAG 720
 882 GTTTCATTCGAG 941
 721 GTTTCATTCGAG 780
 942 TGGAG 1001
 781 TGGAG 840
 1002 TGGAG 1061
 841 TGGAG 900
 1062 ACAAG 1121
 901 ACAAG 960
 1122 TCAAG 1181
 961 CCAAG 1020

1182 GCCACACTGAG 1220
 1021 GCCACACTGAG 1080
 1221 -----TCAG 1274
 1081 AAGCAG 1140
 1275 TATTAG 1334
 1141 CATTAG 1200
 1335 CGAG 1394
 1201 CGAG 1260
 1395 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
 1261 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 1455 TGGCAG 1514
 1321 TGGCAG 1380
 1515 CACCCACAG 1574
 1381 CACCCACAG 1440
 1575 ACGAG 1634
 1441 GCGAG 1500
 1635 TGTGAG 1694
 1501 TGTGAG 1560
 1695 TCTTGAAG 1754
 1561 TCTTGAAG 1620
 1755 TGAAG 1814
 1621 CGAG 1680
 1815 GTCCATGAG 1874
 1681 GTCCATGAG 1740
 1875 CTGAG 1934
 1741 CTGAG 1800
 1935 ATGAG 1994
 1801 CTGAG 1860
 1995 CTGAG 2054
 1861 CTGAG 1920
 2055 AAATGAG 2114
 1921 AAATGAG 1980
 2115 AAATGAG 2174
 1981 AAATGAG 2040
 2175 CCAATGAG 2234
 2041 CCAATGAG 2100
 2235 CCAATGAG 2294

Db	2101	CTGGGGCATCAAGACACTTGTCCAGGCCAGAACTCTGCTCTCAAAOCCCAACGGCTTACA	2160
QY	2295	GGAAGACATTTCTGACGTCACCACTGCTTGTGCTCCAGGAAAATGTCAGGTTGC	2354
Db	2161	AGAGAGATATTTCTATGTCACCACTGCTTGTGCTCCAAAGAAAGTGTTCAGTTTGC	2220
QY	2355	ACAGTCAAAATCTCAACAGGACCCGTTCTATGAGGAAAACGTTGACATGGGAGAGAAAC	2414
Db	2221	ACAGTCAAACTGACCAAGAACCGTTCCCTGAGGAAAAGTTTGACATGGGAGAGAAAC	2280
QY	2415	TCTGTGTCGTCTGTCTGTCCCATGTCGCCAGAGACTTGGGCAAAATCTTGTCTGTGCAAAA	2474
Db	2281	TCTGTGTCGTCTGTCTGTCCCATGTCGCCAGAGACTTGGGCAAAATCTTGTCTGTGCAAAA	2340
QY	2475	CCGTATAGGTCGACCCGAGAACCTAATATACACTTTTACGAGAGTGTCAAGTGCCTC	2534
Db	2341	CCGTATAGGTCGACAGAAACCTGAACTTACAGTTTTCAGGACGAGGAGTCAAGGCGCTC	2400
QY	2535	CAGAGCAGCACAATATTTTACCCTCAAAATGGAGGGAATCCAAATGTTTATCTGATGA	2594
Db	2401	TCCAGAGCAGTCACAGATTTTATTCCTCAAGTGGAGAGATCAAAATGTTTATTAATCTGATGA	2460
QY	2595	AGAGGTGGTGTCCGAGAGACAGACACTTTTGAATGGCCGACCCGACGCTGTGGCAG	2654
Db	2461	GGAGGTGGTGTCCGAGAGACAGAAACAGATATCTTTGACGGGACCCCAACGCGCTGTGGCAG	2520
QY	2655	GGAAGCTGCTTTGTCATCAGACTCTCTAAGCACTGGAGGTCCAGATCATCTCAGACAT	2714
Db	2521	GGAGGTGCTTTTTCATCAGACTCTCTAAGCACTGGAGGTCCAGATCATCTCAGACAT	2580
QY	2715	TTTCTAAGGCGAGAGAAAGTACAGATGCCCTGCGTTCCTCATGTCAAACTGAAATTA	2772
Db	2581	TTTCTAAGGCGAGAGACAGATGACAGACGCCCTCAGTTTGCCTCAGCTCAAACTGAACTTA	2638
RESULT 11			
LOCUS	HSAA272519	1691 bp	DNA
DEFINITION	Homo sapiens partial KCNQ5 gene, exon 14.	linear	PRI 21-FEB-2002
ACCESSION	AJ272519		
VERSION	AJ272519.1	GI:18873690	
KEYWORDS	KCNQ5 gene; KCNQ5 protein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and Steinlein, O.K.		
TITLE	The new voltage gated potassium channel KCNQ5 and early infantile convulsions		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1691)		
AUTHORS	Steinlein, O.K.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-FEB-2000) Steinlein O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY		
FEATURES	location/Qualifiers		
source	1. 1691		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="6"		
	/map="6q14"		
gene	286..1248		
	/gene="KCNQ5"		
exon	286..1248		
	/gene="KCNQ5"		
	/number=14		
BASE COUNT	508 a 397 c 337 g 448 t		1 others
ORIGIN	/usedln-AJ272506:KCNQ5.cds		

Query Match	34.8%	Score 965	DB 9	Length 1691	
Best Local Similarity	100.0%	Pred. No. 3	4e-198		
Matches 965	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1808	AGGTACAGTCCATGAAATCCAAAGTGGAGTGGCTGCTACTAGACATCTATCAACAGGTCCTTC	1867		
Db	284	AGGTACAGTCCATGAAATCCAAAGTGGAGTGGCTGCTACTAGACATCTATCAACAGGTCCTTC	343		
QY	1868	GGAAGAGCTCTGCTCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTG	1927		
Db	344	GGAAGAGCTCTGCTCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTG	403		
QY	1928	AACGACATCTGACATCATCAAAACCCCTGTTGGATAGCAAAAGATCTTTGGGTTCCGCACAAA	1987		
Db	404	AACGACATCTGACATCATCAAAACCCCTGTTGGATAGCAAAAGATCTTTGGGTTCCGCACAAA	463		
QY	1988	ACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAAACATCTTCGAGAGGCCCTCAGTTCAATTC	2047		
Db	464	ACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAAACATCTTCGAGAGGCCCTCAGTTCAATTC	523		
QY	2048	TGAGGCCAAATGAGTTCAGTGGCCAGACTTTTCTAGCGGCTTACGCCCTACTATGACAGTTC	2107		
Db	524	TGAGGCCAAATGAGTTCAGTGGCCAGACTTTTCTAGCGGCTTACGCCCTACTATGACAGTTC	583		
QY	2108	AAGCACACAGTGGCCAAATTTAGTCAAGGGATGGCTCAGCAGTGGCAGCCACCAACACA	2167		
Db	584	AAGCACACAGTGGCCAAATTTAGTCAAGGGATGGCTCAGCAGTGGCAGCCACCAACACA	643		
QY	2168	TTGCAAAACCAATTAATATCGGCACCCCAAGCCAGCAGCCCAACACTTTACAGATCCAC	2227		
Db	644	TTGCAAAACCAATTAATATCGGCACCCCAAGCCAGCAGCCCAACACTTTACAGATCCAC	703		
QY	2228	CTGCTCTCCAGCCATCAAGGATCTGCCAGGCGAGAAATCTGCACCCCTAACCCCTGACG	2287		
Db	704	CTGCTCTCCAGCCATCAAGGATCTGCCAGGCGAGAAATCTGCACCCCTAACCCCTGACG	763		
QY	2288	GCTTTACAGAAAGCATTTCTGACGTCAACCTGCTGCTTGGCTCCCAAGAAATGTC	2347		
Db	764	GCTTTACAGAAAGCATTTCTGACGTCAACCTGCTGCTTGGCTCCCAAGAAATGTC	823		
QY	2348	AGGTGCACAGTCAAAATCTCACCAAGAACCCCTTATGAGAAACCTTTGACATGGGAG	2407		
Db	824	AGGTGCACAGTCAAAATCTCACCAAGAACCCCTTATGAGAAACCTTTGACATGGGAG	883		
QY	2408	GAGAAACTCTGTTGCTCTGCTGCCAGTGGTCCGAGAGACTTGGCCAAATCTTGTCTG	2467		
Db	884	GAGAAACTCTGTTGCTCTGCTGCCAGTGGTCCGAGAGACTTGGCCAAATCTTGTCTG	943		
QY	2468	TGCAAAAACCTGATCAGGTCCGACCCGAGAACTGAAATATACACTTTTAGGGATGAGTCAA	2527		
Db	944	TGCAAAAACCTGATCAGGTCCGACCCGAGAACTGAAATATACACTTTTAGGGATGAGTCAA	1003		
QY	2528	GTTGGTCCAGAGGCGCAAGCATTTTTCACCAATTTGGGGGAATCCAAATTTTATTA	2587		
Db	1004	GTTGGTCCAGAGGCGCAAGCATTTTTCACCAATTTGGGGGAATCCAAATTTTATTA	1063		
QY	2588	CTGATGAAAGAGTGGGTCCGAGAGACAGACACTTTTGAATGCCGACCCGAGC	2647		
Db	1064	CTGATGAAAGAGTGGGTCCGAGAGACAGACACTTTTGAATGCCGACCCGAGC	1123		
QY	2648	CTGGCCAGGGAGGCTCTTTCATCAAGCTCTTAAAGACTGGAAGGTACAGTCAATCTC	2707		
Db	1124	CTGGCCAGGGAGGCTCTTTCATCAAGCTCTTAAAGACTGGAAGGTACAGTCAATCTC	1183		
QY	2708	AGAGCAATTTGTAAGGACGAGAAAGTACAGATGGCCCTCAGCTTGCTCATGTCAAACTGA	2767		
Db	1184	AGAGCAATTTGTAAGGACGAGAAAGTACAGATGGCCCTCAGCTTGCTCATGTCAAACTGA	1243		
QY	2768	AATTA 2772			
Db	1244	AATTA 1248			

RESULT 12
AL365232
LOCUS
DEFINITION
AL365232
ACCESSION
AL365232
VERSION
AL365232.24
KEYWORDS
GI:13234949
SOURCE
HTG.
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 120846)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Mar 5, 2001 this sequence version replaced g1:13160293.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/chr6
Rpl1-257K9 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
Rpl1-257K9 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone Rpl1-257K9 is at 1 in this sequence. The
true left end of clone Rpl1-319022 is at 120747 in this sequence.
The true right end of clone Rpl1-380K3 is at 18652 in this
sequence.

FEATURES
source
1. Location/Qualifiers
1. .120846
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="Rpl1-257K9"
/clone_lib="RPCI-11.1"
2592. .2964
/note="MLTIB repeat: matches 4. .390 of consensus"
4469. .4695
/note="MIR repeat: matches 28. .261 of consensus"
7930. .8258
/note="MIR repeat: matches 1. .365 of consensus"
8713. .9200
/note="MLTIF repeat: matches 1. .568 of consensus"
9523. .9826
/note="Alusg repeat: matches 1. .304 of consensus"
11484. .11893
/note="MIR repeat: matches 72. .536 of consensus"
12067. .12277
/note="MIR repeat: matches 8. .245 of consensus"

repeat_region 12626. .12979
/note="THEIC repeat: matches 1. .371 of consensus"
repeat_region 13234. .13542
/note="Alub repeat: matches 3. .309 of consensus"
repeat_region 13931. .14179
/note="MIR repeat: matches 21. .262 of consensus"
repeat_region 14522. .14579
/note="L2 repeat: matches 2655. .2710 of consensus"
repeat_region 16405. .16696
/note="Alusg repeat: matches 1. .295 of consensus"
repeat_region 16697. .16722
/note="L3 copies 2 mer ga 92% conserved"
repeat_region 16801. .17320
/note="L1 repeat: matches 5188. .5745 of consensus"
repeat_region 17437. .17496
/note="L1 repeat: matches 5751. .5810 of consensus"
repeat_region 17506. .17660
/note="L1 repeat: matches 5753. .5906 of consensus"
repeat_region 17738. .18052
/note="L1 repeat: matches 5908. .6223 of consensus"
repeat_region 18473. .18730
/note="L1 repeat: matches 890. .1179 of consensus"
repeat_region 18829. .19080
/note="L1 repeat: matches 797. .1052 of consensus"
repeat_region 19213. .19412
/note="L1 repeat: matches 161. .360 of consensus"
repeat_region 19507. .19632
/note="L1 repeat: matches 2. .133 of consensus"
repeat_region 21835. .21924
/note="L2 repeat: matches 2542. .2634 of consensus"
repeat_region 23241. .23537
/note="Alus repeat: matches 1. .308 of consensus"
repeat_region 24751. .25402
/note="Cpg Island"
misc_feature /evidence="not_experimental"
25146. .25454
/note="Alus repeat: matches 1. .312 of consensus"
repeat_region 25963. .26384
/note="L1 repeat: matches 5719. .6156 of consensus"
repeat_region 26891. .27204
/note="Alu repeat: matches 1. .311 of consensus"
repeat_region 27647. .27824
/note="MERSB repeat: matches 1. .178 of consensus"
repeat_region 27854. .28504
/note="L1 repeat: matches 5646. .6295 of consensus"
repeat_region 28796. .29115
/note="Alus repeat: matches 1. .310 of consensus"
repeat_region 29598. .29996
/note="MERSB repeat: matches 2. .404 of consensus"
repeat_region 29997. .30290
/note="Alu repeat: matches 1. .288 of consensus"
repeat_region 30291. .30303
/note="MERSB repeat: matches 404. .415 of consensus"
repeat_region 30340. .30353
/note="MERSB repeat: matches 384. .396 of consensus"
repeat_region 30354. .30668
/note="Alus repeat: matches 1. .312 of consensus"
repeat_region 30669. .31120
/note="MERSB repeat: matches 396. .861 of consensus"
repeat_region 31872. .32173
/note="Alu repeat: matches 1. .294 of consensus"
repeat_region 32560. .32851
/note="Alus repeat: matches 9. .311 of consensus"
repeat_region 32905. .33039
/note="MIR repeat: matches 31. .159 of consensus"
repeat_region 33040. .33441
/note="Alu repeat: matches 1. .298 of consensus"
repeat_region 33342. .33369
/note="MIR repeat: matches 159. .187 of consensus"
repeat_region 33488. .33929
/note="MIR repeat: matches 1. .466 of consensus"
repeat_region 34294. .34511
/note="MIR repeat: matches 20. .226 of consensus"

repeat_region 34539..34893
/note="MT1A1 repeat: matches 1..365 of consensus"
repeat_region 35310..35611
/note="Alusx repeat: matches 1..293 of consensus"
repeat_region 37310..37357
/note="8 copies 6 mer cacaca 93% conserved"
repeat_region 37456..37487
/note="16 copies 2 mer aa 87% conserved"
repeat_region 37541..37849
/note="Alusx repeat: matches 1..309 of consensus"
repeat_region 38162..38286
/note="MER9 repeat: matches 1..128 of consensus"
repeat_region 38394..38608
/note="MER3 repeat: matches 1..209 of consensus"
repeat_region 39165..39277
/note="Alus4/x repeat: matches 196..308 of consensus"
repeat_region 40557..40691
/note="FLAM_C repeat: matches 1..132 of consensus"
repeat_region 41582..41761
/note="MIR repeat: matches 81..262 of consensus"
repeat_region 42045..42340
/note="Alusp repeat: matches 1..295 of consensus"
repeat_region 42559..43025
/note="L2 repeat: matches 2359..2707 of consensus"
repeat_region 43026..43412
/note="WSTA repeat: matches 1..426 of consensus"
repeat_region 43413..44100
/note="L2 repeat: matches 1311..2359 of consensus"
repeat_region 45195..45326
/note="FLAM_C repeat: matches 1..133 of consensus"
repeat_region 46031..46446
/note="WSTC repeat: matches 1..405 of consensus"
repeat_region 46634..46899
/note="L2 repeat: matches 2463..2710 of consensus"
repeat_region 47119..47215
/note="L2 repeat: matches 2687..2750 of consensus"
repeat_region 47523..47688
/note="MER5B repeat: matches 1..178 of consensus"
repeat_region 48486..48532
/note="L2 repeat: matches 2701..2747 of consensus"
repeat_region 48636..48789
/note="MIR repeat: matches 15..175 of consensus"
repeat_region 49033..49260
/note="MER5A repeat: matches 1..224 of consensus"
repeat_region 50163..50239
/note="MIR repeat: matches 73..150 of consensus"
repeat_region 50321..50438
/note="L2 repeat: matches 2584..2702 of consensus"
repeat_region 51415..51791
/note="L2 repeat: matches 2289..2710 of consensus"
repeat_region 51865..52076
/note="L2 repeat: matches 2465..2679 of consensus"
repeat_region 52079..52370
/note="Aluud repeat: matches 1..289 of consensus"
repeat_region 52410..52691
/note="L2 repeat: matches 2130..2411 of consensus"

Query Match 34.8%; Score 965; DB 9; Length 120846;
Best Local Similarity 100.0%; Pred. No. 6.9e-198;

Matches 965; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 AGGTACAGTTCATAGATCCAGCTGGAGCTGCTACTGACATCTATCAACAGGCTCTTC 1867
DB 61339 AGGTACAGTTCATAGATCCAGCTGGAGCTGCTACTGACATCTATCAACAGGCTCTTC 61398
QY 1868 GAAAGGCTTCGCTCAGCCCTCGCTTGGCTCTTCATCCAGATCCCACTTTGATGTG 1927
DB 61399 GAAAGGCTTCGCTCAGCCCTCGCTTGGCTCTTCATCCAGATCCCACTTTGATGTG 61458
QY 1928 AACAGACATCTGATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGACAAA 1987
DB 61459 AACAGACATCTGATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGACAAA 61518

QY 1988 ACAGTGGCTGCTTATTCAGATCAACTAGTGGCAACATCTCGAGAGCCGTCAGTTCAATTC 2047
DB 61519 ACAGTGGCTGCTTATTCAGATCAACTAGTGGCAACATCTCGAGAGCCGTCAGTTCAATTC 61578
QY 2048 TGAGGCCCAATVGATTCAGTGGCCAGACTTTCACGGCTTAGGCTTACTATGACAGAGTC 2107
DB 61579 TGAGGCCCAATVGATTCAGTGGCCAGACTTTCACGGCTTAGGCTTACTATGACAGAGTC 61638
QY 2108 AACCAACACAGTGGCCCAATTAGTCAAGCGATGGCTGACGATGGCCAGCCCAACACCA 2167
DB 61639 AACCAACACAGTGGCCCAATTAGTCAAGCGATGGCTGACGATGGCCAGCCCAACACCA 61698
QY 2168 TTGCAAAACCAATAAATATGAGGACCCAGAGCCAGAGCCCAACACTTACAGATCCCAAC 2227
DB 61699 TTGCAAAACCAATAAATATGAGGACCCAGAGCCAGAGCCCAACACTTACAGATCCCAAC 61758
QY 2228 CTCCTCTCCAGCCATCAACATCTGCCCAGGCGAAGAACTCTGACCCCTAACCCCTGAG 2287
DB 61759 CTCCTCTCCAGCCATCAACATCTGCCCAGGCGAAGAACTCTGACCCCTAACCCCTGAG 61818
QY 2288 GCTTACAGAAAGCATTTTGCAGGTCAACCACTGCTGTTGCTCCAGAGAAATGTTTC 2347
DB 61819 GCTTACAGAAAGCATTTTGCAGGTCAACCACTGCTGTTGCTCCAGAGAAATGTTTC 61878
QY 2348 AGTTGCACAGTCAATATCTCACCAGAGACCGTTCTATGAGGAAAAAGTTGACATGGAG 2407
DB 61879 AGTTGCACAGTCAATATCTCACCAGAGACCGTTCTATGAGGAAAAAGTTGACATGGAG 61938
QY 2408 GAGAAACTG 2467
DB 61939 GAGAAACTG 61998
QY 2468 TGCAAAACCTGATCAGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2527
DB 61999 TGCAAAACCTGATCAGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 62058
QY 2528 GTGGCTCCAGAGGACCAAGATTTTACCCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 2587
DB 62059 GTGGCTCCAGAGGACCAAGATTTTACCCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 62118
QY 2588 CTGATGAGAGAGTGGTCCCGAAGAGACAGACAGACACTTTTGATGCGCGACGAGC 2647
DB 62119 CTGATGAGAGAGTGGTCCCGAAGAGACAGACAGACACTTTTGATGCGCGACGAGC 62178
QY 2648 CTGCCAGGAGACTGCTTGTGATCAGACTCTGTAAGGAGCTGGAAGGTCAGATCATCTTC 2707
DB 62179 CTGCCAGGAGACTGCTTGTGATCAGACTCTGTAAGGAGCTGGAAGGTCAGATCATCTTC 62238
QY 2708 AGAGCATTTGTAAAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 2767
DB 62239 AGAGCATTTGTAAAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 62298
QY 2768 AATAA 2772
DB 62299 AATAA 62303

RESULT 13
AC115920/c 162123 bp DNA linear HTG 21-JUN-2002
LOCUS Mus musculus clone RP24-496H1, WORKING DRAFT SEQUENCE, 9 ordered
DEFINITION pieces.
ACCESSION AC115920
VERSION AC115920.3 GI:21536151
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-496H1
JOURNAL Unpublished


```

Db 136143 AACAGCGGCTGTTTAAAGAGGTGACAGCAGTGGCAACATCTCAAGAGAGCCGACATTCATC 136084
QY 2047 CTGACGCCAATGAGTATGAGTCCAGACATCTTCTACGCCGCTTACGCCCTACTATGACAGT 2106
Db 136083 CTACACACCAAGAGTATGAGTCCAGACATCTTCTACGCCGCTTACGCCCTACTATGACAGT 136024
QY 2107 CAGCAACACAGAGTCCCAATGATGATCAAGAGGCTGACAGTGGAGGAGCAGCAGCAGC 2166
Db 136023 CAGACTACCCAGAGTACCATGATGATCAAGAGGCTGCTCCGCTGCTGAGCAGCAGCAGTAC 135964
QY 2167 ATTGCAACCAATTAATTAATAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2226
Db 135963 ATTGCAACCAATTAATTAATAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 135904
QY 2227 CCTGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2286
Db 135903 CCTGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 135844
QY 2287 GGCCTTACAGAAAGCAGTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2346
Db 135843 GGCCTTACAGAAAGCAGTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135784
QY 2347 CAGTTTGCACAGTCAATCTCAACAGACCTGCTTATGAGAGAAAGCTTTGACATGGA 2406
Db 135783 CAGTTTGCACAGTCAATCTCAACAGACCTGCTTATGAGAGAAAGCTTTGACATGGA 135724
QY 2407 GGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2466
Db 135723 GGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135664
QY 2467 GTGCAAAACCTGATGAGTGCAGCAGGAACTGAATATACAACTTTCAGGAGTGAATCA 2526
Db 135663 GTGCAAAACCTGATGAGTGCAGCAGGAACTGAATATACAACTTTCAGGAGTGAATCA 135604
QY 2527 AGTGGCTCCAGAGGAGCAGCAGATTTTATACCCCAATGAGAGAAATCCAAATGTTTATA 2586
Db 135603 AGTGGCTCCAGAGGAGCAGCAGATTTTATACCCCAATGAGAGAAATCCAAATGTTTATA 135544
QY 2587 ACTGATGAGAGAGTGGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2646
Db 135543 ACTGATGAGAGAGTGGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135484
QY 2647 CTTGCCAGGAGAGTCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2706
Db 135483 CTTGCCAGGAGAGTCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 135424
QY 2707 CAGAGCAATTTGTAAGGAGGAGAAAGTACAGATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2766
Db 135423 CAGAGCAATTTGTAAGGAGGAGAAAGTACAGATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135364
QY 2767 AAATTA 2772
Db 135363 AACTAA 135358

```

```

RESULT 14
AC095904/c 179192 bp DNA linear HTG 10-JUL-2002
LOCUS Rattus norvegicus clone CH230-10L20, *** SEQUENCING IN PROGRESS
DEFINITION *** 57 unordered pieces.
AC095904
VERSION AC095904.4 GI:21722989
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 179192)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshbrook,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barberia,J., Benton,J., Bimberg,K., Blankenburg,K., Bonnin,D.,

```

```

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,X., Dint,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earmhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,D., Huylb,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kover,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Matindale,A., Martinez,E.,
Massey,E., Maxwell,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oqub,M., Okunolu,G.,
Oragunye,N., Oyedro,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Qulles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojudoan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umanli,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 179192)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 179192)
Worley,K.C.
Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17943539.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVD
Center clone name: CH230-10L20
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 128957 bases at least Q40
Consensus quality: 135269 bases at least Q30
Consensus quality: 140867 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is

```


Db	176948	CTCTCTCTCTCAACCATCAAGCATCTATCCAGGCCGGAACCCCTCTCTCCAAACCCCT	176888
QY	2287	GGCTTACAGGAAGCATTTCTGACGTCACCACCTGCTTTGTTCCTCCAGGAAAAATGTT	2346
Db	176888	GGCGTACACGAGATATTTCTGACGTCACCAACCTGCTTTGTTCCTCCAAAGAAACGTT	176829
QY	2347	CAGGTTGACAGTCAAAATCTCACCAAGGACCGTTCTATGAGGAAAG-CTTGACATGGG	2405
Db	176828	CAGTTCCGCCAGTCAAAACCTGACCAAGACCGCTTCCCTGAGGAAAAATTTTGACATGGG	176765
QY	2406	AGAGAAAACCTGTTGTCTGTCTGTCTGCCATGTGTCGCAAGGACTTGGGCAATCTTTGTC	2465
Db	176768	AGGGGAAAACCTGTGTGTCTGCCCTCGCCCATGTGTGCCAAGGACTTGGGCAATCTCTGTC	176709
QY	2466	TGTGCAAAACCGATCAGGTCGACCGCAGAACCTGATATACACTTTTACGGAGTGAATC	2525
Db	176708	TGTACAAAACCGATCAGTATCGACAGAGAACTGAATTTACAGTTTTCGGGCAAGTGAATC	176649
QY	2526	AAATGCTCCAGAGGACGACCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTAT	2585
Db	176648	AAATGCTCTGAGGACGACCAAGATTTTAAACCCCAATGAGGGAATCCAAATTTGTTAT	176589
QY	2586	AACGATATGAAGAGTGGTCCCGAGAGACAGACACACTTTTGATGCGCACCGCA	2645
Db	176588	AACGATATGAAGAGTGGTCCCGAGAGACAGAAACGATCTTTTGACGCGCACCCAC	176529
QY	2646	GCTCGCCAGGAAAGTGCCTTTGATCAGACTCTCTTAAGGACTGGAAGCTCAGATATC	2705
Db	176528	GCTCGCCAGGAAAGTGCCTTTGATCAGACTCTCTTAAGGACTGGAAGCTCAGATATC	176469
QY	2706	TCAGAGCATTTGTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACT	2765
Db	176468	TCAGAAACATTTGTGAAGCAGGAGACAGTACGATGCCCTCAGTTGCTCATGTCAAACT	176409
QY	2766	GAATAA 2772	
Db	176408	GAACATA 176402	
RESULT 15			
AX318576			
LOCUS	AX318576	548 bp	DNA
DEFINITION	Sequence 81 from Patent WO01771155.	linear	PAT 06-JUL-2002
ACCESSION	AX318576		
VERSION	AX318576.2	GI:21713342	
KEYWORDS			
SOURCE	human.		
ORGANISM	homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	Fernandes, E., Vernet, C. A., Mishnu, V. S., Leach, M. D., Shinkets, R. A.,		
JOURNAL	zerhusen, B. D. and Kekuda, R.		
COMMENT	Orfx polynucleotides and polypeptides		
FEATURES	Patent: WO 01771155-A 81 18-Oct-2001;		
	Curagen Corporation (US)		
	On Jul 8, 2002 this sequence version replaced gi:17900990.		
	location/Qualifiers		
	1. 548		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	83 a 152 c 194 g 119 t		
ORIGIN			
Query Match	18.0%;	Score 498.6;	DB 6;
Best Local Similarity	97.2%;	Pred. No. 2.6e-97;	Length 548;
Matches	518;	Conservative 0;	Mismatches 14;
			Indels 1;
			Gaps 1;
QY	74	CGCGCGCGCGCGCGCGCGCTTGGGACACGCGATGAAGATGTGAGATCGCGCGCGGCA	133
Db	12	CGCGCGCGCGCGCGCGCGCTTGGGACACGCGATGAAGATGTGAGATCGCGCGCGGCA	71

QY	134	GGGTGCTGCTGCACTCGGACGCGCCAGGGGGACACGGCCCTGCTACGTGCTGGGACCGGG	193		
Db	72	GGGTGCTGCTGCAACTCGGACGCC - CCAGGGGGACACGGCCCTGCTACTGCTGGACCGGG	130		
QY	194	CGGCCACGCTCGGTGCGCGCGGGGTCGTCGAGGAGAGCCGCGGGGCAACAGAGGGG	253		
Db	131	CGGCCACGCTCGGTGCGCGCGGGTGGCCCTGAGGAGAGCCGCGGGGCAACAGAGGGG	190		
QY	254	CCCGGATGAGCCGTGCGGGGAACCGCCCTCTTACACGAGTACCGAGCTGCGCGCGCA	313		
Db	191	CCCGGATGAGCCCTGCTGGGGAAACCGCTCTCTTACACGAGTACCGAGCTGCGCGCGCA	250		
QY	314	ACGTCAAGTACCGCGCGGTGACAGAACTACCTGTACACAGTGTGAGAGACCCCGCGCT	373		
Db	251	ACGTCAAGTACCGCGCGGTGACAGAACTACCTGTACACAGTGTGAGAGACCCCGCGCT	310		
QY	374	GGGCGCTTACATACCAACGCTTCGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG	433		
Db	311	GGGCGCTTACATACCAACGCTTCGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG	370		
QY	434	TGTTTCTTCCATCCCTGAGACACACAAATTTGGCCCTCAAGTTGGCCCTTGATCCGTGAGT	493		
Db	371	TGTTTCTTCCATCCCTGAGACACACAAATTTGGCCCTCAAGTTGGCCCTTGATCCGTGAGT	430		
QY	494	TGCTATGATTTGTCGTTTGGTTTGGAGTTATCATTCGAAATCTGCTGCGGGTTGCT	553		
Db	431	TGCTATGATTTGTCGTTTGGTTTGGAGTTATCATTCGAAATTTGCTGCGGGTTGCT	490		
QY	554	GTTTGTGAAATGAGAGATGGCAAGCAAGACTGAGTTTCTCGAAAGCCCTTC	606		
Db	491	GTTTGTGAAATGAGAGATGGCAAGCAAGACTGAGTTTCTCGAAAGCCCTTC	543		
RESULT 16					
AX18764		548 bp	DNA	linear	PAT 14-DEC-2001
LOCUS	AX18764				
DEFINITION	Sequence 269 from Patent WO0177155.				
ACCESSION	AX18764				
VERSION	AX18764.1				
KEYWORDS	GI:17901084				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1. Fernandes, E., Vernet, C.A., Mishra, V.S., Leach, M.D., Shimkets, R.A., Zetser, B.D. and Kekuda, R.				
TITLE	Orix polynucleotides and polypeptides				
JOURNAL	Patent: WO 0177155-A 269 18-OCT-2001; Curagen Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..548 /organism="Homo sapiens" /db_xref="taxon:9606" /note="Expressed in Bone, Osteosarcoma, Lymphoid tissue, Lymph node-Internal ID: FLC:2498 - accnos=11755212/11755212 correct-Encodes a protein in sequence listing 270 that is 47% similar to g14758632 potassium voltage-gated channel, KQT-like subfamily, member 4"				
BASE COUNT	83 a 152 c 194 g 119 t				
ORIGIN					
Query Match	18.0%;	Score 498.6;	DB 6;	Length 548;	
Best Local Similarity	97.2%;	Pred. No.2.6e-97;			
Matches 518;	Conservative 0;	Mismatches 14;	Indels 1;	Gaps 1;	
QY	74	CGGCGCGCGCGCGGCGCGCTTGCGGCAAGCGCATGAAGATGTGAGTCGCGCGGGGCA	133		
Db	12	CGGCGCGCGCGCGGCGGCGCTTGCGGCAAGCGCATGAAGATGTGAGTCGCGCGGGGCA	71		
QY	134	GGGTGCTGCTGCAACTCGGACGCC - CCAGGGGGACACGGCCCTGCTACTGCTGGGACCGGG	193		

Db	72	GGGTGCTGTGTAACCTGCGAGGC -CCAGGGGGCGAAGGGCGTGTACTGTGTGGGCAACCCGG	130
QY	194	CGCCACGCTCGGTGGCGCGCGGTGGCTCTGAGGAGAGCCGCCGGGGCAAGCAGGGG	253
Db	131	CGGCACGCTCGGTGGCGCGCGGTGGCTCTGAGGAGAGCCGCCGGGGCAAGCAGGGG	190
QY	254	CCCGATGAGCCGTGCTGGGGGAACCGCTCTCTTACAGAGTAAAGCAGAGTGGCGGGCGA	313
Db	191	CCCGATGAGCCGTGCTGGGGGAACCGCTCTCTTACAGAGTAAAGCAGAGTGGCGGGCGA	250
QY	314	ACGTAAAGTACCGGGCGGTGACAGAACTACTCTGTAACAGTGGCTGGAGACCCCGGCT	373
Db	251	ACGTAAAGTACCGGGCGGTGACAGAACTACTCTGTAACAGTGGCTGGAGACCCCGGCT	310
QY	374	GGGCGTTCATCTACACAGCGCTTCGTTTCTCTTGTCTTGTGGTCTTGATTTGTCA	433
Db	311	GGGCGTTCATCTACACAGCGCTTCGTTTCTCTTGTCTTGTGGTCTTGATTTGTCA	370
QY	434	TGTTTCTTCAATCCCTGAGCACACAATAATGGCTCAAGTGGCTCTTGATCTGGAGT	493
Db	371	TGTTTCTTCAATCCCTGAGCACACAATAATGGCTCTTGATCTGGAGTCTGGAGT	430
QY	494	TGCTGATGATTTGTCTCTTGTGGTGGATTCATTCGAATCTGATCTGGCGGTGCT	553
Db	431	TGCTGATGATTTGTCTCTTGTGGTGGATTCATTCGAATCTGATCTGGCGGTGCT	490
QY	554	GTTTCGATATGAGAGATGGCAAGAAAGTCTGAGTTGCTCGAAGCCCTTC	606
Db	491	GTTTCGATATGAGAGATGGCAAGAAAGTCTGAGTTGCTCGAAGCCCTTC	543
RESULT 17			
LOCUS	AX032994	2335 bp	DNA linear PAT 21-SEP-2000
DEFINITION	Sequence 1 from Patent WO0044786.		
ACCESSION	AX032994		
VERSION	AX032994.1	GI:10279897	
KEYWORDS			
SOURCE			
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 2335)		
AUTHORS	Jentsch,T.J.		
TITLE	Novel potassium channels and genes encoding these potassium channels		
JOURNAL	Patent: WO 0044786-A 1 03-AUG-2000;		
	NEUROSEARCH AS (DK)		
FEATURES	Location/Qualifiers		
source	1..2335		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	83..2170		
CDS	/note="KCNQ4"		
	/codon_start=1		
	/protein_id="CAC09957.1"		
	/db_xref="GI:10279898"		
	/translation="MAEAPPRRLGPPPGDAPRAELVALTAVQSEGEAGGGSPRR		
	LGILGSLPPGAPLPGPGSGSGSAGCGSSAAHKRYRLQNNVYVNLERGRMAFYH		
	VTFLLVFSCLVLSVLSITIOHOLANCLILEPMVYVLEGLYIVRWASACCRR		
	RGQGRFRFAKRPFCVIDFVAVSAVYIAAGTQGNITRTSALRSRFLQILKMYRD		
	RGGTGWKLGSVYVAHSELITVAVYIGFLVLIFAFVLVLAERDANSVDSDLSMW		
	GTTTLTITGGDKPTHTWLGRLVLAAGFALGTSFALPGILSGFALKVQDOHROKH		
	FERRMPMAIICAMRLYIDMSRAVLTATWYVYDSILSPRELLALEFHQVORANG		
	GLRDLFVRAPVPPGAPSRYPVATCHRGSSSEFCQEGSSRMGIKDIRMSSORRTG		
	PSNOQLAPMPMPSPSEQNGEATSPYVOKSMSPNDRTPASILRLKPTSAEDAS		
	EEVAEEKSTOCELTVDDIMPAVKYIYRSIRILKELVARKKFKETLEPYVKVDIETS		
	AGHIDILGRKISLTQTRVDQIVRGGRGDKAREKGDGSDAEVDDISIMKGRVYKVK		
	QVQSIIEHKDLILGFTYRSLRSGLTASLGAOVPLFDPDITSDYHSVPVHEDISVSAQ		
	TLISRSVSTVMD"		
BASE COUNT	396 a	812 c	719 g 408 t
ORIGIN			

Query Match	17.7%	Score 492	DB 66	Length 2335	
Best Local Similarity	59.3%	Pred No. 8	Re-96		
Matches 1087	Conservative	0	Mismatches 555	Indels 192	Gaps 7
QY	322	TACCGCGGGGTGCAGAACTACCTGTACCAAGTGTCTGAGAGACCCCGGGCTTGC	381		
Db	320	TACCGCGGGCTGCAGAACTGGGCTCTCAACAGTCTGGAGCGGGCCCGCGGCTTGC	379		
QY	382	ATCTACCAAGCTTCTCTTTTCTCCCTTGCTTGGTTGGTTGGTTTGGTCAAGTCTTC	441		
Db	380	GTCTACCAAGCTTCTCAATTTTGGTGGCTTCAAGTCTGGTGGTGTGTGTCTGC	439		
QY	442	ACCATCCCTGAGACACAAATTTGGCGCTCAAGTTGGCTCTGATTCCTGAGTCTGATG	501		
Db	440	ACATCTCAGAGAGACCAAGAACTTGGCAAGATGTCTCTCATCTTGGAAATCGATG	499		
QY	502	ATTGTGCTTTGGTTTGGAGTTCAATTCATTCGATCTGGTCTCGGGTCTCTTGTCCA	561		
Db	500	ATGTGTGGTTTCCGGCTTGGAGTACATCGTCCGGGTGTGGTCCCGCGATCTCTCGCG	559		
QY	562	TATAGAGGANTGGCAAGAACACAGAGTTTGTCTCGAAAGCCCTTGTGTATAGATAC	621		
Db	560	TACCGAGATGGCAAGGTCCTTCGCTTTGCCAAGAAAGCCCTTGTGTATCGACTTC	619		
QY	622	ATTGTTCTTATCCCTTCAATAGCAGTTGTTTTCGAAAACTCAGGCTAATATTTTGC	681		
Db	620	ATGTGTTCTGTGCTCTGGTGGCGGCTGATCGCGCGGGTACCCAGGGCAATCTTCGC	679		
QY	682	ACCTGTCACTCAAGAACTCCGTTTCCATCACTCCACATCCCTCGCATGGGCTATGACGA	741		
Db	680	ACCTCGCGCTGGCGACATATGCTTCTCTCAATCTCTGGCATGTGGTCCCATGAGACGC	739		
QY	742	AGGGAGGACCTTGGAAATTTACTGGGTTCAGTGGTTTATGCTCAACAGAAATTAATC	801		
Db	740	CGGGGGCGACCTGGAAAGTGTGGGCTCAGTGGTACCGGATATCAGAGAGCTGATC	799		
QY	802	ACAGCTTGGTACATATGATTTTGGTGTCTAATTTTGGTCTTCTGTCTATCTGATG	861		
Db	800	ACGGCTGTACATCGGGTCTGGTGCTATCTTCCGCTCTCTTCTGTGTACTGTGCC	859		
QY	862	GAAGAAGATCCCAATAAAGATTTTCTACATATGACAGATGCTCTGTGGGGCACATT	921		
Db	860	GAGAAGAGCCCAACTCCGACTTCTCTCTACAGCCGACTGCTGTGGGGACGATT	919		
QY	922	ACATTTGACATATTTGGCTATGAGACAAAACTCCCTAATCTGGTGGGAAATTTGCT	981		
Db	920	ACATTTGACCAACTCGGCTATGAGACAAAGACACCGACACATGTGGGGAGGGTCTG	979		
QY	982	TCTGACAGGCTTTGGACATCTTGGCATTTCTTTCTTCCACTTCTCGCGGATCTTGGC	1041		
Db	980	GCTGCTGGCTTGGCTTACTGGGATCTCTTTCTTTGGCCCTGGCGGATCTTATGGC	1039		
QY	1042	TCAGGTTTGCATTTAAAGTACAGAAACAACCCGACAGAAACACTTTGAAAAAGAG	1101		
Db	1040	TCCGGCTTTTCCCTGGAAGTCCAGAGACAGACCGGAGAAAGCACTTCGAAACCGGAGG	1099		
QY	1102	AACCCAGCTGCAACATCATTTCACTGTGGTGGGCTGTATAGAGAGTATGAAATCT	1161		
Db	1100	ATGCGCGAGCAACCTCATCTCAAGGCTGCTGGGCGCTGTACTCCACGATATAGCGCG	1159		
QY	1162	GTTTCCATTGCAACTGGAAAGCCCACTTGAAGGCTTGCACAC-----	1205		
Db	1160	GCTTACCTGACAGCACCTGTACTACTATGACATATCCCTCCATCTTCCAGAGACTG	1219		
QY	1206	-----	1205		
Db	1220	GCCCTCTTGTTTGAGCACTGCAAGGAGGCGCCGCAATGGGGCTTACGGCCCTTGGAGGTG	1279		
QY	1206	-----	1205		
Db	1280	CGGGGGGGCGCGTACCGAGCGAGCAACCTCCCGTTAACCGCGCGTTGCACCTGCGAC	1339		
QY	1206	-----CTGCAGCCCTTACCAATCAGAAGCTAAGTTTAAAGAGGGA	1245		

Db 1340 CGCCGCGGACGACGCTCTCTCTGCGGGAAGCAGCCGCGATGGGATCATCAAGACCGC 1399
 QY 1246 GTGGCATGGTACGCCCCAGGGGCGAGAGATTT-----AGAGCCGCAAGACCTCAGTA 1299
 Db 1400 ATCCGATGGGACGCTCCAGCGCGGAGCGGCTCTCCAGAGCAGCAGCTGGCAGCTTCCA 1459
 QY 1300 GGTGACAGGAGGTCCCAAGCACCAGCATCAGACCGCAGG---GAGTCCCAAGAGTG 1356
 Db 1460 ACAATGCCCCACCTCCCAAGCAGCAGCAGAGTGGGTGAGGCGACAGGCCACCAAGAGTG 1519
 QY 1357 CAGAGAGGTGAGCTTCAACGACCAAGCCGCTTCCGCGCTGCGTCCGCTCAGAAAGT 1416
 Db 1520 CAAAGAGGTGAGCTTCAATGACCGCAGCCGCTTCCGCGCATCTCAGAGCTC----- 1573
 QY 1417 TCTCAGCCAAACAGGTAGATGATGACACAGCCCTTGGCAGTGAATGATGATGATG 1476
 Db 1574 -----AAMCCCGGACGCTCTGCTGAGAGATGCC---CTTAGAGGAAGTACAGAG 1621
 QY 1477 GAAAAAGATGCCAGTGTATGTATCAGTGAAGACCTCAGCCAGCACTTAAAGTGTG 1536
 Db 1622 GAGAAAGACTACGAGTGTAGCTCAGGAGCAGACATCATGCTGCTGTGAGACAGT 1681
 QY 1537 ATTGAGCTATCAGATTTGAATTTGAAATTTGATTTGCAATTTGCTGATGAGACATGTA 1596
 Db 1682 ATCCGCTCATCAGATTTCTCAAGTCTGTGTGGCCAAAGGAATTTCAAGAGACACTG 1741
 QY 1597 CGTCCATATGATTAAGAGTGTATGAAATTTGCTGATGATGATGATGATGATGATG 1656
 Db 1742 CGACCGTACGAGTGAAGAGCTCANTGAGCACTACTGAGCAGAGCCAGCTGGACATGCTG 1801
 QY 1657 TGTAGATTTAAAGCTTCAACAGCTGTGATCAAAATTTCTTGGAAAAAGGC---AAATC 1713
 Db 1802 GCGCGGATCAAGAGCTGTGAACCTGCGGTGAGCAAAATTTGTGGTGGGGGCGGGGAC 1861
 QY 1714 ACATCAGATGAAGAGCGGAGAGAAATAAGCAGCAAGCATGAGACCAAGACATGCTC 1773
 Db 1862 AGGAAGCGCCGAGAGAGGCGACAGAGGGGCTCTCGAGCGGAGGTGTGAGAGAAATC 1921
 QY 1774 AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1833
 Db 1922 AGCATGATGAGGAGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
 QY 1834 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1893
 Db 1982 GACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
 QY 1894 TTGGCTTATTCAGATGCCAAGCTTTGATGATGATGATGATGATGATGATGATGATGATG 1953
 Db 2036 CTGGGCGCGGTGCAAGTCCGCTGTTCAGACCCCGCATCATCCTCCGACTACACAGCCT 2095
 QY 1954 GTGATAGCAAGATCTTTGGGGTTCGCGACAA 1987
 Db 2096 GTGAGCACGAGGACATCTCCGTCCGACAGA 2129

RESULT 18
 AX456863
 LOCUS AX456863 2335 bp DNA linear PAT 06-JUL-2002
 DEFINITION Sequence 4 from Patent W00232960.
 ACCESSION AX456863
 VERSION AX456863.1 GI:21715730
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 AUTHORS Argenti, T.M. and Sheldon, J.H.
 TITLE Methods of selecting compounds for modulation of bladder function
 JOURNAL Patent: WO 0232960-A 4 25-Apr-2002;
 Wyeth (US)
 FEATURES Location/Qualifiers

source 1..2335
 /organism="Homo sapiens"
 BASE COUNT 396 a 812 c 719 g 408 t
 ORIGIN
 Query Match 17.7%; Score 492; DB 6; Length 2335;
 Best Local Similarity 59.3%; Pred. No. 8.8e-96;
 Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

QY 322 TACCGGGGGTGCAGAACTACCTGTACAGCTGTGAGAGAGACCCCGGCTGGGCTTC 381
 Db 320 TACCGGGGGTGCAGAACTACCTGTACAGCTGTGAGAGAGACCCCGGCTGGGCTTC 379
 QY 382 ATCTACAGCTTTCGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 Db 380 GTCTACAGCTTTCGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
 QY 442 ACCATCCCTGAGACACAAATTTGGCTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
 Db 440 ACTATCCAGAGACACAAATTTGGCTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
 QY 502 ATTGCTGCTTGTGTTGAGTTGATCATTTGAAATTTGCTGCTGCTGCTGCTGCTGCTGCT 561
 Db 500 ATGCTGTTTGTGTTGAGTTGATCATTTGAAATTTGCTGCTGCTGCTGCTGCTGCTGCT 559
 QY 562 TATAGAGAGTGAAGAGAACTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
 Db 560 TACGAGAGTGAAGAGAACTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
 QY 622 ATTGCTTATTCGCTTCAATAGAGTTGTTTCTCAAAATTTGCTGCTGCTGCTGCTGCTGCT 681
 Db 620 ATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
 QY 682 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
 Db 680 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
 QY 742 AGGGGAGGCACTGGAATTTAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801
 Db 740 CCGGGGAGCACTGGAATTTAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
 QY 802 ACAGCTTGTATACATAGATTTTGTGCTTATTTTGTGCTTATTTTGTGCTTATTTTGTGCT 861
 Db 800 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 QY 862 GAAAGAGTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
 Db 860 GAAAGAGTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919
 QY 922 ACATTGACAACTATTTGCTATGAGACAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
 Db 920 ACATTGACAACTATTTGCTATGAGACAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
 QY 982 TCTGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1041
 Db 980 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
 QY 1042 TCAGTTTGTGCTTAAAGTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
 Db 1040 TCAGTTTGTGCTTAAAGTGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1099
 QY 1102 AACCGAGTGCACACCTGCTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
 Db 1100 ATGCGGAGGACCAACTGCTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
 QY 1162 GTTTCATTTGCAACCTGGAAGCCACACTTGAAGGCTTGGACAC----- 1205
 Db 1160 GCTTACCTGACAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
 QY 1206 ----- 1205
 Db 1220 GCCCTCTTGTGAGCAAGTGTGCAAGCGGCGCGCAATGAGGGGCTTACGGCCCTGAGAGTG 1279

QY 1206 ----- 1205
 Db 1280 CCGCGGGGCGGGTACCGGAGACACCTCCCGTTACCGCCGCTTGCACCTGCCAC 1339
 QY 1206 -----CTGAGCGCCCTACATGCAAGAGCTAAAGTTTAAAGAGCGA 1245
 Db 1340 CCGCCGGGCGACACCTCTCTCTGCGCTGGGGAAGACCGCGGATGGGATCAAGACCGC 1399
 QY 1246 GTGCGATGAGCTTACCGCCAGGGGCGAGATTT-----AAGACCGCAAGACCTCAGTA 1299
 Db 1400 ATCCGATGGGAGCTCCAGCGGCGAGCGGCTCTTCAAGACAGACACTGGACCTTCCA 1459
 QY 1300 GGTGACAGAGGCTCCCAAGCACACCATCAGCAGGAGG---GAGTCCCAACCAAGG 1356
 Db 1460 ACAATGCCACCTCCCAAGCACAGAGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGG 1519
 QY 1357 CAGAGAGCTGAGCTTCAACGAGACCGGCTTCCGGCCCTGCGCTCGCCCTCAAAAGT 1416
 Db 1520 CAAAGAGCTGAGCTTCAATGACCGGAGCGGCTTCCGGGATCTGAGACT----- 1573
 QY 1417 TCTCAGCCAAACAGTATGATGCTGACACAGCCCTTGGCACTGATGATATATGAT 1476
 Db 1574 -----AAACCCCGACCTCTGCTGAGGATGCC---CCTGAGAGAGTACAGAG 1621
 QY 1477 GAAAGAGATGCCAGTGTGATGATCAAGTGGAGACCTCACCCCACTTAAACTGTG 1536
 Db 1622 GAGAGAGCTACAGTGTGATGATGACGCTGACGCTGACGATCATCTGCTGTGAGACATG 1681
 QY 1537 ATTGAGACTATCAAGATTTATGAAATTTGATGCAAGAGGAGGAGGAGGAGGAGGAGG 1596
 Db 1682 ATCCGCTCCACAGATTTCTCAATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1741
 QY 1597 CGTCCATATATGTAAGAGATGCTATGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTG 1656
 Db 1742 CGACCGTACACGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1801
 QY 1657 TGTAGATTTAAACCTTCAACACAGTGTGATGATCAATTTTGGAAAGAGG---AAATC 1713
 Db 1802 GCGCGGATCAAGAGCTGCAAGCTGCGGTGAGACCAATTTGCTGCTGCGGGGCGCGGAGC 1861
 QY 1714 ACATCAGATAGAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1773
 Db 1862 AGGAGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1921
 QY 1774 AGTATGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1833
 Db 1922 AGCATGATGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1981
 QY 1834 GACTGCTTACTAGACATCTATCAACAGGCTCTCGGAAAGGCTTGCCTCAGCCCTCGCT 1893
 Db 1982 GACTGCTGCTGAGGCTTCTATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2035
 QY 1894 TTGGCTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1953
 Db 2036 CTGGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2095
 QY 1954 GTGATAGCAAGAGCTTTGGGCTTCCGACAAA 1987
 Db 2096 GTGAGACACGAGGAGCATCTCGTCTCCGACAGA 2129

RESULT 19
 AF105202 2335 bp mRNA linear PRI 11-FEB-1999
 LOCUS Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA,
 DEFINITION complete cds.
 ACCESSION AF105202
 VERSION AF105202.1 GI:4262522
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2335)
 Kubiisch,C., Schroeder,B.C., Friedrich,T., Luejohann,B.,
 El-Amraoui,A., Matlin,S., Petit,C. and Jentsch,T.J.
 KCNQ4, a novel potassium channel expressed in sensory outer hair
 cells, is mutated in dominant deafness
 Cell 96 (3), 437-446 (1999)
 JOURNAL MEDLINE 99148276
 PUBMED 10025409
 REFERENCE 2 (bases 1 to 2335)
 Kubiisch,C., Schroeder,B.C., Friedrich,T., Luejohann,B. and
 Jentsch,T.J.
 Direct Submission
 Submitted (10-NOV-1998) Zentrur fuer Molekulare Neurobiologie
 Hamburg (ZMNH), University of Hamburg, Martinistrasse 85, Hamburg
 20246, Germany
 FEATURES
 source location/Qualifiers
 1..2335
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..2335
 /gene="KCNQ4"
 83..2170
 /gene="KCNQ4"
 /codon_start=1
 /product="voltage-gated potassium channel KCNQ4"
 /protein_id="AA14680.1"
 /db_xref="GI:4262523"
 /translation="MAEAPPRRLGPPEDDAPRAELVALTANOSGEAGGSGSPR
 LGLGSPPLPGAPLPDGGSGSACGGRSSAAHRRYRLQWVYVNLBRPGMAFYH
 VFELVFLVSCVLVSTIQEHLAECLILEFVMI VFGLEYIVKWSAGCCRY
 RQMGGRFRFRKPCVDFIVFAVSVAIVAGTQGNFASLSMRLOLRLVLRMD
 RGTGTMWLLGSSVYVAHSEKLITAWYIFLVIIFASFLVLAEXKANSDFSSYADSLM
 RCTTITLIGYGDTPHTMLGRVLAAGALGISFPAFLGSGFALKVQEHOROK
 FERRRMAALIAAMRLYSTDSRAVLTWYYSILPSFRELALEFVEVORARG
 GLRPLEYRAAPVDPGAPRRYPVATCRPSTSPCRPSSRMGKIDRLRMSSORRG
 PSKQOLAPTPMTPSPSEQVEATSPTRVQKSMFSNDRTRRSLRLKPRISAEDAP
 EYVAEKSYYOCELVDDIMPAVKVVISIRLKLVAKRKETLRPLRDLVLEQYS
 AGHLDMLGRISLQTRVDOIVRGPGDKRAEKEDKGSDEAVDELSMORVYKVK
 QVOSIEHKLDLLGFGYSRLCRSGTSASISAGAVVLPDPDIRSDYHSPVDHSDISVAQ
 TLSISRVSSTNMD"
 BASE COUNT 396 a 812 c 719 g 408 t
 ORIGIN
 Query Match 17.7% Score 492; DB 9; Length 2335;
 Best Local Similarity 59.3%; Pred. No. 8.8e-96;
 Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;
 QY 322 TACCGGCGGTCGAGAACTACCTGTACACGCTGTGAGAGACCCCGGCGGTTC 381
 Db 320 TACCGCGCGCTCGAGAACTGGGTCTACAACTGTGTGAGCGCGCCCGGCGGTTC 379
 QY 382 ATCTACACGCTTCTGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 Db 380 GTCTACACGCTTCTGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
 QY 442 ACCATCCCTGAGCACACAAAATTGGCTCAAGTTGCTCTTGAATCTGGAATTCGTGATG 501
 Db 440 ACTATCCAGGAGCACACGAACTTGCACAGAGTCTCTCAATCTTGAATTCGTGATG 499
 QY 502 ATTGTCTCTTGTGTTGGAGTTATCATTTTGAATCTGCTGCGGGTCTGCTGTGCA 561
 Db 500 ATCTGTGTTTGGCTTGGAGTATCATCTCGGGGCTGCTGCGCGGAGTCTGCGCGC 559
 QY 562 TATAGAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
 Db 560 TACCGAGAGTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
 QY 622 ATTGTCTTAAAGCTTCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 681
 Db 620 ATCTGTGTTGTTGGCTTGGAGTATCATCTCGGGGCTGCTGCGCGGAGTCTGCGCGC 679
 QY 682 ACGTCTGACCTCAGAAAGTCTCCGTTTCTCTACAGATCTCCGAGTGTGCGATGAGACGA 741

```

Db      680  ACGTCCGCGCTGCGAGCATGCGCTTCAGCATCTGCGCATGGCGCATGGACCGC 739
QY      742  AGGGAGGACCTTGGAAATTTACGGGTTCAGTGGTTCATGCTCAGACAGCAAGAAATTAATC 801
Db      740  CGCGGCGGACCTTGGAAATTTACGGGTTCAGTGGTTCATGCTCAGACAGCAAGAAATTAATC 799
QY      802  ACAGCTGGTACATAGATTTTGGTTCATTTTTCGCTTCCTGCTGCTATCTGCTG 861
Db      800  ACCGCTGTCATATGAGGTGCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
QY      862  GAAAGAGTGGCAATAAAGAGTTTCTTACATATGACAGATGCTCTGCTGCTGCTGCTG 921
Db      860  GAGAGAGGACGCAATCCGACCTTCCTCCTACGCGACCTGCTGCTGCTGCTGCTGCTG 919
QY      922  ACATTGACAACTATTTGGTATGAGACAAAGTCCCTTAATGCTGGTGGGAAATTTCTT 981
Db      920  ACATTGACAACTATTTGGTATGAGACAAAGTCCCTTAATGCTGGTGGGAAATTTCTT 979
QY      982  TCTGACGCTTTGACCTCTTGGCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1041
Db      980  GCTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1039
QY      1042  TCAAGTTTGCATTAAGAATGACAAACAGACAGCCGCAAGAAACGTTTGAAGAAAGAG 1101
Db      1040  TCGGCTTTGCTTGAAGGCTCAGAGAGACACCGGCAAGAGCACTTCGAAAGCGGAGG 1099
QY      1102  AACCCAGCTGCACTATTCATGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
Db      1100  ATGCGGCGGACCAACCTATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1159
QY      1162  GTTTCATTTGCACTGAGACCCACCTTGAAGGCTTGCACAC----- 1205
Db      1160  GCCTACCTGACAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
QY      1206  ----- 1205
Db      1220  GCCCTCTTTGTTGAGCAGCTGCACAGGCGCCGCAATGGGGGCTTACGCGCCCTGAGAGTG 1279
QY      1206  ----- 1205
Db      1280  CGGCGGCGCGCGGTACCCGAGGACACCCCTCCGTTACCCGCCCTTGCCACCTGCCAC 1339
QY      1206  -----CTGCAAGCCCTTACCAATTCAGAACTTAAGAGCGA 1245
Db      1340  CGGCGGCGGACGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1399
QY      1246  GTGCGCATGGCTAGCCCGAGGCGGCGAGAGTAT-----AAGAGCGGACAGGCTCAGTA 1299
Db      1400  ATCGGATGGGCGAGCTCCAGCGGCGGCGAGGCTCTTCCAGACAGCAGCTGGCAGCTCCA 1459
QY      1300  GTGACAGAGAGTCCCAAGCAGCAGCAATCAGAGCGAGG---GCAATCCCAAGAGTG 1356
Db      1460  ACAATGCCCTCCCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1519
QY      1357  CAGAAGCTGGGAGCTTCAACGAGCGAAGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 1416
Db      1520  CAAAAGAGCTGGAGCTTCAATGAGCCGACCCGCTTCCGCGGCACTTCTGAGACTC----- 1573
QY      1417  TCTCAGCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1476
Db      1574  -----AAACCCGCGACCTCTGCTGAGAGATGCC-----CCTCAGAGAGAAATAGAGAG 1621
QY      1477  GAAAAAGATGCCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1536
Db      1622  GAGAAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1681
QY      1537  ATTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1596
Db      1682  ATCCGCTCAATGAGATTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
QY      1597  CGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1656

```

```

Db      1742  CGACGCTAGACGCTGAAGAGAGCTGATGAGAGTACTGACAGAGCCACCTGGACATGCTG 1801
QY      1657  TGTAGAAATTAAGCCCTTCAACACAGCTGTTGATCAATTTCTTGGAAAGGCG---AAATC 1713
Db      1802  GCGCGGATCAAGAGCGCTGCAAACTCGGGGTGAGCAAAATTTGAGCTGGGGGCGCGGAGC 1861
QY      1714  ACATCAGATTAAGAGAGCCGAGAGAAATAACACAGCAATGACATGAGACAGAGCATGCTC 1773
Db      1862  AGGAAGGCGCGGAGAGAGGCGAGACAGAGGCGCTCCGACGCGGAGAGTGTGATGATGATG 1921
QY      1774  AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1833
Db      1922  AGCATGATGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
QY      1834  GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1893
Db      1982  GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
QY      1894  TTGCTTCAATTCAGATCCACCTTTTGAATGTAAGACAGACATGATGATCAAAAGCCCT 1953
Db      2036  CTGGGCGCGCTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2095
QY      1954  GTGATAGCAAAAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1987
Db      2096  GTGACACAGAGAGACATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2129

RESULT 20
AB000497
LOCUS      2827 bp      mRNA      linear      ROD 23-JAN-1999
DEFINITION Mus musculus mRNA for alternative splicing: see accession between
AB000494 and AB000504, complete cds.
ACCESSION  AB000497
VERSION    AB000497.1 GI:4176399
KEYWORDS   mKOR2.4; alternative splicing.
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (sites)
AUTHORS   Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,
          Sasai,H. and Nishii,Y.
          KOR2, a new putative potassium channel family produced by
          alternative splicing. Isolation, genomic structure, and alternative
          splicing of the putative potassium channels
          Recept. Channels 5 (5), 255-271 (1998)
          98330948
JOURNAL    2 (bases 1 to 2827)
MEDLINE    Watanabe,H.
REFERENCE  Direct Submission
AUTHORS   Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
          Pharmaceutical Basic Research Lab.; 6-2, Umeagoko, Aoba-ku,
          Yokohama, Kanagawa 227, Japan (E-mail: watanabe@etcl.jti.co.jp,
          Tel:045-972-5741)
FEATURES
source
CDS
1..2827
/organism="Mus musculus"
/db_xref="taxon:10090"
87..2258
/note="mKOR2.4"
/codon_start=1
/product="alternative splicing: see accession between
AB000494 and AB000504"
/protein_id="BAA37159.1"
/db_xref="GI:4176400"
/translation="MVQSRNGVYPTSGEKKLVGPGIDGADPSTRDGALLING
SEARRGVLSKPRTGAGAGAPPRMAYRKLQNLVYVLEPRMAYFVHAIVFLL
VFSCVLSVSTFKYERKSEEGALVLEIVTVVEVEYFVIRMAAGCCCRYGWRGR
LKPARKPCVIDIMVLIASIVLAAGSQNVATLSRISRFQIILIMIMDRGGTW
KLISVYVAHSEKELVTAVYIGFLCLISLSEVLAKEGNDHDFDYADALMVGILITL
TIGGDKYPTQWNGRLAATFTLIGVSEFALPAGLIGSGFALKVQBOHPRKREKRN
PAQLIOSAMFYRANLSTRDISHWYTERVYVPMYRFLIPLNDLELRNLKSKSG
LTFRKEPPEPSPKSVSLKDKRVSSPRMAGKSGPOAQTVRRSPSADQSLDSSPS

```

polya_site

BASE COUNT 589 a 830 c 816 g 592 t
 ORIGIN /note="20 a nucleotides"

Query Match 17.6%; Score 488.4; DB 10; Length 2827;
 Best Local Similarity 57.0%; Pred. No. 5.4e-95;
 Matches 1023; Conservative 0; Mismatches 666; Indels 105; Gaps 3;

KVPSWSFGDPSRSTRQAFRIKGAASRQNSEASLPJEDI VEDNKSCEFEVTLPLG
 LKVSIRAVCVMRFLVSKRFEKSLRPLDYMDVLEJOXSGHMLDMLRISKLSDVHIV
 GRSPTIDKDRKRGKAEERLEPEDBSMGRLKVEKOVLSMEKKLPIKSLITYROMKIP
 PAETREAFKGAKEPRAPYHPSPEDSRIDADHGCITIKYRSTSSSGQRYNAPPAIRP
 AACPSTSMOOSHORHGTSPVGDHSLVLRLEBSAGMMSCH
 2827

169 GGCCTGCTACGTGCGGCGACCGGCGGCGCAACGCTGCGTGGGGGGGGGGGCTGGAG 228
 153 GGGCTTCGGGGGCTGGAGCCCGGCGCGCCGACCTCCACGCGAGCGCGCGCTACTCATC 212
 229 GAGAGCCGCGGCGGCGGCGGCGGCGGATGAGCTGCTGGGGAAGCGCTCTCTTAC 288
 213 GCGGGCTCCGAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 272
 289 ACGAGTACCGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 273 GAGAGCCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332
 349 AAGCTGCTGAGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 333 AAGCTGCTGAGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
 409 GTCCTTGGCTGCTGATTTTGTCACTGTTTCTACACCTGAGCACAACAAATTGGCC 468
 393 GTCCTTGGCTGCTGATTTTGTCACTGTTTCTACACCTGAGCACAACAAATTGGCC 452
 469 TCAAGTTCCTCTTATCTGAGAGTTCGATGATGTTGCTTGGTGGAGTTCATC 528
 453 GAGGAGGCGCTCTATCTTGGAAATCGTACTATGCTGATTCGCTGTTGCTACTTT 512
 529 AATGCAATCTGATGCGGAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 588
 513 GTGAGAGTCTGAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
 589 TTTGCTGCAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
 573 TTTGCTGCAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
 649 GTTCTGCAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 633 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
 709 CTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 693 TTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 752
 769 TCAGTGTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 753 TCGGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
 839 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 813 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
 889 ACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 873 ACCTACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
 949 AAAACTCCCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
 933 AAGTACCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
 1009 TCTTCTTCTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
 993 TCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052

1069 CAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCTCATTCAGTGT 1128
 1053 CAGATATGGCCAAACAACTTTGAGAAAAGGAGAAACCTGGGCGAGCTGATCCAGTCT 1112
 1129 GTTTGGCGGTAGTTAGCGACGCTGATGAGAAATCTGTTCCATTGCAACCTGGAGCCAC 1188
 1113 GCGTGAAGATTTCTGCTACTTACCTTCCAGCAGCCAGCTGCACTCCAGCTGGCAGTAC 1172
 1189 T----- 1189
 1173 TAGAGCGGAGACGTCTACTCTCCATGTACAGACTATCCACCTTATACAGCTGGAG 1232
 1190 -----TGAGGCTTGGCAGACCTGCG 1209
 1233 CTGCTGAGGAATCTCAAGAGCAATCTGAGCTCACTTCAAGAAAGAGCCAGCCAGAG 1292
 1210 AGCCCTACCAATCAAGAGCTTATTTTAAAGAGCGAG---TGCGCATGGCTAGCCCGAG 1266
 1293 CCATCACCAAGTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1352
 1267 GCGCAGATTTAGAGCGCAGCAAGCCCTCAGTATGAGTGAAGAGGTCGCCAGCAGCCAG 1326
 1353 GCTGCCAAGGAGAAAGGGTCTTCCAGGCGCAGAGCGTCCGCGGTCCCCAGTGGGAT 1412
 1327 ATCACAGCCGAGGCGAGTCCACCAAAAGTGAAGAGCTGAGAGCTTCAAGCAGCGAAC 1386
 1413 CAGAGTCTTATGACAGCCGAGAGAGTGGCCAGAGAGCTGAGAGCTTGGTGAACGCGAC 1472
 1387 CGCTTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
 1473 CGCAGAGCGCCAGGCTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1532
 1447 ACAGCCCTTGGCAGTATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1506
 1533 AGCTCCCTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1592
 1507 GAGAGCTCAGCCCAACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGAT 1566
 1593 GAGAGTCTTACCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1652
 1567 GTTCAAAAGGAGAGTATTAAGAAACATTTAGCTCCATATGATGATGATGATGATGATGATG 1626
 1653 GTATCTAAGCCAAAGTTCAAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGATG 1712
 1627 CAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686
 1713 CAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1772
 1687 GATCAAAATCTTGGAAAGGGGCAATTCACATCAGATTAAGAAAGCCGAGAGAAATTAACA 1746
 1773 GACCAATTTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1829
 1747 GCAGAACATGAGACCAAGAGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1806
 1830 GCGGAAAGGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1889
 1807 CAGTACAGTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 1890 CAGGCTTGTCCATGAGAAAGAGCTCGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1943

RESULT 21

AX456861

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Sequence 2 from Patent WO0232360.
 AX456861.1 GI:21715728
 2750 bp DNA linear PAT 06-JUL-2002

LOCUS	AF110020	2750 bp	mRNA	linear	PRI 03-MAR-1999
DEFINITION	Homo sapiens potassium channel (KCNQ2) mRNA, complete cds.				
ACCESSION	AF110020				
VERSION	AF110020.1	GI:4324686			
KEYWORDS	.				
SOURCE	Homo sapiens.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 2750)				
AUTHORS	Wang,H.-S., Pan,Z., Shi,W., Brown,B.S., Wymore,R.S., Cohen,I.S., Dixon,J.E. and McKinnon,D.				
TITLE	KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of the M-current				
JOURNAL	Science 282 (5395), 1890-1893 (1998)				
MEDLINE	99053598				
PUBMED	9836639				
REFERENCE	2 (bases 1 to 2750)				
AUTHORS	Wang,H.-S., Pan,Z., Shi,W., Brown,B.S., Wymore,R.S., Cohen,I.S., Dixon,J.E. and McKinnon,D.				
TITLE	Direct submission				
JOURNAL	Submitted (30-NOV-1998) Neurobiology, SUNY Stony Brook, Life Sciences Building, Stony Brook, NY 11794-5230, USA				
FEATURES	Location/Qualifiers				
source	1..2750				
gene	/organism="Homo sapiens"				
CDS	/db_xref="taxon:9606"				
	1..2750				
	/gene="KCNQ2"				
	47..2572				
	/gene="KCNQ2"				
	/codon_start=1				
	/product="potassium channel"				
	/protein_id="AADI6988.1"				
	/db_xref="GI:4324687"				
	/translation="MVQSKRNGGVYPGSGEKKLVGVGLDPDPAIDSTRGALLIA SEAPRGSLIKPRAGGAGCPPKRNFAFRLOLNLNLEPRPGMAFTIATVFL VFSCVLVSFSTIKREYKSSBGALILITVIVVEGFAPVIMAGGCCCRGRG LKFAKPEPCVIDIMVLISAVLAGSGGNFATLSRLSLQLTIRMI RMDRRGTG KLGSVVYAHSEKELVTANYIGFLICFLSVLAKEENDEHFDTVAALMLGITLL TLTGDXKYPOTMNGRLAAATFLIGSFLLPDLGILGSGFALKVOEORHKHEKRRI PAGLIOSAMRPYARNLSRTPLSHMOWYERYRVTPMYSSOTQYGASRLIPLNOLIL LRNIUKRSGLAFRKDDPPSPSPRGTAAKGSGPOQTARYSRPSADQSLEDPSKT PKSWSGDRSRAKQAFLTKGASRONSSASLPEGDIYDKSCPCEVTEIDTFGLKV IRAVCMRFPLEAKRKFESLRYDYMDYIEDYSACHLMLSIKLSKLDVDIVRG AITDDRTKGAEALLPEDPSMWGRIGVYEKVLSEMKLDFLTVINIQRMGIPTEFE EAYFARKPEEPAPPHSPEDSRHHVDRHGCIYKIYRSSSTGEENSAFPAPVOCI PSTMOPSHPDROGHGTSPVGDHGSLVIRPPPAHERSLISAAGGNRAMSELRDED PGCRPREGNLRDSDPTSIPTSYDHELIRTSFGESGISOSKEULDALNSCYAAVACA VRPIAGESTDSDLCIFPCGPPEPCKATGEGFFGDVMAGPRK"				
BASE COUNT	493 a	910 c	891 g	456 t	
ORIGIN					
Query Match	17.2%: Score 475.6: DB 9: Length 2750:				
Best Local Similarity	56.6%: Pred. No. 3.2e-92:				
Matches 1075:	Conservative 0: Mismatches 714: Indels 111: Gaps 6				
Oy	63	CGCAGCGGGCGGC	GCGCGGGCGGGGGCGCTTTGGGACAGCGCATGAAGATGTGGAGTC	122	
Dd	1	CCCCCTGAGCTTGAGACC	CGACCCCGGGGCGCCTCCCGCACCAACCATGTGCAGAAATC	60	
Oy	123	GGGCGGGGCGAGGTCGTGCTGAAC	TCGGCACACCGCCA-----GGGCGGACGGCGCTGCT	176	
Dd	61	GGCGAACGGCGCGGTATACCCCGGCGCGGCGGGGAGAAGAACTGAAGTGGCGCTTGCT	120		
Oy	177	ACTGCTGGGACACCGCGGCGGCACGCTCGATTGGCGGCGGCTTGCGCTTAGGAGAGACCG	236		
Dd	121	GGGGCTGGAGCCCCGGGCGCCCGACTCCAGATCCACCGGGGACGGGCGCTGTGATGCGCGCTC	180		
Oy	237	CCGGGGCAAGACAGGGGGGCCCGGATAGAGCTGCTGGGGAACCCGCTCTTTACAGAGTAG	296		
Dd	181	CGAGGCCCCCAAGCGGGGAGGATCTTCAGCAAACCTCGCGGGGGGCGCGGGCGCGG	240		

[illegible]

QY 1301 -----GTACAGAGAGTCCCAACACGACATCAGACCGAGG 1340
 Db 1321 GGGGTCCCGCAGGCGCCAGACTGTGAGCGGTCACCCACGCGGACGCTCGAGGA 1380
 QY 1341 CAGTCCCAACCAATGAGAGAGTGTGAGCTTCAACGACCGACCCGCTCCGCCCTC 1400
 Db 1381 CACCCCGACAGAGTGTCCCAAGAGCTGTGAGGAGCCGACGCGGACGCGAGG 1440
 QY 1401 GCTGCGGCTCAAAAAGTTCTCAGCCAAAACAGTGTAGTGTGACACAGCCCTTGAC 1460
 Db 1441 TTTCGGCATCAGAGGTGCCGG-----TCAAGGACAACTAGAAAGCAAGCTCCCGG 1494
 QY 1461 TGTATGATGTATGATGAAAAAGATGCCAGTGTGATGTATCAGTGAAGACCTCACCC 1520
 Db 1495 AGAGGACATTTGTGATGACAAAGAGCTGCCCTGCGAGTTTGTGACAGAGACCTGACCC 1554
 QY 1521 ACACATTAAGACTGTATGAGTATCAGATCAGAAATTAATTCATGTTGCAAAACGGA 1580
 Db 1555 GGGCTTCAAGTACAGCTACAGAGCCGCTGTGTCTATGCGGTTCTGTTGTCAGAGGGA 1614
 QY 1581 GTTTAAGAAACATTTACGTCATATGATGATAAAGATGTATGAACATATTTCTG 1640
 Db 1615 GTTCAAGAGAGCTGCGGCGCTCAGAGTATGAGACTCAGACGACTACTCAGCCG 1674
 QY 1641 TCATTCGAGATGTGTGTAGATTAAGACCTTCAAAACAGCTGTGATCAAAATCTG 1700
 Db 1675 CCACCTGAGATCTCTGCTCCGAATTAAGAGCTGACAGTCCAGAGTGAACAGATGCTG 1734
 QY 1701 AAAAGGCAAAATGACATCAGATAGAAAGCCGAGAGAAATTAACAGAGCAATGAGAC 1760
 Db 1735 GGGGCGCCAGGATCAGCGACGACAAAGAA---CCGACCAAGAGGCGCGCGAGAGT 1791
 QY 1761 CACAGCAGATCTAGATGCTCGGTGCGGTGCAAGTTGAAAAAAGCAGTACATC 1820
 Db 1792 GCCCGAGAGCCCGAGATGATGAGCGCTCGGAGAGTGAAGAGCAGAGTCTTGCCAT 1851
 QY 1821 AGAATCCAGCTGAGCTACTAGACATCTATCAGAC 1860
 Db 1852 GGAGAGAAAGCTGACTTCTGTTGAATTCATCATGAG 1891

RESULT 23
 AB000496 2899 bp mRNA linear ROD 23-JAN-1999
 LOCUS AB000496 and AB000504, complete cds.
 DEFINITION AB000496 and AB000504, complete cds.
 ACCESSION AB000496.1 GI:4176397
 VERSION mKOT2.3; alternative splicing.
 KEYWORDS Mus musculus cDNA to mRNA.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (sites)
 AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T., Sasaki, H. and Nishi, Y.
 TITLE KOT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
 JOURNAL Recept. Channels 5 (5), 255-271 (1998)
 MEDLINE 98330948
 JOURNAL 2 (bases 1 to 2899)
 REFERENCE Watanabe, H.
 TITLE Direct Submission
 AUTHORS Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umeogaki, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
 FEATURES
 SOURCE Location,Qualifiers
 1..2899
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 CDS 87..2330

polyA_site
 BASE COUNT 606 a 864 c 830 g 599 t
 ORIGIN
 Query Match 17.1%; Score 474.8; DB 10; Length 2899;
 Best Local Similarity 57.9%; Pred. No. 4.8e-92;
 Matches 925; Conservative 0; Mismatches 607; Indels 66; Gaps 2;
 169 GCGCTGCTACTGCTGGGACCGCGCGGACGCTGCGGCGCGGCGGCTGAGG 228
 153 GCGTCTGCTGGGCGTGGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTG 212
 229 GAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 288
 213 GCGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 272
 289 ACGAGTACCGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 273 GAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332
 349 AAGCTGCTGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 333 AAGCTGCTGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
 409 GCTCTGCTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
 393 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
 469 TCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
 453 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
 529 ATTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
 513 GTAGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
 589 TTGCTGTAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
 573 TTGCGCAGGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
 649 GTTCTGCAAAAACCTGATATATTTTTCACAGCTGCTGCTGCTGCTGCTGCT 708
 633 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 709 CTACAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 693 TTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 752
 769 TCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 753 TCGGTAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812

QY 829 CTTATTTTTCCTTCCTGCTATCTGTTGAGAAAGATGCAATTAAGATTCT 888
 DB 813 CTCATCTGGCCCTCATTTCTGTTGTTACTTGCGACAAAAGGTGAGATGACCTTTGAC 872
 QY 889 ACATATGAGANTGCTCTGTTGGGGGACATATTCATTTGACACTATTTGGCTATGAGAC 948
 DB 873 ACTATGAGAGTACACTGCTGTTGGGCTGATACCCCTGACGACATTTGGCTAGGGGAC 932
 QY 949 AAAAATCCCTTAATCTGCTGGGAGATGCTTTCTGACGCTTTGCACTCTTGCGACT 1008
 DB 933 AAGTACCTCTGACAGCTGGAGAGGAGCTGCTGACACGACCTTTACCTCATTTGCTC 992
 QY 1009 TCTTTCTTTCACATCTCTGCGGATCTTGGCTCAGGTTTGGATTAAAGTACAAAGA 1068
 DB 993 TCGTTCTTTCCTCTCTGCTGCTGATTTGGATCCGGCTTTGCCCTGAAAGTCCAAAG 1052
 QY 1069 CAACACCGCCAGAAACATTTGAGAAAAGAGAACCCAGCTGCGCAACCTCATTCAGTGT 1128
 DB 1053 CAGCATCGGGCAAAACATTTGAGAAAAGGAGAACCCGCGGAGGTCTGATCCAGTCT 1112
 QY 1129 GTTTGGCTGTTACGAGCTGATGAGAAATCTTTTCATTTGCACTGCAAGCCACAC 1188
 DB 1113 GCTTGAGATTTCTATGCTTACTTAACCTTCACGACCGACCTGCACTGCGAGTAC 1172
 QY 1189 TTGAGAGCTTGCACACCTGACGCTTACCAATCAGAAAGTAAAGTTTAAAGAGGAG 1248
 DB 1173 TACGAGCGGACACTGCTGCTCCATGATACAGACTCATCCACTCTCAACACCTGAG 1232
 QY 1249 CCGATGGCTAGCCCT-----AGGGCCAGAGTATTAA 1280
 DB 1233 CTGCTGAGAAATCTCAAGAGCAATCTGACTCACCTTCAGAAAGAGCCACAGCAGAG 1292
 QY 1281 GACCCGACACCTCACTAGT----- 1302
 DB 1293 CCATTCACACCCCTCCAGAGGATGGCTGCCAAGGAAAGGGCTCTCCAGGCCACAGACG 1352
 QY 1303 GACAGAGAGTCCCAACACCGACATCACACCGAGGAGCTCCCAACCAAGTGCAGAG 1362
 DB 1353 GTCCGGAGGTTCCCAAGTGGGATCAAGTCTTATGAGACGCGAGAGAGTGGCCAG 1412
 QY 1363 AGCTGAGCTTCAACGACCCGCTTCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
 DB 1413 AGCTGAGCTTGGTGGACCGGACGCGACGCGCTTCCGCTCATCAAGGCTGTGCA 1472
 QY 1423 CCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1482
 DB 1473 TCCCGGAGATTTAGAAAGAACAGCTCCCTGAGGAGGACATGCTAGAGACACAGAG 1532
 QY 1483 GATGCGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1542
 DB 1533 AGCTGTAAGTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1592
 QY 1543 GCTATGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1602
 DB 1593 GCTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1652
 QY 1603 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1662
 DB 1653 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1712
 QY 1663 ATTTAAAGCTTCAACAGCTGTTGATCAAAATTTCTGG 1700
 DB 1713 ATCAAGAGCTGCGAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATG 1750

RESULT 24
 HSKCNO2
 LOCUS HSKCNO2 7420 bp mRNA linear PRI 12-FEB-1998
 DEFINITION Homo sapiens mRNA for voltage gated potassium channel.
 ACCESSION Y15065
 VERSION Y15065.1 GI:2826772
 KEYWORDS KCNQ2: voltage-gated potassium channel.
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 7420)
 Blevvert,C., Schroeder,B.C., Kubisch,C., Berkovic,S.F.,
 Propping,P., Jentsch,T.J. and Steinlein,O.K.
 A potassium channel mutation in neonatal human epilepsy
 Science 279 (5349), 403-406 (1998)
 MEDLINE 98092527
 PUBMED 9430594
 REFERENCE 2 (bases 1 to 7420)
 Steinlein,O.K.
 Direct Submission
 Submitted (09-OCT-1997) O.K. Steinlein, Inst. of Human Genetics,
 University of Bonn, Wilhelmstr. 31, 53111 Bonn, FRG
 Revised by submitter 02-DEC-1997
 Related locations D82343 to D82347.
 FEATURES
 source
 1. 7420
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="20"
 /map="q13.3"
 43..2577
 /gene="KCNQ2"
 43..2577
 /gene="KCNQ2"
 /codon_start=1
 /product="voltage gated potassium channel"
 /protein_id="CAA75348.1"
 /db_xref="GI:2826773"
 /db_xref="SPTREMBL:043796"
 /translation="MYOKSRNGVYPPSPSEKKLVFVGLDPAIDPSTRDALLIG
 SEAPKRGSLISKRPAAGAGKPKPRKALFRIKQNFVYVRIYMAAGCCGRRMRGR
 VESCIYLSVSTIKYEKSESEGLTILEYIYFPGYEVYRIYMAAGCCGRRMRGR
 LKFAKPFVYIDIMVLAVLAAGSGVAFATSAIRSLRFLDILKIRDRRGCTT
 KLGSVYVAHSEKELTAWYIGFLCLILASFLVLAEGENDHFTVADALMHLITTE
 TIGYDKRPOTMNGRLAATFTLIGVAFALPGILSGALKYOEHRORHFEKRRN
 PAAGLQSAWRYATNLSPDLSTWQYERIVYPMYRLIPLNOLLEMLSKSG
 LARNDPPEPSPSOXVSLKDRVSSRGAAGKSGPOATVRSSEPADLSLSPS
 KVPKSWSPGDRSARAFRIKGAARNSSEASLPGDIYDDKSCPEFVEDLPLG
 KSTRVACVRLFLVSKRKFEKSLRPYVYVYIYDSYSGHIDMLSRISLSRNOIYC
 RGAATIDKDKTPAELELDEDSBMGRLEKVEQVLSMEKRLDPLVNTIQKNGIIP
 TETEAIFGAKEPEPAPYHSPEDSRREHVDHRCQIVKSSSTGQNFSAFPAPPV
 OCPSTSMQPSHROGHGTSPYGDHSLRIPIPPPHERLSAYGGGNRSMELFRO
 EDIPGCRPGTGLRSDPTSLSPSDHEELERSPSGSIISQKENDLALNCSYAVALP
 CAKVRYIAGESDTSDLCTPGSPPRSATGEGPFDVGMAGPRK"
 BASE COUNT 1366 a 2325 c 2354 g 1368 t 7 others
 ORIGIN
 Query Match 17.0%; Score 472.2; DB 9; Length 7420;
 Best local Similarity 57.6%; Pred. No. 2,1e-91;
 Matches 1035; Conservative 0; Mismatches 648; Indels 114; Gaps 6;
 QY 169 GGCCTGCTACTGCTGGGCAACCGCGGCGCACGCTCGGTGGCGGCGGCTGTAGG 228
 DB 109 GCGTTCTGCTGGGCTGGGACCCCGGCGCCCACTCCACCCGCGGAGCGGCGCTGTATC 168
 QY 229 GAGAGCGCGCGGCGCAAGCAGCGGCGGATGAGCCTGCTGGGAAACCGCTCTTAC 288
 DB 169 GCGGCTCCGAGGCGCCCAACGCGGCGACATCTCTACAGAAACCTCGCGCGGCGCGG 228
 QY 289 ACAGTAGCAGAGACTCCGCGCGCAGCTCAAGTACCGCGGCTGACAGACTTACTGAC 348
 DB 229 GGGCGCGGGAAGCCGCCCAAGCGCAAGCCTTCTACCGCAGAGCTCAAAATTTCTTAC 288
 QY 349 AACGTGCTGAGAGAACCCCGCGGCGCTTCACTACACAGCTTTCCTTCTCTCT 408
 DB 289 AACGTGCTGAGAGCGCGCGCGGCTGCTTCACTACACAGCTTACTGCTCTCTG 348
 QY 409 GTCCTTGTGCTGATTTTGTCAAGTCTTCTCACTACCTGACAGACACAAATTTGGCC 468
 DB 349 GTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408

QY	466	TCAGTTGGCCCTTATACCTGGAGTTGCGATATATTTGCTGTTGGTTTGGACTTCATC	528
Db	409	GAGGGGGCCCTTCTACATCTGGAAATCGTACATCTGTGGTTGGCGTGAAGTACTTC	468
QY	529	ATTGGAATCTGTCTGCGGGTGTCTGTTGTGCATATATAGAGATGGCAAGAACTGAGG	588
Db	469	GTCGGGATCTGGGGCCGACGGCTGCTCGCGGTACCGTGGCTGGAGGGGGCGCTCAAG	528
QY	589	TTTGGCTGGAAGCCCTTCTGTGTATATAGATACCATTGTCTTATTCGCTTCAATAGCACTT	648
Db	529	TTTGGCCGGAACCGTTCTGTGTGATATGACATATGCTGTGCATTCGCTCCATTTCCGGTG	588
QY	649	GTTTCTGCAAAACACGAGGTAAATATTTTGGCAGCTGCACACTCAGAAAGCTCCGTTTC	708
Db	589	CTGGCCGCGCGCTCCACAGGCAACGCTTTGGCCACATCTCGCTCCGAGCGCTCGCTTC	648
QY	709	CTACAGATCTCCCGATGGTGGCCATGAGACCGAAGGGGAGGCACTTGGAAATTACTGGGT	768
Db	649	CTCCAGATTTCTGCGGATATCCGCATATGACCCGGCGGGGAGGCACTGGAACTGCTGGGC	708
QY	769	TCAGTGGTTATGCTACAGCAAGGAATTAATCAACGCTGGATACATAGAAATTTTGGTT	828
Db	709	TCGTGGTCTATGCCCAAGCAAGAGAGCTGTGACTGCTCGTATCATCGGCTTCTTTGT	768
QY	829	CTTATTTTTTTCGTTCCCTTCTATCTGTCATCTGCTGGAAGAGATCCCAATTAAGATTTTCT	888
Db	769	CTCATCTCGGCTCGTTCTCGTGTATCTTGGCAGAGAAGGGGAGAACGACCACTTTTAC	828
QY	889	ACATATGCAATGCTCTCTGTGGGGGACAAATTAATTCATTAACAATTTGGCTATGAGAC	948
Db	829	ACCTACCGGGATGCACTCTGTGGGGCCGTATCACTGACCAACCAATTTGGCTACGGGGAC	888
QY	949	AAACTCCCTTAACCTTGCTGGGGAAGATTGCTTTTGCAGAGCTTTGGCACTCTTGGCAAT	1008
Db	889	AAGTACCCCAAGACTGGAAAGGACGAGCTCTTGGCGCAACCTTCACTCATCGGTTC	948
QY	1009	TCCTTTCTTTCGACTTCTCGCCGGCACTTCTTGCTCAGGTTTGCATTTAAAGTACAAGAA	1068
Db	949	TCCTTTCTTCGCGCTCGCCGACGAGCACTTGTGGGTTGCGGTTTCCCTGAAGGTTACAGAG	1008
QY	1069	CAACACCGCCAGAAACCTTGAAGAAAGAAAGAACCCGAGCTGCCAACTTCATTCAGTGT	1128
Db	1009	CACACAGSAGAAAGCACTTTGAGAGAGAGCGGAAACCCGACAGGCTGATTCACGTGC	1068
QY	1129	GTTTGGCGTATGTAAGCAGCTGAT-----	1152
Db	1069	GCCTGAGATTTCAAGCCACCACTCTCGCCACAGACCTGCACTCCAGCTGACAGTAC	1128
QY	1153	---GAGAAATCTGTTTCCATTTGCAACTTGGAAGC-----	1183
Db	1129	TACGAGCGAAGGTCACCGTGGTCCCATGTACACACTTATCCCGGCTGAACCAAGCTGGAG	1188
QY	1184	-----CACACTTGAAGGCTTGCACACCTGC-----	1209
Db	1189	CTGCTGAGAACTCAAGAGTAATCTGTGACTCGCTTTAGAGAAAGACCCCCCGCGGAG	1248
QY	1210	AAGCCCTAACCAATAGAAAGCTTAAGTTTAAAGAGCAGATGCGCATGGCTTACGCCAGGGGC	1268
Db	1249	CCGTCTCCAAAGCCAGAAAGGTCTAGTTTGAAGAATCTGTGT---CTTCTCCACGCCCCCGAGGC	1305
QY	1270	CAGAGTATTAAGAGCCGACAAAGCCTCACTAGTAG-----GTGACAGAGAGGTGCCAAGAGAC	1323
Db	1306	GTCGCTGCCAAGGGGGAAGGGGTCCCCCGCAGGCCACAGACTGTGAGGCGGTATCCCAAGCGCC	1365
QY	1324	GACATCAACGCCAGGGCAGTCCCAACAAAGTGCAGAAGAGCTGAGCTTCAACAGCGCA	1383
Db	1366	GACCAAGAGCTTCAGAGCAGACCCCAAGAAAGGTGACCAAGAGCTTGAGGCTTCCGGGAGCCG	1425
QY	1384	ACCCGCTTCGGGCTCTGTCGCGCTCAAAAGTCTCAGCCAAACCACTGATATAGATGCT	1443
Db	1426	AGCCGGGACGCCAGGCTTTCCTCGATCAAGGGGTGCGCGTCAACGGCAGAACTCAGAAAGAA	1485

QY		1444	GACACAGCCCTTGGCAGCATGATGTATGTATGAATAAAGAGATGCCAGTGATGTATCA	1503
Db		1486	G---CAAGCCTCCCCGGAGAGAGACAATTGGATGATCAAGAAGACTGCCTCGGATTTGTG	1542
QY		1504	GTCGAAAGACCTCACCCCACCACCTTAATAAAGTGCATTTCGAGCTATCAGAAATTATGAATTT	1563
Db		1543	ACCGAGAGACCTGACCCCCCGGCTCTCAAAGTCACATTCAGAGCCGTGTGTGCATCGGTTTC	1602
QY		1564	CATGTTCCAAAACGGAATTTAAGGAACATTAACGTCCATATGATGTAAAAAGATGTCA	1623
Db		1603	CTGCTGTCCAGCGGAAAGTTCAAGAGAGACCTCGGCCCTTCAGACGTGATGAGAGCTATC	1667
QY		1624	GAACAATATTTCTGCTGTCATCTGGACATGTTGTGTAGAATTTAAAGCCCTTCAAACACGT	1683
Db		1663	GACACAGTACTCAGCCGGCCGACCTGACATGCTGTCCGAATTAAGAGCCTCGACATCCAGA	1722
QY		1684	GTTGATTAATTTCTTGGAAAAAGGCGCAATTCATCATGATTAAGAAGACCCGAGAAATAA	1743
Db		1723	GTCGACCAGATCTGGGGGGGGGCCACAGATCAACGACAAAGGA--CCGACACCAGAGGC	1779
QY		1744	ACAGCAGAACATGAGACACAGACAGCATCTCAGTATGCTCGTGGGTGGTCAGAGTTGAA	1803
Db		1780	CGGCGCAGGAGGAGCGTCCCGGAGAGACCCACCATATATATGAGACGGCTTCGGAGAGTGCAG	1833
QY		1804	AACAGGTACAGTCCATTAAGAAATCCAAGCTGCACTGCTACTAGACATCTATCAACAG	1860
Db		1840	AACGAGCTCTTGTCCATGAGAGAAAGAGCTGCACTTCCTGTTGAATATCTACATGTCAG	1896
RESULT 25				
AF074247				
LOCUS		AF074247	3195 bp mRNA linear PRI 16-FEB-2001	
DEFINITION		Homo sapiens neuronal delayed-rectifier voltage-gated potassium channel splice variant (KCNO2) mRNA, complete cds.		
ACCESSION		AF074247		
VERSION		AF074247.1	GI:3294576	
KEYWORDS				
SOURCE		Homo sapiens.		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		1 (bases 1 to 3195)		
AUTHORS		Iannotti,C.A., Dargis,P.G., Christian,E.P. and Aiyar,J.		
TITLE		The expression pattern of KCNO2 splice variants in neuronal proliferation and differentiation		
JOURNAL		Abstr. - Soc. Neurosci. (1998) In press		
REFERENCE		2 (bases 1 to 3195)		
AUTHORS		Smith,J.S., Iannotti,C.A., Dargis,P., Christian,E.P. and Aiyar,J.		
TITLE		Differential expression of kcno2 splice variants: Implications to m current function during neuronal development		
JOURNAL		J. Neurosci. 21 (4), 1096-1103 (2001)		
MEDLINE		21114072		
PUBMED		11160379		
REFERENCE		3 (bases 1 to 3195)		
AUTHORS		Iannotti,C.A. and Aiyar,J.		
TITLE		Direct Submission		
JOURNAL		Submitted (24-JUN-1998) Target Discovery Department, Zeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19850-5437, USA		
FEATURES				
SOURCE		Location/Qualifiers		
		1..3195	/organism="Homo sapiens"	
			/db_xref="taxon:9606"	
			/tissue_type="brain"	
		1..3195	/gene="KCNO2"	
		176..2740	/codon_start=1	
			/product="neuronal delayed-rectifier voltage-gated potassium channel splice variant"	
			/protein_id="AA025921.1"	
			/db_xref="GI:3294577"	
			/translation="MYOKSRNGGVYPGPSEKKLVGFVGLDPGAPDSTRDALIANG	
gene				
CDS				

SEAPKRSILSKPRAGGACGCPPKRNAFRKILONFLENYLNERAGCAATYHAIVFRL VSCCIIIVSVSTIKEYKSSSEGLILIEITIVYEGVEYVIRIAAGAACCCCRHYMRBR LNRARRPFCYIDIDIMVLASTAVIAVLAGSGQVFAISARSRLRFDIOLIEIMIDREGTMM KLIGSVYVAHSKELEVTAMVIGFLDILLIASTLVIAESGDNDHPTYDAILMWCILITLT TIGAGVYQPTWMGRLLAATFTLLIGVSEFVLPALIELSGRLKVOEORHOFKERRRN PAAGLLOSARFVATNLNRDLHSTWQYERTVAVPWSQSOTQYVGSRLPLPINOIE LNRNKSISGLAPKDPDPPEPSQKSLMDRVSFSPVAAKSGSPQAOQYVRSFS ADSLDEPSPKVSMSFGDRSARAFORFKILGAARVONSEASLPGDIYDCKCPCE FVLEIDLPJGKSCVMARPLVRSKFKFSEKFLIIPALRYMDEIYSGHILMDSRIS LOSRYDQIVRCRAPIIDKDKTKPAEAELEPDEPSMRRLKVEKQVLSMEKKLDFLVN IYKORMEIPPLETEATIFGAKEPEPAPVHSDEBRESHVDRGLVTKIVRSSSTLYQKX FSAPAPAPVQCEPSTISWQPSHROGHSIPVGDHSLVRIPPPAAHRSLSVYGGG NRSAMELROEDIPGCRPEPGLRDSOTISIPVDEHELEERSGFSISQSKNLDPA LNSVYAEADCAKVRPIYIAGESPTDSDLCTPCGPPPRSATGEPGFDVGMACPRK"	BASE COUNT	559 a	1048 c	1068 g	520 t
ORIGIN					
Query Match	16.3%;	Score 451.4;	DB 9;	Length 3195;	
Best Local Similarity	55.7%;	Pred. No. 5.7e-87;			
Matches 1113;	Conservative 0;	Mismatches 736;	Indels 150;	Gaps 7/;	
QY	3	GCCCCGCGACACCGCGGGAGAGAGAGAGGGGGGGCGCGCGCGCTCTGGGTGAAGAGCGG	62		
DB	70	GCCATTTGGGCTCCCGCGCGGGGGCGCTGGGGGGCCCGCGCGCGCCCCCGCTCCGC	129		
QY	63	CGCAGCGCGCGCGCGCGCGGGGGCGCTTGGGCGAGCGGCATGAAGATGTGAAGTC	122		
DB	130	CCCCGCTGAGCGCTAGCCCGAGCCCGGGGGCGCTCCCGCAGGCAACATGRTGAGAAATTC	189		
QY	123	GGGCGGGGGCAGGCTGCTGCTGAACCTGGCAGCGGCCA-----GGGGCGAGCGCTCTCT	176		
DB	190	GCGCAGGCGCGCGCTATACCCCGCGCGAGCGGGGAGAAAGCAAGCTGAAGGCTTGCTGT	249		
QY	177	ACTGCTGGGCAACCGCGCGGGCGCGCTGGTGGGGGGCGCGGTGAGCTGAGAGGAAAGCGG	236		
DB	250	GGGGCTGGACCCCGCGCGCGCCGAGCTCCACCCGGAGCGGGCGCGCTGCTGATGCCGGCTC	309		
QY	237	CGGGGGCAGCAGGGGGCGCGGATGAGCCTCTGGGGAAGCGCGCTCTTACACAGTAG	296		
DB	310	CGAGCGCCCAAGCGCGCGCAGCATCTCAGCAAACTCGCGGGCGCGCGCGCGCGCG	369		
QY	297	CCAGAGCTGCGGGCGCAACGTCMACTACCGGGCGGTGCAAGAACTACCTGTAAACAGTCT	356		
DB	370	GAAAGCCCCCAAGCGCAAGCGCTTCTACCGCAAGCTGAGAAATTTCTCTACAAAGTGT	429		
QY	357	GGAGAGACCCCGCGCGCTGAGGCTTCATCTACCAAGCTTCTGTTTTCCTCTCTTTGG	416		
DB	430	GGAAGCGCGCGCGCGCTGCGGCTTCATCTACCAAGCTTCATCGTTCCTCTCTGTTTCTC	489		
QY	417	TTGCTTGAATTTTGTCAGTGTTTTCACATCCCTGAGCACACAAATATGGCCCTCAAGTTG	476		
DB	490	CTGCTCTGCTGTCTGTGTTTTCACCATCAAGAGATGATGAGAGAGCTCGAGGGGGC	549		
QY	477	CCTCTGATCCTGAGAGTTCGTGATATGTGCTCTTTGGTTGGAGTTTCATATTCGAT	536		
DB	550	CCTTACATCCTGGAAATCGTACATCGTGTGTGTTTGGCGGAGTATCTTGCGGGAT	609		
QY	537	CTGCTCTCGGGTCTCTGTTGCGATATAGAGATAGGCAAGAGAACTAGAGTTTGCTCG	596		
DB	610	CTGGGCGCGCAGGCTCTGCTCGCGGTACCGTGGCTGAGAGGGGGCGGCTCAAGTTTGCCG	669		
QY	597	AAAGCCCTCTGTGTTATAGATACATATGTTCTTATCGCTTCAATAGCAGTTGTTTCTG	656		
DB	670	GAAACCGTGTCTGTGATGTGATCATATGTTGCTCATCGCTCATATGCGGTCTGGCCCC	729		
QY	657	AAAACTCAGGGTAAATTTTGGACACGCTCAGCTACAAGCMTCOCGTTTCTCTACAGAT	716		
DB	730	CGGCTCCAGGGCAACGCTTTTGCCACATCTCGCTCCGGAAGCTTGGCTTCTCGAGAT	789		
QY	717	CTCTCGCATGTGCGCATGAGCAGGAAGGGAGGCACTTGGAAATTACTGGGTTCACTGTG	776		
DB	790	CTTGGGAGATGATCCGATGAGCCGGGGGGGAGGACCTGGAAGCTGTGGGCTCTGTGGG	849		

QY	777	TTATGCTACAGCAGCAAGAAATTATTAATCAGAGCTGGTACATAGATATTTTGGCTCTATTTT	836
Db	850	CTATGCCCCACAGCAGAGGAGCTGGCTACTGCTGTATCATGGCTTCTTGTCTCATCTCT	909
QY	837	TTGCTCTTCTCTGTCTATCTGTGTGGAAAAAGATAGCCAAATTAAGATTTTCTATCATATGC	896
Db	910	GGCCTCGTCTCTGGTGTACTTTGGCAGAGAAAGGGGGAGAACGACCACTTGTATACACTACGC	969
QY	897	AGATGCTCTCTGGTGGGGGCACATTTACATTTGACAACTATTTGGCTATGTGAAACAAACTCC	956
Db	970	GGATGCACTCTGGTGGGGCCGTGATCAGCTGACCCACTTTGGCTTACGGGGACAAATACCC	1029
QY	957	CCTAACCTTGGCTGGGAGATATTCCTTTTCGAGAGCTTTTGACACTCTCTTGGCATTTCTTTCTT	1016
Db	1030	CCAGACCTTGGACAGCGGACGGCTCTTTGGGGCAACCTTACCTCATGGGTCTCTCTCTT	1089
QY	1017	TGCATCTTCTGCGGGCATTCCTTGGCTCAGGTTTTTGCAATTAAAGTACAAACAAACACCG	1076
Db	1090	CGCCCTCTCTGACAGCATCTTGGGGGTCTGGTTTGCCCTTAAGATTTACAGAGACGACAG	1149
QY	1077	CCAGAAACACTTTAGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAGTGTATTGGCG	1136
Db	1150	GCAGAGACACTTTTAGAAGAGAGCGGAAACCCGGCAGCAGGCTGATCCAGTGGGCTGGAG	1209
QY	1137	TAGTTACGCACTGAT-----GAGA	1157
Db	1210	ATTCTACGCCCAACCTCTGCGCACAGACCTGCATCCAGCTGAGTACTACGAGCG	1269
QY	1158	ATCTGTTTCCATTCGAACCTGGAGGACACACTTAAAGCCCTTGACACTGCAGCC----	1213
Db	1270	AAGGTCACCGTGCACATGTACAGTTGCAAACTCAAACTACGGGGCTTCCAGACTTAT	1329
QY	1214	-----	1213
Db	1330	CCCCCGCTGAACCAAGCTGAGCTGCTGAGGAACCTCAAGATTAATCTGACTCGCTTT	1389
QY	1214	-----CTACAAATCAAGAAGTAGTTTAAAGGCGCAGT	1247
Db	1390	CAGGAAGGACCCCCCGCGGAGCCGTCTCCAAAGCAGAGAGGTCAAGTTTGAABAGATCGTGT	1449
QY	1248	GCGCATGGCTATGACCCACAGGGGCTCAGAGATTATTAAGGCCAGACAACTCAGTAG-----G	1301
Db	1450	---CTTCTCCAGCCCCCGAGGCGTGGGTGCCAAGAGGGGAGGGGGTCCCGCAGGCCACAG	1506
QY	1302	TGACAGGAGGTGCCCAAGCACCAGCATCAGACCGGAGGGGAGTGTCCCAACAAAGTGCAGAA	1361
Db	1507	TGTGAGGGGGTACCCACCGCCGACAGAGCCTGAGAGACAGCCCAAGGAGTGGCCAA	1566
QY	1362	GAGCTGGAGCTTCAACGACGACCGACCCGGTTCGGGGCTCGCTGGGCCCAAAATTTCTCA	1421
Db	1567	GAGCTGGAGCTTCCGGGAGCCCGCAGCGGGGACGCGCAGGCTTTCCGCATCAAGGGTGGCCG	1626
QY	1422	GCCAAACCAAGTAGATGCTGTGACACAGCCCTTGGCAGTGAATGTATATGTGAAAA	1481
Db	1627	GTCACGGCAGAACTAGA---AGAAAGCAAGCCTCCCCGAGAGGACATTTGTGATGACAA	1683
QY	1482	AGGATGCCAGTGTGATGTATCAGTGGAGAACTTCAACCCACACACTTAATAACTGTCAATCG	1541
Db	1684	GAGCTGCCCCCTGCGGATTTGTGACCGAAGACCTGACCCCGGGCTCAAAAGTCAGCATGAG	1743
QY	1542	AGCTATCAGAAATTAATTAATTTTCATGTTGCAAAACGAAAGTTTAAGAAACATTACGTCG	1601
Db	1744	AGCGGTGTGTGCATGCGGTTCTGTGTGCCAAAGGGAAGTTTCAAGAGAGACCTGCGGCC	1803
QY	1602	ATATGATGTAAAAAGATGTTCATTTGAAACATATTTCTGCTGGTCAATGCGCATGTGTGTAG	1661
Db	1804	CTACAGACGTGAGGACGTATCTAGCAGAGTACTCAGCCGGCACTTGGACATGTCTGCCG	1863
QY	1662	AATTAAGACCTTCAACACAGCTGTGTGATCAATTTTGGAAAGGGCAAAATCACATCAGA	1721
Db	1864	AATTAAGACCTTGCAGTCCAGAGTGGACCAAGATCTGTGGGGGGGGCCACAGGATACCGA	1923
QY	1722	TAAAGAGACCGAGAGAAAATATACAGCAGAACATAGACACACAGACATCTCAGTACTCT	1781

```

Db      1924  CAAAGG---CCGACCAAGGCGCCGCGAGGAGCTGCCAGAGACCCACACATAT 1980
QY      1782  CGGTGCGGTGTCAGAGTGAAGAAACAGTACAGTCCATGATCCAGCTGAGTGCCT 1841
Db      1881  GGGAGCGGCTCGGGAGGAGGAGGAGGCTGCTCCATGAGAGAGAGAGTGCAGTCTCT 2040
QY      1842  ACTAGACATCTATCAACAG 1860
Db      2041  GGTGAATATCTACATGCAG 2059

RESULT 26
AF087453 4165 bp mRNA linear ROD 27-SEP-2001
LOCUS Rattus norvegicus potassium channel (KCNO2) mRNA, complete cds.
DEFINITION AF087453
VERSION AF087453.2 GI:15795325
KEYWORDS
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4165)
AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Cloning and sequencing of the Rattus norvegicus potassium channel
JOURNAL KCNO2
REFERENCE 2 (bases 1 to 4165)
AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) University of Marburg, Inst. for
Physiology, Deutschnaust. 2, Marburg 35037, Germany
REFERENCE 3 (bases 1 to 4165)
AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) University of Marburg, Inst. for
Physiology, Deutschnaust. 2, Marburg 35037, Germany
REMARK Sequence update by submitter
COMMENT On Sep 27, 2001 this sequence version replaced gi:3641299.
FEATURES
source
1..4165
location/Qualifiers
1..4165
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="brain"
1..4165
/gene="KCNO2"
123..2681
/gene="KCNO2"
/codon_start=1
/product="potassium channel"
/protein_id="AAC36722.1"
/db_xref="GI:3641300"
/translation="MVQSRMGVYVPGTSGEKKLVGVGVDLPDGPADSTRDGLIAG
SEAPKRSVSKPTGCGAGAKPRKRNFKLQNFVLEPRKMAITIAVYVL
VECVLIVSTIKETKSSGALYIEIVIVGVEYEVVIMAGCCCRKRGWGR
LKRARPCVVIDWLVASIAVLAGSGNENFATSLRLQLRLMRMRGSGTW
KLGSVVAASKELVAMVIGFCLILASFLVLAKEGENDFDYADLMGLITLV
TIGYDKYPTQWNGRLAATFTLIGVFFALIGSGFALKVOEHOHKEREN
PAGLIOSARFYATNSRDLSTWQYESTVVPMTSSQCTGASLPIINDLE
MLNLTSGSLTRKEPQSPSPQKYSLKRVSSPGVAKGKSPDAOTVRSPS
ADSLDPSKVRKSMFSGDRARQARIRIGASRONSSEASLFGEDVDNKSNC
EFTEDTLPGLKYSIRAVCVARFLVSKRKFESLAPYVMDVTEQYSAHLMLSIK
SLASRDQIVRGPTITDKDRKGPAETELDEDSMGRLGVEKQVLSMEKLDLIV
SITQRMGIPAEETFAFGAKPEPAPYHSDRQADKHCITIKIVRSSTGR
KYAAPVMPPEACPEPSTSMOOSHQRHGSFVGDHSIVIRIPPAHERSLISVSGNR
ASFEPLRGSTPACRSEALRDSPTISITSPYHEHLERSSGSISQSKENLNLAA
SCAAAVPCKAVPYRIAGESDPTSDICTPCGPPPRSATGEGFEDVAMAGPRK"
BASE COUNT 866 a 1194 c 1203 g 902 t
ORIGIN
Query Match 16.2%; Score 448.4; DB 10; Length 4165;

```

```

Best Local Similarity 56.1%; Pred. No. 2.6e-86;
Matches 1023; Conservative 0; Mismatches 666; Indels 135; Gaps 4;
QY      169  GGCCTGCTACTGCTGGGACCCGCGGCGCACACGCTGGTGCGGCGGCTGGAGG 228
Db      189  GCGTTGGTGGGCTGAGACCCGCGGCGCGCCGACATCCACTCCGAGCGGCGTACTCATC 248
QY      229  GAGAGCCCGCGGCGCAAGCAGCGGGGCGCGATGAGCTGTGGGAGACCGCTCTTAC 288
Db      249  GCGGCGTCCGAGCGCCCGCAAGCGCGGCGCATTTTGAACAAGCGCGAGCGGCGGCG 308
QY      289  ACGAGTAGCCAGAGCTGCCGCGGAGGAGTGAAGTGAAGTGGGAGCAACACTGATAC 348
Db      309  GGAAGCGGGAAGCGCCCAAGCGGAGCGCTTCTACGCGAAGCTGCAAAATTTCTATAC 368
QY      349  AACGCTCTGAGAGACCCCGCGGCTGGCGCTTCACTACACAGCTTGGTTTCTCTCT 408
Db      369  AACGCTCTGAGAGCGGCGCGCGGCTGGCGCTTCACTACACAGCTTGGTTTCTCTCT 428
QY      409  GTCTTGGTGGCTTGAATTTTGTCAAGTGTCTTACATCCCTGAGACACAATAATYGGCC 468
Db      429  GTCTTCTCTGCTCTGCTTGTCTTCCGCTTTCCACATCAAGAGATAGAGAAGATYCC 488
QY      469  TCAAGTGGCTCTTGAATCCCTGGAGTGGTGTGATGATGATGATGATGATGATGATG 528
Db      489  GAAAGGCGGCGCTCTACATCTTGAATGATGATGATGATGATGATGATGATGATGATG 548
QY      529  ATTGATCTGTCTGCGGCGGCTGCTGTGATATGATGATGATGATGATGATGATGATG 588
Db      549  GTGAGATCTGGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY      589  TTTGCTGGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
Db      609  TTTGCTGGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
QY      649  GTTCTGCAAAAACCTCAGGAGTAATATTTTCCACATCTGCTGCTGCTGCTGCTGCTG 708
Db      669  CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
QY      709  CTACAGATCTCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db      729  TTACAAATCTTACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 788
QY      769  TCAGTGGTTATGCTACACAGCAAGAAATTAATACAGCTTGTATAGATGATGATGAT 828
Db      789  TCGGTGCTTACGCTACACAGCAAGAGCTGATGATGATGATGATGATGATGATGATG 848
QY      829  CTATTTTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
Db      849  CTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
QY      889  ACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
Db      909  ACCTAGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY      949  AAACTCCCTTAACCTTGGCTGGGAGATTTCTTTCGACGGCTTGGCATCTTGGCAT 1008
Db      969  AAGTACCTTCAGACCTGGAAGGAGGCTGTTAGACGACGCTTACCCATCTGCTGCT 1028
QY      1009  TCTTTCTTTCGACCTTCTGCGCGCATTTCTTGGCTCAGGTTTTCATTAAGATCAAG 1068
Db      1029  TCATCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
QY      1069  CAACAGCGCGCAACACTTTAGAGAAAGAAAGAACCGGAGCCCAACCTCATCTAG 1128
Db      1089  CAGATCGGCAAAAACACTTTAGAGAAAGCGGAAATCTGCGGAGGCTGATCCAGTCT 1148
QY      1129  GTTGGCGGTACTTACGAGCT----- 1149
Db      1149  GCTGAGATATCTATGCTACTTACCTTCACGACCGACGACCTGACCTGACGAGTAC 1208
QY      1150  GATGAGAAATCTGTTTCCATCTGCAACCTGGAAGCCACACTTGAAGGCTTGCACAC 1209

```



```

Db      1027 GCCTGAGATCTACGCCACCAACCTCTGGCGACAGACCTGACCTCCAGCTGGCACTAC 1086
Qy      1153 ---GGAATATCTGTTCCATTGCAACCTGGAGGCCACTTGAAGCCCTTGCACACCTGC 1209
Db      1087 TACGAGCGCAACGCTACCGCTGCCATGTACAGTTTCCAAACTCAACCTACGGGGCTCC 1146
Qy      1210 AGCC----- 1213
Db      1147 AGACTTATCCCCCGCTGACACAGCTGGAGCTGCTGAGAACCTCAAGAGTAAATCTGCA 1206
Qy      1214 -----CTACCAATCAGAAGCTTAAGTTTAA 1239
Db      1207 CTCGCTTTCAGGAGAGACCCCCCGCGGAGCCGCTCCAAAGCAGAGAAGCTTGTGAA 1266
Qy      1240 GAGCAGTGGCGATGGCTGAGCCCGAGGGCCAGAGATTAAAGACCCGACAGAGCTTCACTA 1299
Db      1267 GATCGTGT---CTTCTCAAGCCCCCGAGCGCTGGCCCAAGGGGAGGGGCTCCCGCAG 1323
Qy      1300 G-----GTGACAGAGAGTCCCGCAAGCAACGACATCACAGCCGAGGAGAGTCCACCAAA 1353
Db      1324 GCCCAGACTGTGAGCGGCTGACCCAGCGCGGACAGAGCTGAGAGACAGCCCGACAG 1383
Qy      1354 GTGAGAGAGCTGAGAGCTTCAACAGCAGACCCGCTTCCGCGCTCCGCTGCGCTCAAA 1413
Db      1384 GTGCGCAAGAGCTGAGCTTGGGGAGCCGACCCGCGGACGCGCAGGCTTTCGCGATCAAG 1443
Qy      1414 AGTTCTAGACCCAAACAGTATAGATCTGACACAGCCCTTGGCACTGATGATATAT 1473
Db      1444 GGTGCGCGGTC---ACGGCAGACACTCAAGAGAGAGAGCTCCCGGAGAGACATTTG 1500
Qy      1474 GATCAAAAAGAGTCCCACTGTGATGTATCAGTGAAGACCTCCACCCACTTAAACT 1533
Db      1501 GATACACAAGAGCTGCGCTGCGAGTTTGTGACCCGAGAGAGCTGACCCCGGCTCAAAAGTC 1560
Qy      1534 GTCATTTGAGCTATCAGATTAATGATTAATTTGATTTGCAAAAGGAGTTTAAAGAACA 1593
Db      1561 AGCATCAGAGCGCTGTGTGTATGCTGCTGCTGCTCAACCGGAGTTCAAGAGAGAC 1620
Qy      1594 TTACGTCATATGATGTAAGAAAGATGTCATTAATTTGCTGCTGCTGCTGCTGCTGCTG 1653
Db      1621 CTGCGCGCTTACGAGCTGATGAGCTGATGAGCTGATGAGCTGATGAGCTGATGAGCTG 1680
Qy      1654 TTGCTGATTAATTAAGCTTCAAAACAGCTGATGATCAATTTCTTGAAAGAGGCAATTC 1713
Db      1681 CTGTCCTCCATTAAGCTGCTGATGCTGAGAGTGAACGATCTGCGGCGGCGCCAGCG 1740
Qy      1714 ACATCAGATTAAGAGAGCCGAGAGAAATAACAGACAGAAATGAGACACAGAGATCTC 1773
Db      1741 ATCAGGAGCAAGGA---CCGACACAGAGGCGCGCGGAGGAGCTGCCGAGAGACCC 1797
Qy      1774 AGTATGCTCGGTGGGTGCTGAGGTTGAAAGAGAGTACAGTACAGTAAATCCAGCTG 1833
Db      1798 AGCATATGAGGAGCGCTCGGAGAGGAGTGTGAGAGAGAGCTGCTCATGAGAGAAAGCTG 1857
Qy      1834 GACTGCTACTAGACATATATCAACAG 1860
Db      1858 GACTTCTGCTGATATCTACATGACAG 1884

```

```

RESULT 28
AF087454      5927 bp  mRNA  linear  ROD 27-SEP-2001
LOCUS      AF087454
DEFINITION  Rattus norvegicus potassium channel (KCNQ3) mRNA, complete cds.
ACCESSION  AF087454.2 GI:15795326
VERSION    AF087454.2 GI:15795326
KEYWORDS
SOURCE     Rattus norvegicus.
ORGANISM   Rattus norvegicus.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 5927)

```

```

AUTHORS      Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE        Cloning and Sequencing of the Rattus norvegicus potassium channel
              KCNQ3
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 5927)
AUTHORS      Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE        Direct Submission
JOURNAL      Submitted (26-AUG-1998) University of Marburg, Inst. for
              Physiology, Deutschausstr. 2, Marburg 35037, Germany
              3 (bases 1 to 5927)
AUTHORS      Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE        Direct Submission
JOURNAL      Submitted (27-SEP-2001) University of Marburg, Inst. for
              Physiology, Deutschausstr. 2, Marburg 35037, Germany
REMARK       Sequence update by submitter
COMMENT       On Sep 27, 2001 this sequence version replaced gi:3641301.
FEATURES
source
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
    /tissue_type="brain"
    1..5927
gene
    /gene="KCNQ3"
    428..3049
    /gene="KCNQ3"
    /codon_start=1
    /product="potassium channel"
    /protein_id="AAC36723.2"
    /db_xref="GI:15795327"
    /translation="MGAKARRAAGAGAGGGGGGGGGGGAANPAGDSAVAGDERV
    GLADVEQVETALGTGADKDTLLGGGREGGRRPQIGLILATPLSRPKRN
    AKYRIOTLIYDLERGRWALYHALYPLIVLACLLAVITTEKEIVSGDWLL
    ERTAIFTEGEPALRTIACCCCKRYKMRGLKFAKPLCLMLDFVLAIVAVAGN
    OGNVLAISLRFLOTLRLMDRREGTWKLISATCAHSEKELITMYIGFLILIS
    SFVLYVEKDPMDAGEEMKEFEYAAALMGLITLATITGYDPTKTEGRLIA
    ATESLIGVSFFALPAGLISGLALVQEOHOKFEKRRPAELIOAAMRYATNP
    RLDVATWREYSESVSPFPRKDELAASOKGLDRVRLSNRGSNTGKLTPTN
    VDAIESPSKEPVGILNKRERTATRAKAAVAFWSSDEAGCTDPTMBDGYNDPL
    IEMIPITKAIRAVRIORRYLKKKKETLRLPDVADYIEQYSAGHLDMLSRKTLQ
    KYRQVDMKKLIDFLVDMHOMERLQVHTLEYYPKLGASSPAEGKAKDNRYSDK
    TIIICNSESQPPDPYSFHQVPIDRVGPYFPHADPYKLRGSGSTRAADNPSSGS
    TYAERPLVILILDLSCVSHSQTELOGYSPIHISPRORSITRDSDTPLMSVNH
    EELERSPGFSISQDRDDYVFPGSGSSMREKRYLAEGFTDITDPTFGSMPMS
    TGDIDSDIWTPTNKPT"
BASE COUNT   1530 a 1455 c 1430 g 1512 t
ORIGIN
Query Match      15.9%; Score 440.4; DB 10; Length 5927;
Best Local Similarity 57.1%; Pred. No. 1.5e-84;
Matches 969; Conservative 0; Mismatches 669; Indels 58; Gaps 7;
Qy      50 GGGTGAAGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCTTGGGACGCGCATGA 109
Db      460 GGGCGGCGGGGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
Qy      110 AGGATGTGAGATCGGCGCGCGGAGGAGGCTGCTGAACCTCGGAGCGCGCAAGGGGCGAGC 169
Db      520 AGG-GGACTCGGCAAGTGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
Qy      170 GCCTGCTACTGCTGGGACCCGCGCGCCACAGCTCGGTGGGAGGCGGCGGCTGAGGG 229
Db      579 TGGAGCAAGTCACTTGCGCGCTGAGGACGAGACCAACAAAGACGGGAGACCTGCTGTG 638
Qy      230 AGAGCGCGCGGGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
Db      639 AGGGCGGTGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
Qy      290 CGAGTAGCAGAGAGCTGCC-----GGCGCAAGCTCAAGTCCGCGGGGCGAGAGT 340
Db      699 AGACCCCGCTGAGCGCTGCAAGTAAAGAGAAACAGCCCAAGTACAGGCGCATCAACCTT 758
Qy      341 ACCTGTACAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 400

```

```

Db      759 TGAATATGAGCGCCCTGAGAGAGACCGAGGGGCTGGGGCTCTACACACGGCGCTTGT 818
QY      401 TTCTCCCTGCTTGGTGGCTGATTTTGTAGTTTCTACCATCCCTAGACACAA 460
Db      819 TCGTGAATGTCCTGGGATGCTTGTGCTGGCCGCTGACACATTTCAAGGATATGAGA 878
QY      461 AATTGGCCTCAAGTGGCTCTGATCTGATCTGATGATGATGATGATGATGATGATGAT 520
Db      879 CTGTGCTGAGAGACTGGCTTGTGCTGGGAAACATTTGATTTTCACTTTGAGAGCTG 938
QY      521 AGTTTCATCATTCGATTTGCTGCGGGTTCCTGTTGCAATATAGAGAGATGCAAGAA 580
Db      939 AGTTTGGTTCGAGATCTGGGCTGACAGATGCTGCTGATACAAAGCGCTGGCTGAC 998
QY      581 GATGAGGTTTGGCGAAGCCCTTGTGTTATAGATACATTTGTTTTCCTTCA 640
Db      999 GCGTGAAGTTTGCAGAGAGCCCTGTGATGATGATGATGATGATGATGATGATGAT 1058
QY      641 TAGCAGTTTGTTCGAAAACTCAGGATATATTTTTCACGCTGCTCAGTACAGAGTC 700
Db      1059 TGGCAGTGGTGGCGGTAACCAAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1115
QY      701 TCGCTTTCCTACAGATCTCCGCAATGCTGCGCATGAGACGAGGGGAGGCACTTGAAT 760
Db      1116 TCGCTTTCCTGAGATCTCCGCAATGCTGCGCATGAGAGAGGGGAGGCACTTGAAT 1175
QY      761 TACTGGTTCAGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
Db      1176 TCGTGGCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1235
QY      821 TTTTGGTTCATTTTTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 871
Db      1236 TCTGACACATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1295
QY      872 -----CCAATAAGATTTTCTACATATGACATGCTCTCTGCT 910
Db      1296 TGGATGCCCAAGAGAGAAATGAAGAGATTTGAACCTATGCTGATGCTGCTGCTG 1355
QY      911 GGGGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 970
Db      1356 GGGGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1415
QY      971 GAAGATGCTTTCAGAGCTTTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1030
Db      1416 GAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1475
QY      1031 GCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Db      1476 GCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1535
QY      1091 AGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1150
Db      1536 AGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1595
QY      1151 ATGAGAAATGCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
Db      1596 ACCCAAGAGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1655
QY      1202 ACACCTGAGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
Db      1656 CATTTCTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1715
QY      1262 CAGAGGCTGAGATTAAGAGCGGACAGCTCAGTGTGAGAGAGAGAGAGAGAGAGAG 1321
Db      1716 GGGTGGCTTTCATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1775
QY      1322 CCGACATCAAGAGCGAGGAGAGCTCCACCAAGTGCAGAAAGAGCTGAGCTTCAAGAG 1381
Db      1776 ATGTAGATGCTATGAAGAAAGCGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAG 1835
QY      1382 GAACCCGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441

```

```

Db      1836 AAGAGCGTTTCGACACCGCTTCGCGCATGAAGCT-----ACGCTTTCGCAAGTT 1889
QY      1442 CTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1501
Db      1890 CTGAAATGCGGGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1949
QY      1502 CAGTGAAGAGCTTACCCACAGCACTTAAACCTGATTCGATGATGATGATGATGATGAT 1561
Db      1950 TCATTAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
QY      1562 TTTATGTTGAAAACGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 1621
Db      2010 TCGCTGATTAATAAAAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 2069
QY      1622 TTGAACAAATTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681
Db      2070 TTGAGCAGATTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY      1682 GTGTTGATCAAAATCT 1697
Db      2130 GAATGATATGATTTT 2145

RESULT 29
AB000494
LOCUS
DEFINITION
AB000494 Mus musculus mRNA for alternative splicing; see accession between
AB000494 and AB000504, complete cds.
ACCESSION
AB000494
VERSION
AB000494.1 GI:4176393
KEYWORDS
mKOT2.1; alternative splicing.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
Sasai, H. and Nishi, Y.
KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
Recept. Channels 5 (5), 255-271 (1998)
98330948
2 (bases 1 to 2935)
Watanabe, H.
Direct Submission
Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
Pharmaceutical Basic Research Lab., 6-2, Umeogoka, Aoba-ku,
Yokohama, Kanagawa 227, Japan (E-mail: watanabe@ctrl.jti.co.jp,
Tel: 045-972-5741)
FEATURES
source
location/Qualifiers
1..2935
/organism="Mus musculus"
/db_xref="taxon:10090"
87..2366
/note="mKOT2.1"
/codon_start=1
/product="alternative splicing; see accession between
AB000494 and AB000504"
/db_xref="GI:4176394"
/protein_id="BA37156.1"
/translation="MWOSNRNGGVPTGSEKKLVGVGLDGPAPDSTRDGLLIAG
SEAPKRSVLSKPRTGAGAGKPKRAAFRLKQNFVLYNLERGAFVTHAVFLL
VESCILVSTSTKEYKESSEGLALILEITVIVGVEYVRIYTAACCCGYSRMBGR
LFAKRPFCVIDIMVLAVLAVLAAGSGVAFATSAIRLSRFLDILMIRDRRGCTH
KLGSVVAHASKELVTAWYIGFLCLILASFLVLAEGENDHPTVDALWGLITLT
TIGGDKRYDPTWNGRLAATFTLIGVFPALPGIILSGFLAKVOBHRPHEKRRN
PAAGLIOSARFATJNLSTDLSTWYERYVAPYRLPLPLNOLELLNLKSKSG
LFRKREPOPEPSPOKYSVLTDYVSSRGAAGVSGROQTVRSRPSADSLSDSSG
KPKSKSFGDRSTRQAFRIKGAASRNSSEASLPGDYLIEDNKSCEPVEDLTRC
LKVSIKAVCWRLVLSKRFKESURPDMVDVLEQVSGHLDMLSKLSQSRIDMLY
GPPSPTRDCKYPTKGPATPSRSPDYSPRVHIVGSGPTIDDKRTKGAELELPE
DPSMGRILKVERQVLSMEKKLDFLVSITYORMGIPPALETEAYGAEPEPAPYHSP

```

polyA_site
 EDSRDHAKHCIIIVKIRSTSSIGORNYAPPAIPACPPSTSMOOSHORHGTSPVG
 DHGSLVRLERSAGMSCH*
 2935
 /note="20 a nucleotides"
 BASE COUNT 615 a 871 c 839 g 610 t
 ORIGIN

Query Match 15.8%; Score 437.2; DB 10; Length 2935;
 Best Local Similarity 56.5%; Pred. No. 6,6e-84;
 Matches 924; Conservative 0; Mismatches 608; Indels 102; Gaps 2;

169 GGCCTCTACTGCTGGGACACCCGCGCCACAGCTCGGTGGCGGGGGGCTGAGG 228
 133 GGCCTCTGAGGCTGACCCCGCGCCGCTCCTACACAGCGAGCGGCGCTACTCATC 212
 229 GAGAGCCCGCGGGGCAAGAGGGGCGCGGATGAGCCTGCTGGGGAGCCGCTCTTAC 288
 213 GGGGGCTCGAGAGGCCCGCCAGCGGAGCTTTGAGCAAGCGCGGAGCGGGCGCG 272
 288 ACGAGTACCCAGAGCTGCGCGCCAGCGTCAAGTACCGGGGCTGACAGACTACCTGAC 348
 273 GAGCGCGGAGAGCCCGGAGGCGCTTCTACAGCGCTGAGCAAGTTCCTCTAC 332
 349 AACGCTGAGAGAGACCGCGGCTGCGCTTCTACATTCACAGCTTTGTTTCTCTT 408
 333 AACGCTGAGAGAGCGCGCGCGCTGCGCTTCTACATTCACAGCGCTTCTCTTCTT 392
 409 GCTTCTGCTGCTGATTTTGTGCTGCTTCTACATTCCTGAGCAGACAAATTTGCGC 468
 393 GCTTCTGCTGCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 452
 469 TCAAGTCTGCTCTGATTCCTGAGGCTGCTGATTTCTGCTTCTGCTTCTGCTTCTG 528
 453 GAGGGGCGCTTCTACATTCCTGAGGAGTCTGCTGCTTCTGCTTCTGCTTCTGCT 512
 529 ATTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 513 CTGAGAGATCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 589 TTTGCTGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 573 TTTGCTGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 649 GTTCTGCAAAAAGTATGATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
 633 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 709 CTACAGATCTCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 693 TTGCAAACTCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 769 TCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 753 TCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 829 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
 813 CTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 889 ACATATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
 873 ACCTATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 949 AAAATCTCCCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
 933 AAGTACCTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
 1009 TCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 993 TCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 1069 CAACAGCCCGCAAGACCTTGTAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128

Db 1053 CAGCATGCGCCAAAACACTTTGAGAAAGCGGAGAACCTTGCGGACAGTCTGATCACTCT 1112
 QY 1129 GTTGGGCTACTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACAC 1188
 Db 1113 GCTGGAGATTCTATGCTACTTACCTCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1172
 QY 1189 TT----- 1190
 Db 1173 TACAGAGGAGACGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 QY 1191 -----GAGGCTTGCACACTGC 1209
 Db 1233 CTGCTGAGAACTCAAGAGCAAAATCTGAGACTCACCTTGAGAGAGGACACAGCAGAG 1292
 QY 1210 AGCCCTACATCAAGAACTGATTTTAAAGGCGAG---TGCATGCTGCTGCTGCTGCTGCT 1266
 Db 1293 CCATCACCAGTCAAGAGGCTGATTTGAAAGTCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1352
 QY 1267 GGCAGAGTATTAGAGCGCGAGAGCCCTCAGTAGGTGACAGAGAGTCCCAAGCAGCAGAC 1326
 Db 1353 GCTGCCAAGGAGAAAGGGGTCTCCCAAGGCGCAGAGCGGTCCGGCGTCCCGCAGTGGGAT 1412
 QY 1327 ATCAGACCCGAGGAGCTCCACCAAGTGCAGAAAGCTGAGCTTCAACGACGCAACC 1386
 Db 1413 CAGAGTCTTATGACAGCCGAGGAGAGGCTGCCAAGAGCTGAGCTTTGCTGACCCAGC 1472
 QY 1387 CGCTTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
 Db 1473 CGCAGACGCCAGGCTTTCCGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1532
 QY 1447 ACAAGCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
 Db 1533 AGCCTCCCTGGGAGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1592
 QY 1507 GAAGACCTCAACCCACACACTTAAAGCTCATGAGCTATGAGATTTGAATTTTCAT 1566
 Db 1593 GAAGATCTTACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1652
 QY 1567 GTTGCAAAAGGAGATTAAAGAAACATTAGCTCATGATGATGATGATGATGATGATGAT 1626
 Db 1653 GTTGTAAAGGAAAGTTCAAGAGAGTGTGCGCCCATGATGATGATGATGATGATGATGAT 1712
 QY 1627 CAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
 Db 1713 CAGTACTCGGCTGAGCACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1772
 QY 1687 GATCAATCTCTG 1700
 Db 1773 GATATGATGATGATG 1786

RESULT 30
 A94974
 LOCUS A94974 3029 bp DNA linear PAT 26-JUN-2000
 DEFINITION Sequence 1 from Patent WO9931232.
 ACCESSION A94974
 VERSION A94974.1 GI:6779160
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 3029)
 AUTHORS Christian, E.P. and Alvar, J.
 TITLE HUMAN BRAIN DERIVED KCNO2 POTASSIUM CHANNEL
 JOURNAL Patent: WO 9931232-A 1 24-JUN-1999;
 ZENECA LTD (GB)
 FEATURES
 source location/Qualifiers
 1..3029
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 546 a 972 c 1004 g 507 t
 ORIGIN

QY 1622 TTGAACATATTTCTGCTGTCATCTGACATGTTGTAGATTAAGCCTTCAACAC 1681
 DB 1643 TTGAGAGATTTGCGCGGACATCTTGACATGTTTCCAGAGTAAGTACTACACACA 1702
 QY 1682 GTCTGATCAATTCCT 1697
 DB 1703 GATATGATATGATTTT 1718
 RESULT 32
 AB000495
 LOCUS
 DEFINITION AB000495 2920 bp mRNA linear ROD 23-JAN-1999
 AB000494 and AB000504, complete cds.
 ACCESSION AB000495
 VERSION AB000495.1 GI:4176395
 KEYWORDS mKOT2.2; alternative splicing.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (sites)
 Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,
 Sasai,H. and Nishii,Y.
 KOT2, a new putative potassium channel family produced by
 alternative splicing. Isolation, genomic structure, and alternative
 splicing of the putative potassium channels
 Recept. Channels 5 (5), 255-271 (1998)
 98330948
 2 (bases 1 to 2920)
 Watanabe,H.
 Direct Submission
 Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
 Pharmaceutical Basic Research Lab., 6-2, Umeogoka, Aoba-ku,
 Yokohama, Kanagawa 227, Japan (E-mail:watanabe@crl.jti.co.jp,
 Tel:045-972-5741)
 FEATURES
 source
 location/Qualifiers
 1..2920
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 87..2351
 /note="mKOT2.2"
 /codon_start=1
 /product="alternative splicing; see accession between
 AB000494 and AB000504"
 /protein_id="BA37157.1"
 /translation="MVOKSRNGVYPTGSGERKLVGFVGLDPGAPDSTRDGLIAG
 SEAPRGSVLSKPTGAGAGKPKRNALFRLNLFVNLPRGMALFYHAYVELL
 VESGLIVSESTIEKESSEGLYIEIVIVGVFVRYVMAAGCCFRGMGR
 LKAPRKPCVYDIDVILASTIVLAAGSGNPAISALSLRIOLIRMRMRGGTW
 KLGSVYVANSKELVTAYITGFLIILASFLVYLAKEENHFDIYADALMGLITLT
 TIGGDKYPTQWNRLLAATTLIGVSFFALPGILGSGFALKVOQHPRKFERRN
 PAAGLIOSAMFYATNLSTLDHSTWOYERIVPMYRLIPLMLLELRMLKSKS
 LTFPEKEQPEPSPQKSLKDRVSPRGMAGKSGPOAQRSPSPADSDIDSPS
 KVPKSWSEGRDSTROAFRIKGAARONSEASLGEEDIVEDNKCNCFEVEDLTPG
 LKSVIRACVWRPRTVSRKREKESLRPYDVYVITEOYSAHLDMLSRKISLOSREP
 VQSGHEGPPRONAMHKHGGGLGDRVDHYVGRPTITDKDKTKPAETLEPDBSM
 GRUKVERKOVLSMKKLDLVSITYTORMGIPPAETEAFLGAEPEAPAPYSPEDSRD
 HADHGCIILIKIVRSTSTGORNPAIPAACPSPSTWSDSHORHGHSPGDHGL
 VLRLERSAGMWSCH"
 2920
 /note="20 a nucleotides"
 BASE COUNT 611 a 858 c 849 g 602 t
 ORIGIN
 polyA_site
 Query Match 15.6%; Score 433; DB 10; Length 2920;
 Best Local Similarity 56.4%; Pred. No. 5.4e-83;
 Matches 921; Conservative 0; Mismatches 610; Indels 102; Gaps 2;
 QY 169 GGCCTGCTACTGCTGGGACCCGCGGACGCTGCTGGCGGCGGCTGAGCCTGAGG 228
 111 1 1 1111 1 11111 1 111111 1111111 11 1

DB 153 GCGTTCGTGGGCTGAGACCCCGCGCCGAGCTCCACAGCGAGCGGCTACTATC 212
 QY 229 GAGAGCGCGCGGCGAAGAGGCGCCGGATAGAGCTGCTGGGGAAGCGGCTCTTAC 288
 DB 213 GCGGGCTCGAGAGCCCGCAAGCGCGAGGTTTGAGCAAGCCGCGAGCGGCGCGC 272
 QY 289 ACGAGTAGCCAGAGTGCAGCGCCGCAACGTCAGTACGCGCGGCGGAGCAAACTACTATC 348
 DB 273 GAGCGGGAAGAGCCCGGAGAGCGCAAGCGCAAGCGCTTCTACGCAAGCTGCAATTCCTCTAC 332
 QY 349 AACGCTGAGAGAGACCCGCGGCTGGCGCTTACATCTACACGCTTTCCTTCTCT 408
 DB 333 AACGCTGAGAGAGCGCGCGGCTGGCGCTTACATCTACACGCTTTCCTTCTCT 392
 QY 409 GCTTGTGCTGCTGATTTTGTGAGTGTTCACATTCCTGAGCAACAAAATTTGACC 468
 DB 393 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452
 QY 469 TCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
 DB 453 GAGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
 QY 529 ATTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 DB 513 GTGAGGATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 QY 589 TTGCTGCGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 DB 573 TTGTCAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 QY 649 GTTTCGCAAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
 DB 633 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 QY 709 CTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 DB 693 TTGCAAAATCTGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 QY 769 TCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 DB 753 TCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 QY 829 CTTATTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
 DB 813 CTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 QY 889 ACATATCCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
 DB 873 ACCTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 QY 949 AAAATCCCTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
 DB 933 AAGTACCTCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
 QY 1009 TCTTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 DB 993 TCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 QY 1069 CAACACGCGCAAGAACTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1128
 DB 1053 CAGATAGGCGCAAAACCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1112
 QY 1129 GTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
 DB 1113 GCGTGAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
 QY 1189 TT----- 1190
 DB 1173 TAGAGAGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 QY 1191 -----GAAGGCTTGGACACACTGC 1209
 DB 1233 CTGCTGAGGATCTCAAGAGCAAAATCTGACTACCTTTCAGAGAGGAGCAGAGCAGAG 1292

QY	1210	AGCCCTAACCATCGAAGCTAAGTTTAAAGAGCGAG---	-TGGCATTNGGTATGCCACG	1260
Db	1293	CCATTCACCAAGTCAAGAGGTAGTTTGAAAGTTCGTCTTCCACGCCCCGAGGGATG	1352	
QY	1267	GGCCAGAGTATTAGAGCCGACCAAGCCCTCAGTAGGTGACAGAGAGTCCCAACACCGAC	1326	
Db	1353	GCAGCCAAAGGAAAGGGGGTCTCCCAAGGCCACGAGAGGTCCGGGGGTCCCCAGTGGCGAT	1412	
QY	1327	ATCCACAGCCGAGGGCACTCCACCAAGTGCAGAAAGAGCTGGAGCTTCAACGACCGAAC	1386	
Db	1413	CAGAGTCTTGATATACACAGCCGAGCAAGGTGCCAAGAGCTGGAGCTTGGTGAACCGCAGC	1472	
QY	1387	CGCTTCGGGCGCTTCGCTGCGCCTCAAAAAGTTCTCAGCCAAACCAATGATAGATGCTGAC	1446	
Db	1473	CCGACACGCCAGGCTTCCCGCATTAAGGGTGTGCATCCCGCAGATTCAGAAAGAGCA	1522	
QY	1447	ACAGCCCTTGGGCACTGATGATGATATGATGATAAAAAGATGCCAGTGTATGATCATGTG	1506	
Db	1533	ACCTCTCCCTGGGAGAGCATCTGTAGAGGACAAACAGAGCTGTAACTGCCAGTTGTGACT	1592	
QY	1507	GAAAGACCTACCCACACACTTAAACGTCTCATTCAGCTATACGAATTATGAAATTTTCAT	1566	
Db	1593	GAGAGTCTTACCTCCCTGGCTCAAAAGTTAGCATCAGAGCTGTGTGTATTGCGCTTCTTG	1652	
QY	1567	GTTCGCAAAACGGAAGTTTAAAGAAACATTACGATATGATGATTAAGATGTCATTGAA	1626	
Db	1653	GTATCTAAGGGAAGTTCMAAGAGAGTCTGGCCCATATGATGTATGACATGCTATCGAA	1712	
QY	1627	CAATATTTCTGCTGTGTCATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTGT	1686	
Db	1713	CAGTACTCCGGCTGGACACTGTGATATGTGTGCCGATCAAGAGCTGTGCAATCCAGGCA	1772	
QY	1687	GATCAAAATTCCTTG	1699	
Db	1773	GAGCCCTGCTG	1785	
RESULT 33				
AB000498				
LOCUS	AB000498	2382 bp	mRNA	linear
DEFINITION	Mus musculus mRNA for alternative splicing: see accession between			
ACCESSION	AB000498			
VERSION	AB000498.1	GI:4176401		
KEYWORDS	mk02.5; alternative splicing.			
SOURCE	Mus musculus cDNA to mRNA.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;			
AUTHORS	1 (sites)			
TITLE	Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,			
JOURNAL	K02, a new putative potassium channel family produced by			
MEDLINE	alternative splicing. Isolation, genomic structure, and alternative			
REFERENCE	splicing of the putative potassium channels			
AUTHORS	98330948			
TITLE	2 (bases 1 to 2382)			
JOURNAL	Watanabe, H.			
FEATURES	Direct Submission			
SOURCE	Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,			
	Pharmaceutical Basic Research Lab., 6-2, Umeogoka, Aoba-ku,			
	Yokohama, Kanagawa 227, Japan (E-mail:watanabecrl.jti.co.jp,			
	Tel:045-972-5741)			
	Location/Qualifiers			
	1..2382			
	/organism="Mus musculus"			
	/db_xref="taxon:10090"			
	87..1799			
	/note="mk02.5"			
	/codon_start=1			
	/product="alternative splicing: see accession between			

[illegible]

Db	873	ACCTAGCGAATGACACTCTGTTGGGGGCTGATACACCTGACGACCAATTGGCTACGGGGAC	932
Oy	949	AAAACCTCCCTAACTTGGTGGGAAGATTCTTTTCTGAGAGCTTTGACATCTTTGGCATTT	1008
Db	933	AACTAACCTTGAACCTTGGAAAGGGAGGCTCTGGACAGCACTTTTACCTTCATTGGTGTG	992
Oy	1009	TCCTTCTTTTGCACATCTCCCTGGGCACTTCTTGGCTCAGGTTTTCATTAAGAATGACAAGA	1068
Db	993	TCGTTCTTTCTCTCTCTCTCTGCTGGCATTTTGGGATCCGGCTTTTGCCCTGGAAGTCCAAAG	1052
Oy	1069	CAACACCCGCAAGAAACATTGTGAAAAAGAGAACCCACCTGGCAACTTCATTACGTG	1128
Db	1053	CAGATCTGGGCAAAAACCTTTGGAGAAAGCGCGGAACCTCTCGGAGAGTCTGATTCAGACT	1112
Oy	1129	GTTTGGGCTAGTTACCGAGCTGATGGAAGAAATCTGTTTCCATTTGCATCTGGAAGCCACAC	1188
Db	1113	GCTTGGAGATTCTTGTCTACTTAACCTCTCAGCGACCGACCTGCACTTCACGTGGCACTAC	1172
Oy	1189	TT-----	1190
Db	1173	TACGAGCGGACAGTCACTGTCCCATGTACAGACTCATCCACCTGTGAACCAAGCTGGAG	1232
Oy	1191	-----GAAAGCCTTGCACACCTGC	1209
Db	1233	CTGCTGAGGAATCTCAAGACCAATCTGCACTACCTTCAGGAAAGAGCCACAGCCAGAG	1292
Oy	1210	AGCCCTTACCAATCAGAAAGCTAAGTTTTTAAAGAGCGAGTGGCG-----ATGGCTAAGCCCCA	1264
Db	1293	CCATCACCACAGTGAAGAGTCAAGTTTAAAGATGTTCTTCTTCACAGCCCCCGAGGATG	1352
Oy	1265	GGGGCCAGAGTAATTAAGACCGGACAGCCCTCAGTAGTGACAGAGAGGTCCCAAGCACCG	1324
Db	1353	GCTGCCAAGGAAAGGGGGTCTCCCAAGGCCACAGGCT--CCGGCGGTCCCCCAAGTCCGG	1410
Oy	1325	ACATCACAGCGCGAGGGGAGTCCACCAAGAGTGCAGAGAGCTGGAGCTTCAACAGCCGAA	1384
Db	1411	ATCAGAGCTTTGATGAGACGCCGAGCAAGGTGCCCAAGAGCTGGAGCTTTGTGTGACCGCA	1470
Oy	1385	CCGGCTTCCGGCCCTCGCTGGGCTCAAAAAGTTCACGCAAAAACAGTGATAGATCTG	1444
Db	1471	GCCCGCACAGCGCAAGCTTTCCGCATCAAGGGTGTGTCATCCCGCAGAAATTCACAAAGAG	1530
Oy	1445	ACACAGGCGTTGGCAGCATGATGATTAATGATGAAAAAGATGTCAGTGTGATATACAG	1504
Db	1531	CAAACCTTCCTCGGGAGGAGACTCTGTAGGGCAACAAAGAGCTGTACCTGCGAGTTTGTGA	1590
Oy	1505	TGGAAGACCTCACCCACACACTTAAATGTCTATTCAGACTATCAGAAATTAATGAATTTTC	1564
Db	1591	CTGAAGATCTTAACCCCTGGCCCTCAAAAGTTAGCATCAGACGCTGTGTGTTATGCGGTTCT	1650
Oy	1565	ATGTTGCAAAACGGAAGTTTAAAGAAACATTACGTCCATATGATGTAAAGATGTCAATG	1624
Db	1651	TGATATCTTAACCGAAATTCATAAAGAGAGTGTGCCCATATGATGATGATGACGTCAATCG	1710
Oy	1625	AACAATATTTCTGTGTCATCTGGACATGTGTGTAGAAATTAAGACCTTGA	1676
Db	1711	AACAGTACTGGGCTGGACACTTGGATATGTGTCCCGCATCAAGAGCCTGCA	1762
RESULT 34			
AB000499			
LOCUS			
DEFINITION			
AB000499.1			
ACCESSION			
AB000499.1			
VERSION			
AB000499.1			
KEYWORDS			
MKQT2.6; alternative splicing.			
SOURCE			
Mus musculus			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE			
1 (strets)			
AUTHORS			
Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,			

TITLE	Sasai, H. and Nishii, Y. KOT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels Recept. Channels 5 (5), 255-271 (1998)					
JOURNAL	98330948					
MEDLINE	2 (bases 1 to 2764)					
REFERENCE	Watanabe, H.					
AUTHORS	Direct Submission					
TITLE	Submitted (14-JUN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umesoga, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail: watanabe@ctrl.jtl.co.jp, Tel: 045-972-5741)					
FEATURES	Location/Qualifiers					
source	1. .2764 /organism="Mus musculus" /db_xref="taxon:10090" 87. .1958 /note="mKOT2.6" /codon_start=1 /product="alternative splicing; see accession between AB000494 and AB000504" /protein_id="BA037161.1" /db_xref="GI:4176404" /translation="MVQSRNGVYPTGSGKKIKVGFVGLDPAQDPSDRGALLINGSEARSGVLSKPRPTGGAGKPRPKRPAFTKLDLFLNVLERGRWAFITHAVFLVLFSCFLPVEITLIEYKESSEGLYILEIVTIVEGFEPRIMAAAGCCCKYRWGRGLKFLRPKSPFVDIVLLASIVLAAGSGNFAISALSLFLDILIMRIDRGGTGTLKLSVYVAHSEKLEVTAMYIGFLCLILASFLVLAKEENHPETVADALWMLGTLTLTIGDGKVPOTMKNRLIAAFTPLIGVSEFAPLIGLGGFALQVQEOHRRHFEKRRPAALIOSARAFRYANNTSRDILHSTMOYRETVYPMYRLPLNQLLELNLSKSGSLTEKEPQPEPSPQKYSIKDRVFSRPGMAKKGSGQADOTYRSPADSUDSPSRKVPKSWFSDRSRTROARIRGASRONSSEASLPEDIVDNKSCNEFVTEUPLRELKVSIRAVCYMRPLVSKRKEESLDPYDMVIMBOYSAGHLDMLSRKLSQSRPLEVOSHEDGPPQONQAMHKGHOGLDRCADQGOYOLMWRILPTLASCFLLCFHYCF"					
CDS						
BASE COUNT	586 a 753 c 771 g 654 t					
ORIGIN						
Query Match	15.6%; Score 431.4; DB 10; Length 2764;					
Best Local Similarity	56.3%; Pred. No. 1.2e-82;					
Matches	920; Conservative 0; Mismatches 611; Indels 102; Gaps 2;					
169	GGCCCTGCTACGCTGCGGACCCGGCCGACACGCTCGGTGCGGCGGCTGAGG	228				
153	GCGTTCGTGGGCGTGAACCCCGCGCCGCCACCTCAACACGCGAGCGGCGCTACTATC	212				
229	GAGAGCCCGCGGCGCAAGCAGGGGCGCGGATGAGCTGTGGGGAAACCGCTCTTAC	288				
213	GCGGCGTCCGAGGCGCCCGACGCGCGGCGCTTTGACAAACCGCGGACGGCGCGCG	272				
289	ACGAGTACCGAGAGTGTCCGCGCGCAAGCTCAAGTACCGCGGCGTCCAAACTACCTGAC	348				
273	GGAGCGGGGAAAGCCCCGACAGCGCAAGCGCTTACCCGAAAGCTGCAAAATTTCTCTAC	332				
349	AACGTGCTGGAGAGACCCCGCGGCGGTGATCACTACCAAGCTTTGTTTCTCTCT	408				
333	AACGTGCTAGAGCGGCGCCCGCGGCGTTCATCACTACCAAGCGCTAGGTGTTCTTTA	392				
409	GCTTTGGTGTGATTTTGTCAAGTGTTCACATCCCTGAGCACACAAATTTGGCC	468				
393	GCTCTCTCTGCTGTGCTTCTGTGTTTCCAAACAAAGGAATACAGAGAGCTCT	452				
469	TCAAGTTCGCTCTGATCTGGAGTTCGATGATTCGATTCGCTTTGGTTGGAGTTCATC	528				
453	GAGGCGCCCTCTACTATCTTGGAAATCTGTACTATCTGTGATTTGGTTGAGTACTTT	512				
529	ATTGCAATCTGCTGCGGGTTCCTGTTGTCGATATAGAGATGCGCAAGAACTGAGC	588				
513	GTGAGAGATCTGGGCTGACAGGCTGCTGTTCGCGGTTCAGAGCGCTGAGGCGGAGCTCAAG	572				
589	TTTGCTGCAAGACCTCTGTTGTTTAAATACCATCTGTTTATGCTTCAATATACAGTT	648				
573	TTTGCCAGGAAGCCCTTCTGTGTGATTAATATACATGAGTGTCTGATTTGCTTCCATTTCTGTG	632				

QY	649	GTTTTCGCAAAAAC	TGAGGTAATATTTT	TGCAAGCTGAC	CGACAGAAAGCTCCGTTTC	708
Db	633	CTGGCTCTGTGTT	CCGAGGCAATGCTT	GTGCACATCTCGCTT	CGAGGTTGGGTTTC	692
QY	709	CTACAGATCTCT	CCGCATGGTGGC	ATGACCCG	AAAGGAGGACACTTGGAAATTA	ACTGGGT 768
Db	693	TTGCAAAATCTTG	CGGATGATCCGT	ATWGACCGG	AGGGGTGCACCTGGAAAGCTCTTGGGA	752
QY	769	TCAGTGGTTAT	TGCTCAGCAAGGAATTA	TACAGCTTGGT	ATCATAGATTTTGGTT	828
Db	753	TCGGTACTACGCT	CACAGCAAGGAGCTGGT	ACTGCTGGTATCATTTGGCTTC	CGC 812	
QY	829	CTTATTTTTT	CGTTTCTTGTCTATCT	ATGCTGGGAAAGATGCCATTA	AAAGATTTTCT 888	
Db	813	CTCATCTGGCC	TCATTTCTGCTGATCT	GTGACGAGAAAGG	GTAGATGACACTTTTGAC 872	
QY	889	ACATATGCAAT	GCTCTCTGTTGGG	GCACAAATTACATTGCA	CACTATTTGGCTATGAGAC 948	
Db	873	ACCTAGCAAT	GTGACTTGGTGGGCTG	ATCACACCTCGACACCAATTTGGCT	TACGGGAC 932	
QY	949	AAAACTCCCT	TAATTTGGCTGGG	AGATTTGCTTTCGACAGGCTTTGG	CACTCCCTGGCACT 1008	
Db	933	AAATACCC	TAGACCTTGAACGGG	AGGCTGTCTGGCAGCCACTTTTAC	CTCATTTGGTCTC 992	
QY	1009	TCCTTTCTT	GCACACTTCTCCCGG	CACTTCTTGCTCAGTTTGCATTTAA	AAAGTACAGAA 1068	
Db	993	TCCTTTCTT	CTCTCTCTCTGCTGGC	ATTTTGGATCCGGCTTTCCCTCG	AAAGTCCAGAG 1052	
QY	1069	CAACACCGG	CAGAAACACTTTGAG	AAAAAGAAAGAACCCGAGCTGG	CAACATTCAGT 1128	
Db	1053	CAGCATGCG	CAAAACACTTTGAG	AAAGGCGGAAACCTCGG	CAGGTCTGATTCAGTCT 1112	
QY	1129	GTTTGGCG	TAGTTACGCACTGAT	GAGAATTCGTTTCCATTTG	CAACCTGGAAAGCCAC 1188	
Db	1113	GCTTGAG	ATTTCTATGCTACT	TAACCTTCACGACCGACCTG	CATCCAGTGGCAGTAC 1172	
QY	1189	TT	-----	-----	----- 1196	
Db	1173	TACGAGCG	CAGTCACTGTCCCAT	TGACAGACTCATCCACCTG	TAACAGCTGGAG 1232	
QY	1191	-----	-----	GAAGGCTTTG	CACACCTGTC 1209	
Db	1233	CTGCTGAG	GAATCTCAAGAGCAAA	CTGAGACTCACCTT	CAGGAAGGACCCACAGCCAGAG 1292	
QY	1210	AGCCCTAC	CAATCAGAAAGCTA	AGTTTAAAGAGCGAG--	TGCGCATGGCTAGGCCAGG 1286	
Db	1293	CCATCA	CCAAAGTGAAGAGT	GTGAGTTGAAGATCTGTCTT	CCACGCCCCCGAGGAGT 1352	
QY	1267	GGCCAA	AGTTTAAAGAGCCG	CAAGACCTCAGTAGGTG	AGACGAGGATCCCAAGACCGAC 1358	
Db	1353	GCTGCC	AAAGGAAAGGGGTCT	CCCCAGGCCACAGAGG	GTCCGGGTCTCCCACTGGCGGAT 1412	
QY	1327	ATTCAC	AGCCGAGGAGGCA	GTCCCAAGAGTGC	AGAGCTTCAACGACGAGC 1386	
Db	1413	CAGAGT	CTTGATATACAC	CCCGAGCAAGGTG	CCCAAGAGCTGTGGTGAACCGAGC 1472	
QY	1387	CACTTCC	CGGCGCTGCTGCG	CTCAAAAAGTTCTC	AGCAAAACCAATGATNGATGCTGAC 1446	
Db	1473	CGCACAC	CGCAGGCTTTC	CCGCATTAAGGGGTG	CTGATCCCGGAGAAATTCAGAAAGAGA 1532	
QY	1447	ACAGCC	CTTGGCACTGAT	TGATGTATGATG	AAAAAGATGCCAGTGTGATCTATCAGTG 1506	
Db	1533	ACCTCT	CCCTGGGAGAGCA	CTGCTAGAGGACA	AAAGAGTGTAACTGGCGATTGTACT 1592	
QY	1507	GAA	GACCTCA	CCGACCACTTA	AAAGTGTCAATGAGCTATCAGAAATTATGAAATTTCAAT 1566	
Db	1593	GAA	GATCTTA	ACCCCTG	CTCAAGGTTAAGCAATCAAGAGCTGTGTGTATTTAGCGATTTCTTG 1652	
QY	1567	GTTTCA	AAAAAGGAAATTTA	AGAAACATTTAG	CTATGATGATTAAGAGTGTGATTTGAA 1626	
Db	1653	GTATCT	AAAGGAAGTTCA	AAAGAGTCTGG	CCCATATGATGTATGAGACGTCACTAGAA 1712	

Query	Best Local Match	Similarity	Score	DB	Length
1627	CANNTATCTCTGCTGATCTGACATGTTGTGTAGATTAATAAAGCCCTTCAAAACAGCTT	1688			
1713	CAGTACTCGGCTGACACTTGGATATATTGTTCCTCCGATCAGACGCTGCAGTCCAGGCAA	1772			
1687	GATCAATTCCTTG	1699			
1773	GAGCCCTGCCTG	1785			
RESULT 35					
A94977	A94977	1425 bp	DNA	linear	PAT 26-JAN-2000
LOCUS	Sequence 4 from Patent WO931232.				
DEFINITION	A94977				
ACCESSION	A94977.1	GI:6779162			
VERSION					
KEYWORDS	unidentified.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1. (bases 1 to 1425)				
AUTHORS	Christian, E. P. and Aiyar, J.				
TITLE	HUMAN BRAIN DERIVED KCMQ2 POTASSIUM CHANNEL				
JOURNAL	Patent: WO 931232-A 4 24-JUN-1999;				
FEATURES	ZENECA LTD (GB)				
source	location/Qualifiers				
BASE COUNT	1. 1425				
ORIGIN	/organism="unidentified"				
	/db_xref="taxon:32644"				
Query Match	15.5%: Score 429.4; DB 6; Length 1425;				
Best Local Similarity	61.5%: Pred. No. 2.9e-82;				
Matches 707; Conservative	0; Mismatches 436; Indels 6; Gaps 1;				
3	GCCTCCGCAACACGCGGAGAGAGAGGCGCGCCCGCGGCTCTGGGTGAAGACGG	62			
72	GCGATCGGCTCCCGCGGGGGGCGTGGGTCGGGCGCGCGCGCGCGCGCTCCG	131			
63	CGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGGCAAGCGGATGATGAGTC	122			
132	CCCCGTGAGCTGAGGCCGACCGCGGCGCGCTCCCGCAGGACACCATGTGCAGAGTC	191			
123	GGGCGGGGAGGGGTGCTGMACTGGCGACCGCCCA-----GGGGGAGCGCTGCT	176			
192	GCGCAACGGGCGGTATACCCCGGCGGAGCGGGGAGAGAACTGMAAGTGGCTTGGT	251			
177	ACTGCTGGGCAACCGCGCGCGCAAGCTGAGTGGCGCGCGCGTGGCTGAGGAGAGCGG	236			
252	GGGGCTGGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGATGATGCGCGCT	311			
237	CGGGGCAACGAGGGGGCCCGATGAGCCCTGCTGGGGAAGCCGCTCTTACAGAGTAG	296			
312	CGAGGCCCCCAACGCGGGGAGCATCTCAGCAAACTGCGCGGGCGGCGCGCGCGG	371			
297	CGAGAGCTCGCGCGCAACGCTCAAGTACCGCGGGGTGAGAACTACTCTACAACTGCT	356			
372	GAAAGCCCCCAACGCGCAACGCTTCAACCGGAACCTGAGAAATTTCTCTPAAACGTGCT	431			
357	GGAGAGACCCCGCGCGGTGGGCTTCAATCAACAGCGTTTCTGTTTCTCTCTGTCTTGG	416			
432	GGAGGCGCGCGCGCGCGCGCTGAGCTTCAATCAACAGCGCTTCTCTCTGTCTTGG	491			
417	TTGCTTGAATTTGTCAAGTGTCTTCTACCAATCCCTGAGCACAAATAATGGCCCTCAAGTG	476			
492	CTGCTCTGCTGCTGTCTGTCTTTCACCAATCAAGAGATAGAGAGAGCTGAGAGGGGCG	551			
477	CTCTTGAATCTGAGATCTGTATGATATGCTCTTGGTGTGGAGTCAATCAATTCGAT	536			
552	CTCTTGAATCTGAGATCTGTATGATATGCTCTTGGTGTGGAGTCAATCAATTCGAT	611			
537	CTGCTCTGCGGGTCTGCTGTCTGATTTAGAGATGGAAGAGAGAGAGAGAGAGAGAG	596			

Db	612	CTGGGCGCCGACGGCTGCCTGCTGGCGGTACCGGCTGGAGGGGGGGGCTCAAGTTGTGCCG	671
QY	597	AAAGCCCTTGTGTGTTATACATACATGTTCTTATGGCTTCAATAGCAGTGTGTTGCG	656
Db	672	GAACCGTTGTGTGTTATGACATCAATGATGCTCATGGCTCCATTCGGGTGGCGCG	731
QY	657	AAAAACTCAGGGAATATTTTTTGGCAGCTGCACCTGAGAAAGTCCGTTTCCACAGAT	716
Db	732	CGGCTCCAGGGCAAGCTTTTGGCAATCTGGCTCCGAGCCTGGCTTCGCMAGAT	791
QY	717	CTCCCGCATGGTGGCATGACCGAAGGGGAGGACATTTGAAATTAAGTTCAGTGGT	776
Db	792	TCGCGGATATATCCGATGAGACCGGGGGAGGACACTGAAAGCTGCTGGGCTGTGTGT	851
QY	777	TATGCTCAGCAGGAATTAATCACAAGCTGGTGTACATAGATTTTTTGGTCTTATTTT	836
Db	852	CTATGCCACAGCAAGAGAGCTGGTCACTGCTGGCTGTACATCGGCTTCTTCATACCT	911
QY	837	TTCGTCTTCTCTTCTCATCTGTGGGAAAGAGATCCAAATTAAGTTTCTACATATGC	896
Db	912	GGCTCTCTTCTGGTGTACTTGGGAGAGAGGGGAGAAACGACCATTTGACACCTAGCG	971
QY	897	AGATGCTCTGTGGGGGACAAATTTACATTGACAACTATGGCTATGGAGACAAATCC	956
Db	972	GGATGCACTGTGGGGGCTGTGATCAGCTGATCACCACATTGTGGTACGGGGACAGTACC	1033
QY	957	CTTAATCTGGCTGGGAAGATTCCTTTCGACAGGCTTTCGACCTCTGGCATTTCTTCTT	1018
Db	1032	CAGACCTTGGAACGCGAGGCTCTTTCGGGCAACCTCATCCCTCATCGGTCTCTCTCTT	1091
QY	1017	TGCACCTTCGCGCGGCAATTCGTGGCTCAGTGTTCGATTAAAGTACAAAGAACACCG	1076
Db	1092	CGGCTCTCTGCAAGCATCTTGGGGGTCTGGGTTTGCCTGAAGTTCCAGGAGCAGCAG	1151
QY	1077	CCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCCTCATTCAGTGTGGCG	1138
Db	1152	GCAGAACACTTTGAGAAAGAGCGGGAACCCGCGACAGAGCTGATCCAGTGGCGCTGGAG	1211
QY	1137	TAGTTACGC 1145	
Db	1212	ATTCTTACGC 1220	
RESULT	36		
LOCUS	D82346	1425 bp	linear
DEFINITION	Homo sapiens mRNA for HNSPC, complete cds.		PRI 18-MAR-1995
ACCESSION	D82346		
VERSION	D82346.1	GI:1841341	
KEYWORDS	HNSPC.		
SOURCE	Homo sapiens Neuroblastoma cell_line:IMR-32	cDNA to mRNA, clone:HNSPC.	
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.		
AUTHORS	1 (stiles)		
TITLE	Yokoyama,M., Nishi,Y., Yoshii,J., Okubo,K. and Matsubara,K.		
JOURNAL	Identification and cloning of neuroblastoma-specific and nerve tissue-specific genes through compiled expression profiles		
MEDLINE	DNA Res. 3 (5), 311-320 (1996)		
REFERENCE	97191543		
AUTHORS	2 (bases 1 to 1425)		
TITLE	Yokoyama,M.		
JOURNAL	Direct Submission		
FEATURES	Submitted (21-DEC-1995) Masahiro Yokoyama, Japan Tobacco, Inc., Pharmaceutical Frontier Research Laboratories: 13-2 Fukuura 1-chome, Kanazawa-ku, Yokohama, Kanagawa 226-0004, Japan (E-mail:masahiro.yokoyama@fms.frl.co.jp, Tel:045-786-7693, Fax:045-786-7692)		
source	Location/Qualifiers		
	1..1425		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		

[illegible]

Db		792	TCGCGGATGATCCGATGAGACCGGGGAGGACCCTGGAACCTGCTGGCTGTGCT	851
OY		777	TTATGCCTCACAAGCAAGAATTAAATACAGACTTGTAACATAGATTTTTGGCTTTATTT	836
Db		852	CATAGGCCAACAGCAAGAGAGCTGCTACTGCTCCGTACATCGCTTCTCTTGTCTCATCT	911
OY		837	TTGCTCTTCTCTTCTATCTATCTGCTGTAAGAAAGATGCAATTAAGAGTTTCTACATATGC	896
Db		912	GCGCTGTCTCTGTTCTGTATCTTGCGCAGAGAGGGGAGAAACGACCATTCTTGACACTCACGC	971
OY		897	AGATGCTCTCTGTTGGGGCACAATTACATTTGACAACATTTGGCTATGAGAGCAAACATCC	956
Db		972	GGAATGCACTGTGGGGGGCCGTGATCACCGCTGACCAACATTTGGCTACGGGGAACAATGCC	1031
OY		957	CCATAATTTGGCTGGGAGATGCTTCTGACAGCTTTGGACGCTTGACGCTTGGCAATTTCTCT	1016
Db		1032	CCAGACCTGGAACGGCAGCGCTCTTGCGGCAACCTTCAACCTCATGCTGTCTCTCTT	1091
OY		1017	TGCACCTTCTGCGGGCATTTCTTGCTCAGGTTTGGCATTTAAAAGTACAAAGAACACACCG	1076
Db		1092	CCGGCTGCCCTGCAGGCAATCTTGGGGGTCTGGGGTCTGCCCTGAAGGTTACAGAGCAGCACG	1153
OY		1077	CCAGAAACACTTTGGAGAAAAAGGAACCCGACCTGCAACCTCATTCACGCTGTTTGGCG	1138
Db		1152	GCAGAAACACTTTTGAGAGAGAGCGGACCCGGCAGCAGGCTGTATCCAGTCGGCTGGAG	1211
OY		1137	TAGTTAAGC 1145	
Db		1212	ATTCTACGC 1220	
RESULT 37				
AF033348				
LOCUS	AF033348	3332 bp	mRNA	linear PRI 21-JAN-1998
DEFINITION	Homo sapiens potassium channel (KCNQ2) mRNA, complete cds.			
ACCESSION	AF033348			
VERSION	AF033348.1	GI:2801451		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 3232)			
AUTHORS	Singh,N.A., Charlier,C., Stauffer,D., Dupont,B.R., Leach,R.J., Mellis,R., Ronen,G.M., Bjerre,I., Quattleben,T., Murphy,J.V., McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and Leperlet,M.			
TITLE	A novel potassium channel gene, KCNQ2, is mutated in an inherited epilepsy of newborns			
JOURNAL	Nat. Genet. 18 (1), 25-29 (1998)			
MEDLINE	98085864			
PUBMED	9425895			
REFERENCE	2 (bases 1 to 3232)			
AUTHORS	Singh,N.A., Charlier,C., Stauffer,D., Dupont,B.R., Leach,R.J., Mellis,R., Ronen,R.M., Bjerre,I., Quattleben,T., Murphy,J.V., McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and Leperlet,M.			
TITLE	Direct Submission			
JOURNAL	Submitted (06-NOV-1997) Human Genetics, University of Utah, 2030E 15N Room 2100, Salt Lake City, UT 84112, USA			
FEATURES				
source	1..3232			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/chromosome="20"			
	/map="20q13.3"			
	1..3232			
	/gene="KCNQ2"			
	128..2746			
	/gene="KCNQ2"			
	/note="KYBN1"			
	/codon_start=1			
	/product="potassium channel"			

Query Match	Similarity	15.5%	Score 429;	DB 9;	Length 3232;
Best Local	61.4%	Pred. No. 4e-82;			
Matches 706;	Conservative 1;	Mismatches 436;	Indels 6;	Gaps 1;	
BASE COUNT	576 a	1054 c	1061 g	533 t	8 others
ORIGIN					
Query Match					
Best Local					
Matches 706;					
Conservative					
1;					
Mismatches					
436;					
Indels					
6;					
Gaps					
1;					
3	GC	CC	CC	CC	CC
22	GC	AT	GC	GC	GC
63	CG	AG	CG	CG	CG
82	CC	CC	CG	CG	CG
123	GG	GG	GG	GG	GG
142	GG	GA	GG	GG	GG
177	ACT	GT	GG	GG	GG
202	GG	GG	CG	CG	CG
237	CG	GG	CG	CG	CG
262	CG	AG	GC	GC	GC
297	CG	AG	CG	CG	CG
322	GA	AG	CG	CG	CG
357	GG	AG	CG	CG	CG
382	GG	AG	CG	CG	CG
417	TT	GC	TT	TT	TT
442	CT	GC	TT	TT	TT
477	CC	CT	TT	TT	TT
502	CC	CT	TT	TT	TT
537	CT	GT	TT	TT	TT
562	CT	GG	CG	CG	CG
597	AA	AG	CG	CG	CG
622	GA	AA	CG	CG	CG
657	AA	AA	CG	CG	CG
682	CG	GC	CG	CG	CG

QY	1024	CCTGCCGGCATCTTGGCTCAGAGTTTGCATTAAAGTCAAGAACACACCCGACAGAA	1083
Db	898	CCAGCGGGCATCTCTGGGGTCCGGGGCTGGGCCCTCAAGGTGCAGAGACCAACCCGTCAAG	957
QY	1084	CACTTTGGAAAAGAAGAACCCAGCTGGCAACCTCATTCAGTGTGTTTGGCGTAGTTAC	1143
Db	958	CACTTTGGAAAAGAAGAGAGCAGCTGCTGACCTATTCAGGCTGCTGGAGGATATAT	1017
QY	1144	GCAGCTGATGAGAAATCTGTTTCCATTG-----CAACCTGGAAGCCACACTTGAAG	1194
Db	1018	GCTACCAACCCCAACGAGATTGACCTGTGGCGACATGAGATTTTATGATCAGTGTCTC	1077
QY	1195	GCTTTGCACACCTGGACGCCCTCCATCATGAAAGCTAAGTTTAAAGAGCAGTGCAGT	1254
Db	1078	TCTTTTCTCTTCTTCAGGAAAAGACAGCTGGAGGGCGCATCCGACCAAAAGCTGGGTCTC	1137
QY	1255	GCTAAGCCCCAGGGGCGCAGATATTAAAGACCACAAGCCCTCAGTAGGTGACAGAGGTCC	1314
Db	1138	TTGGATGGGGTTCGCTTCTTCAATTCCTGTGTGTAGCATATCTAAAGAAAAGCTATTAC	1197
QY	1315	CCAAGCACCGCATCTCACAGCCGAGGGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTC	1374
Db	1198	CTCTTGAAATGATATGCCATAGAAAGAAAGTCTCTTAAAGAAACCAAGCCCTGTGGCTTA	1257
QY	1375	AACGACCGAACCCTTCCTGGGCCCCGCTGGCCCTCAAAAGTTTCTCAGCCAAACCAAGTG	1434
Db	1258	AACAATAAAGAGCGTTTCCGACGGCCCTTCGCAATGAAAGCCCTAGCGTTTCTGGC----	1312
QY	1435	ATGATGCTGACACAGCCCTTGGCAGCTGATGATATATGATGAAAAGAGATGCCAGTGT	1494
Db	1313	-AGAGTTCTAAGATGAGTGGGACAGTGATACCCCATATGGGGAAGACAGGGGCTATGGAGAT	1371
QY	1495	GATGATCACTGGAAGACCTCACCCACCACTTAAACGTCATTCGACCTATCAGAAATT	1554
Db	1372	GACTTCCCATTCGAAAGACATGATATCCCAACCTGGAAGGCCCATCCGAGCCGTGCAAAAT	1431
QY	1555	ATGAAATTTATGTGCAAAAGCGAAGTTTAAAGAAACATTACGTCATATGATGTAAAA	1614
Db	1432	CTACAATTCGCTCTCTATAAAAAAAATTCAAAGGAGACTTTGAGGCCCTTACGATGGAG	1491
QY	1615	GATGTCATGAACAATATTTCTGCTGCATCATGTGGCATGCTGTGTAGAAATTTAAAGCCTT	1674
Db	1492	GATGATTTGAGCAGATTTCTGCGGGGCATCTCGACATGCTTCCAGGATTAAGTACCTT	1551
QY	1675	CAACACAGTGTGATCAAAATCTT 1697	
Db	1552	CAGACGAGATATGATATGATTTT 1574	
RESULT 41			
LOCUS	EL13516	1182 bp	DNA
DEFINITION	Human mRNA for a K+ channel protein.		
ACCESSION	EL13516		
VERSION	EL13516.1 GI:3252321		
KEYWORDS	JP 1997191882-A/1.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1182)		
JOURNAL	Yokoyama, M., Nishi, Y., Matsubara, K., and Ookubo, K.		
	DNA CAPABLE OF CODING HUMAN NEW K+ CHANNEL PROTEIN AND ITS FRAGMENT		
	Japan: JP 1997191882-A 1 29-JUL-1997;		
	JAPAN TOBACCO INC		
COMMENT	OS Homo sapiens (human)		
	PN JP 1997191882-A/1		
	PD 29-JUL-1997		
	PF 16-JAN-1996 JP 1996004726		
	PI YOKOYAMA MASAHIRO, NISHI YOSHISUKE, MATSUBARA KENICHI, PI		
	OOKUBO KIMISAKU		
	PC C12N15/09,C07H21/04,C12Q1/68//C07K14/47;		
	CC strandedness: Double;		

	CC	topology: Linear;	Location/Qualifiers
Query Match	15.3%	Score 425; DB 6; Length 1182;	
Best Local Similarity	64.7%	Pred. No. 2.5e-81;	
Matches 632; Conservative	0;	Mismatches 345; Indels 0; Gaps 0	
BASE COUNT	201 a	372 c	364 g 245 t
ORIGIN			
FEATURES			
source			
		Location/Qualifiers	
		1..1182	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/cell_type="neuroblastoma"	
		/cell_line="IMR32"	
		1..1182	
		/product="K+ channel protein"	
Query	169	GGCCGTACTGCTGGGACACCGCGCGCCACCGTGGGCGCGCGGTGGCGAGG	228
Db	67	GGCTGCTGGGCTGGAGCCCGCGCGCCCGACCTCCACCGGGGCGGTGGCGAGG	126
Query	229	GAGAGCCCGCGGGGCAAGAGGGGGCCGGATGAGCGTGGTGGGAAGCGCTCTTAC	288
Db	127	GCGGCTCGAGGGCCCCAGCGCGGAGATCTCTAGCAAACTGGCGGGCGCGG	186
Query	289	ACAGATGACCAAGCTGCGCGGCCAACGTCAGTACCGGGCGGTGAGAACTACCTAC	348
Db	187	GGCGCGGGAGGCCCCCAAGCCCAAGCGCTTCTACCGCAAGCTCGAATTTCTCTAC	246
Query	349	AAGTGTGAGAGACCCCGCGCGCTGAGCTTATACAGCGCTTGTCTTCTCCCT	408
Db	247	AAGTGTGAGAGCGCGCGCGCTGAGCTTATACAGCGCTTGTCTTCTCCCT	306
Query	409	GTCCTTGGTGTGATTTTGTGAGTGTCTTACATCCCTGAGCACAAATTTGCC	468
Db	307	GTTTCTCCGCTGCTGTGTGTGTCTTCCACCATCAAGAGATGAGAAAGACTCG	366
Query	469	TCAAGTGGCTCTTGAATCTGAGGATGATGATGATGATGATGATGATGATGATG	528
Db	367	GAGGGGGCCCTCTACATCTCGAATCGTACATCTGTTGGCGTGGAGTCTTC	426
Query	529	ATTGCAATGCTGCTGCGGGGTGCTGTGATAGAGATGAGAGAGAGAGAGAGAG	588
Db	427	GTCGGATCTGGGCGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	486
Query	589	TTTGCTCGAAAGCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	648
Db	487	TTTGCGCGGAAACCGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	546
Query	649	GTTTCTGCAAAACTGAGGTAAATTTTGGCACGTGGCACTGAGAAAGTCCGTTTC	708
Db	547	CTGGCGCGCGCTCCCAAGGCAACGCTTTGGCAATCTGGGCTCGGAGCGCTGCTTC	606
Query	709	CTACAGATCTCCGATGCTGGGCGATGACGACGAGGAGGAGGAGGAGGAGGAGG	768
Db	607	CTGCGAGATCTCGGATGATCTCGATGAGAGCGGCGGAGGAGGAGGAGGAGGAGG	666
Query	769	TCAGTGGTTATGCTACAGCAAGAAATTAATCAAGCTGTGTACATAGATTTTGGTT	828
Db	667	TCGTGAGTCTATGCCACAGCAAGAGGCTGTGTACCTGCTGTGTGTGTGTGTGTGT	726
Query	829	CTTATTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	888
Db	727	CTCATCTCGGCTCTGCTCTGCTGTACTTGGCAAGAGGAGGAGGAGGAGGAGGAGG	786
Query	889	ACATATGAGATGCTCTGTGGGGGCAATTTCAATGAACTATTTGGTATGAGAG	948
Db	787	ACATATGAGATGCTCTGTGGGGGCAATTTCAATGAACTATTTGGTATGAGAG	846
Query	949	AAACTCCCTTAACTGGCTGGGAGAGATGCTTTCTGACAGCTTGTGACTCTTGGCAT	1008

Db	Accession	Source	Organism	Reference Title	Journal	Remark	Comment
Db	847	AACTACCCCGACGACCTBGAACGGCAGGCTCCCTTGCGGCAACCTTACCCGTACGCTGTC	906				
Qy	1009	TCCTTCTTTGCACTTCCCTGCGGCACTTCTTGCTCAGAGTTTGTCATTTAAAGTACAGAA	1068				
Db	907	TCCTTCTTCCGCTGCTCGCAGGCACTTCTTGCGGCTTGCGGTTTCCCTGAAAGTTTCAGGAG	966				
Qy	1069	CACACCCGCAAGAAACCTTTGGAAAGAAAGAACCCACCTGSCCAACCTCATTCAGTGT	1128				
Db	967	CAGCAGCAGGAGAGAGCCTTTGGAGAGAGAGGCGGAGAACCCGACAGCAGGCTGATTCAGTGC	1026				
Qy	1129	GTTTGGCTAGTTACGC	1145				
Db	1027	GCCTGGAGATTCATCGC	1043				
RESULT 42							
BC000699							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
REMARK							
COMMENT							

BASE COUNT	239 a	404 c	388 g	283 t	
ORIGIN					
Query Match	15.3%	Score 425;	DB 9;	Length 1314;	
Best Local Similarity	64.7%;	Pred. No. 2.5e-81;			
Matches 632;	Conservative 0;	Mismatches 345;	Indels 0;	Gaps 0;	
Db	169	GACCTGCTACTGCTGGGACACCCGGGGGCCACGCTCGTGGCGGGCGGCTGGAG	228		
Qy	111				
Db	119	GGTTCGTGGGGCTGACCCCGCGGCCCGGACCTCCAGCCGGAGGGGGCGTGTATC	178		
Qy	229	GAGAGCCCGCGGGGCAAGCAGGGGGGCCGGATGAGCTCTGGGGAAAGCGCTCTTAC	288		
Db	179	GCCGGCTCCAGAGGCGCCCAAGCGGAGCATCTCTAGCAAACTCCGGGGCGGGCGG	238		
Qy	289	ACGAGTACGACGACCTCCGGCGCAGCTCAAGTACCGGGGGGTGCAAACTACTGTAC	348		
Db	239	GGCGCCGGGAAGCCCCCAAGCGCAACGCCCTTACCGCAAGCTGAGAAATTCCTTAC	298		
Qy	349	AACGTCTGAGAGACCCCGCGGCTGGGCGTTATCTACACGCTTCGTTTTCTCTTAC	408		
Db	299	AACGTCTGAGAGCGCGCGCGCGCTGGGCGTTCTATCAACAGCTCAGTTCCTCTCTG	358		
Qy	409	GCTTTGGTCTCTGATTTTGTACGTTTCTCAATCCCTGAGCAGCAAAATTTGGCC	468		
Db	359	GTTCCT	418		
Qy	469	TCAAGTCCCTCTTGATCTCGATCTGAGTCTGATGATGTTGTCGTTTGGTTTGGATTC	528		
Db	419	GAGGGGGCGCTCTACATCTGGAATCTGCTACTATCGTGTGTTGGCTGTGACTTTC	478		
Qy	529	ATTGCAATCTGCTCTGGGGTTGCTGTTTCGATATAGAGATGGCAAGAACTGAG	588		
Db	479	GTCGCAATCTGGGCGGAGGCTGCTGCTGCGGTTACCTGTGAGGGGGCGGCTCAAG	538		
Qy	589	TTTGTGCAAAAGCCCTCTGTTATGATATACATATGTTTCTTATCGCTCAATAGAGTT	648		
Db	539	TTTGGCGGAAACCGTTCTGTGTATTAACATCAATGCTCATGCGCTCATGTGCGGTG	598		
Qy	649	GTTTCTGCAAAAACCTGACGGGTATATATTTTGGCACGCTGCACATCAAGATCTCCGTTT	708		
Db	599	CTGGCGCGCGGCTCCCAAGGCGCAACGCTTTTGGCAATCTGGCGCTCCGGAGCTCCGCTTC	658		
Qy	709	CTACAGATCTCCGATGATGGTGGCATGGAACCGAAGGGAGGCACTTGGAAATTA	768		
Db	659	CTGCAAGATCTCGGATGATGCGCATGGAACCGGCGGGAGGCACTGTGAGACTGTGGGC	718		
Qy	769	TCAGTGTTTATGCTACAGCAAGCAATTAATCACAGGCTGGTACATAGATTTTGGTT	828		
Db	719	TCGTGTGCTATAGCCCAAGCAAGAGGCTGTGCTGCTGTATCATGCGCTCTCTTGT	778		
Qy	829	GTTATTTTTCGTTCTTCTCTGTTCTATCTGTTGGAAAAAGATGCCAATAAAGAGTTTCT	888		
Db	779	CTCATCTCTGCGCTCTCTCTCTGTTACTTGGGCAAGAAAGGGGAGAACGACCATCTTAC	838		
Qy	889	ACATATGCAATGCTGCTGTTGGGGCAACATTAATGATGACAACTATTTGGCTATGAGAC	948		
Db	839	ACCTAGCGGAGTACACTCTGTGTGGGGCCGTGATGACGCTGACCAACCATTTGGGTACGGGGAC	898		
Qy	949	AAAAATCCCTAACTTGGCTGGGAAGATTGTTTTCGACAGGCTTTGCACTCTTGGCAATT	1008		
Db	899	AAGTACCCTCAGACCTGGAACGCGAGGCTCTTGGCGCAACCTTCACCTCATCGGTGTC	958		

Db 213 GCGGGCTCCGAGGCCCGCCAGCCGCGCAAGCTTTTGAGCAAAACCGCGAGCGGGCGG 272
 QY 289 ACAGTAGCCAGAGCTGCGCGGCAACGCAAGTACCGCGGGTGCAGACTACCTGTAC 348
 Db 273 GAGAGCGGGAAGCCCGGCAAGCCGCAAGCTTTCACCGAAGCTGAGAAATTCCTCTAC 332
 QY 349 AACGCTGTGAGAGAGACCCCGGGGCTGGCTTCATCTACACGCTTCTCTCTCT 408
 Db 333 AACGCTGTGAGAGAGACCCCGGGGCTGGCTTCATCTACACGCTTCTCTCTCT 392
 QY 409 GTCTTTGCTGTGATTTTGTCACTGTTTCTTCCATCTACCTGAGCACAATAATGGCC 468
 Db 393 GTCTTTGCTGTGATTTTGTCACTGTTTCTTCCATCTACCTGAGCACAAGAGCTCT 452
 QY 469 TCAAGTGTGCTGTGATTTTGTCACTGTTTCTTCCATCTACCTGAGCACAAGAGCTCT 528
 Db 453 GAGGGGCGCTGTACATCTTGTGAATCTGTACATCTGTGTGTTTGGTGTGATCTT 512
 QY 529 ATTGGAATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 588
 Db 513 GTGAGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 572
 QY 589 TTTGCTGTGAGAGCCCTGTGTGTATACATACATCTTCTTATCTTCAATAGCAGTT 648
 Db 573 TTTGCTGTGAGAGCCCTGTGTGTATACATACATCTTCTTATCTTCAATAGCAGTT 632
 QY 649 GTTCTGTCAAAAACCTCAAGGTAATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 708
 Db 633 CTGGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 QY 709 CTACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 Db 693 TTGCAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 QY 769 TCAAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 Db 753 TCGGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 QY 829 CTATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
 Db 813 CTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 QY 889 ACATATGCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
 Db 873 ACCTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 QY 949 AAAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
 Db 933 AAGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
 QY 1009 TCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 Db 993 TCGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 QY 1069 CAACACCGCAGAAACATTTGAGAAAGAAAGAACCCAGCTGCCAATCTATTCAGT 1127
 Db 1053 CAGCATCTGCGCAAAACATTTGAGAAAGCGGAGAACCTCGCGAGCTGTGATCCAGGG 1111
 RESULT 47
 AF325548 2671 bp mRNA linear MAM 19-FEB-2001
 LOCUS Bos taurus potassium voltage-gated channel (KCNQ3) mRNA, complete
 DEFINITION
 ACCESSION AF325548
 KEYWORDS AF325548.1 GI:12963341
 SOURCE Bos taurus.
 ORGANISM Bos taurus.
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; 1 (bases 1 to 2671)

AUTHORS Rae, J.L.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-2000) Physiology and Biophysics, Mayo Clinic, 200
 1st Street SW, Rochester, MN 55905, USA
 FEATURES
 source Location/Qualifiers
 1..2671
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /cell_type="lens epithelium"
 1..2671
 /gene="KCNQ3"
 /note="KOT-1 like subfamily, member 3"
 /product="potassium voltage-gated channel"
 /protein_id="AAK11221.1"
 /db_xref="GI:12963342"
 /translation="MGLKARPPAGAGGGGGGGGGAANPAGDAAAAGDEERKVG
 LAPVEQVETLALGAGADKDTLLLEGGRDEGRPTPOGIGLAKPLSPVRNNA
 KYRIOTLIVDALERRGNALYHALVELIVLCITLAVLTREYETSGDWILLIE
 TPATITFGAEPLRITAAAGCCCKKGRGLKRRKPLCHLIDIVLAVSYAVVAGNO
 GVALATLSLRLPLQILRLMRDRGGTMRLLDSATCAHSKELITWVIGFTLLISS
 FLVLYEKDVPEVDAQEEMKEFEFYADALMGLIATIGYDGKPKTEGRILAA
 TFSLIGVSEFALPAGILGSLALVKVOEHOKHEKRRKPAELIOAMRYATPNR
 IDLVATMREYESVSPFFRKEOLDPAASOKGILDLRLSPNRSNTKRLPLVAV
 DAIESPSKEPPVGSNNKERRPTARRMKVAFMOSEDACTGDPTEDRGVDLI
 EDMITPLKAIKRAVRLQRLRYKKRKTETLRPYDKVITYEDYSAGHLDMSRIKYLQI
 RIDMTFTGPEPSTPKHKSQORGAALFYPSQSPNEEYVARPSTSEEDSOMKREVK
 VERQVHDMKRLDLFDMLQHMERELOVHAPSPSSGASPADEKEDRDLKLT
 ILICNSSETGADPAVPSFHQVPVYKVPYGFADPVLPLGSPSSGHAATPARPT
 VPLITLDRSGRSYQVELHGPCSDRVSRORSITRDSOTPLSLMSVNEELERSP
 SGFSTISODBDIAFSPSGSSSMNRKRYLAEGTDIDTEPFTPGSLPLSTGGCISD
 STWPSGKPT"
 BASE COUNT 585 a 777 c 803 g 506 t
 ORIGIN
 Query Match 14.9%; Score 411.8; DB 4; Length 2671;
 Best Local Similarity 55.6%; Pred. No. 2,1e-78;
 Matches 951; Conservative 0; Mismatches 702; Indels 58; Gaps 6;
 QY 35 GCGCGCGGCTCTGCTGTGAAGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCT 94
 Db 40 GCGCAGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 99
 QY 95 TGGGAGCGGCAATGAAGATGTGAGTCCGGCGCGCGCGCGCGCGCGCTGCTGAATCGGAG 154
 Db 100 CGCTAACCCGCGCGGAGG-GGACGCGCGCAGCGCGCGCGCGCAGAGACCGGAAATGGGGC 158
 QY 155 CCGCAGGAGCGAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
 Db 159 TAGCCCGCGCGCAGCGCGCGCAGGATCACTTGGCGCTGCGGAGCGCGGAGCTACCAAGACG 218
 QY 215 GCGGTGCGCTGAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGATGAGCTGTGGGA 274
 Db 219 GAGCCCTGCTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 278
 QY 275 AGCGCTCTTACAGAGATAGCAGCTGCC-----GGCGAAGCTCAAGTACC 325
 Db 279 TCGGGCTCTGTGCGCAAGACGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 338
 QY 326 GCGGCGTGCAGAACACTGTACAAAGCTGTGAGAGAGACCGCGCGCGCGCTGTCAATCT 385
 Db 339 GAGCGATCCAACTTGTGATCTACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTCT 398
 QY 386 ACCACGCTTGTGCTTCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 445
 Db 399 ACCACGCGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 458
 QY 446 TCCGAGACACCAAAATGGCGCTCAAGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 505
 Db 459 TCAGGAGTACAGAGACTGTTTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 518

OY	506	TCGTCCTGGTGTGGAGATCTCAATTCATTCGAATCTGGCTCCGGGTCCTGTTGCGATATA	565
Db	519	TCATCTTCGGAGCCGAGATTGCTTTGAGAGATCTGGGCTCCGGCTCTTGCTGCCGATACA	578
OY	566	GAGGATGGCAGAAGACAGTAGGTTTGCTCGAAAGCCCTCTGTGTATATAGATACCATG	625
Db	579	AAGGCTTGGCGGGGACGACATGAAGTTTGGCAGAAAGCCCTTGTCATGTTGGACATCTTTG	638
OY	626	TTCTTATCCGCTCAATAGCAGTGTGTTTGCAGAAAACCTAGGGTAATATTTTGGCCAGCT	685
Db	639	TCCTGTATCCGGTCCGCTGCTGTGGTTGCGCTGTGGAAACAGGGGCAACGTCCTGGCCACGT	698
OY	686	CTGCACCTGCAAGGCTCCGTTTCTACAGATCTCCGCACTGGGCGCATGGACGGAAGG	745
Db	699	---CCCTGCCGAGCTCGGCTTCTGCGAGATCTTGAGATGCTGCGCAATATGACCCGGAGGG	755
OY	746	GAGGCACTTGGAAATTACTGGGTTTCAGTGTTTATATGCTACAGCAAGAAATTAATCAAG	805
Db	756	GGGGCAGCTGGAAAGCTCTGGGGCTGGGCATCTGGGCCACAGCAAAAGACCTCATACCG	815
OY	806	CTTGTGACATAGCATTTTGTGTTTATTTTGTCTTTGCTTGTCTATCTGGTGAAA	865
Db	816	CCGTGTACATCGGGTTCCTGACGCTCATCTGTTCATTTCTGCTACCTCGGTTGAGA	875
OY	866	AGGATG-----CCAAATAAGGTTTTCATCATATG	895
Db	876	AAGATGTGCCGAGGTGATGCCCAAGAGAAAGATGAAAGGAAATTTGAGACCTTACG	935
OY	896	CAGATGCTCTCTGATGGGGGCAATTAATGATTTGACAACTATTTGGCTATGAGACAAATCTC	955
Db	936	CAGATCCCTGTGTGGGGCTGTATCAGATCTGCCACCACTTTGGCTACGGAGACAAAGCCG	995
OY	956	CCCTTACTTGGCTGGGAGATTTGCTTTCGACAGGCTTTGCACTCTTGGCATTTCTTTCT	1015
Db	996	CCAAAAGGTGGGAAAGCCGTCGTATCGCAGCCACTTTCTTAACTGAGGTCTCTTTT	1055
OY	1016	TTGCACTTCTGCGCGGCACTTCTTGGCTAGGTTTGTCAATTAAGTACAAAGAACACAC	1075
Db	1056	TTGCGCTGCGAGCGGATCTCTGGGGTCCGGGCTCGCGCTCAAGGTGCAGAGACAGCAC	1115
OY	1076	GCGAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGC	1135
Db	1116	GCCAGAAAGCACTTTGAGAAAAAGGAGAAAGCCGCTGTCTAGCTCATTCAGGCCGCTTGA	1175
OY	1136	GTAATTACGAGCTGATGAGAAATCTGTTCCATTGCAACTGTGAAGCCACACT-----	1189
Db	1176	GGTACTATGTACCAACCCCAACAGAGATTGATCTGTGCGACGTGAGGTTCTATGAAT	1235
OY	1190	---TGAAGGCTTGCACACCTGCAAGCCCTACCACATCAGAAAGTAAGTTTAAAGAGCGAG	1246
Db	1236	CAGTCGCTCTTTTTCACATTTCTTCAGAAAGAACACTGTGATCCAGAGCCAGCCAAAGC	1295
OY	1247	TGCGCAATGGCTAGCCCGCAGAGGAGATTAATTAAGGCGGACAGCCCTCAGTGAAGTGACA	1306
Db	1296	TGGGTCTCTTGGATCGGGTTGCGCTTTTAACTCTGTGTAGCAATACTTAAAGGAAGC	1355
OY	1307	GGAGGTCCCAAGCACCGACATCACAGCCGAGGAGAGTCCACACAAAGTGCCAGAGAAGCT	1366
Db	1356	TATTTACCCCTCTGAATGTAGATGCCATAGAAGAAAGTCTCTTAAAGAACCAAGGCTG	1415
OY	1367	GGAGCTTCAACAGACCGAAGCCGCTTCGGGCCCTGCGTGGCGCTCAAAAAGTTTTCAGCCAA	1426
Db	1416	TTGGCTCAAACAATTAAGAGGTTTCCGACCGCTTCGCGCATGAAAGCATAGCGCTTCT	1475
OY	1427	AACCACTGATAGATGCTGACACAGACCCCTTGGCACTGATGATATGATGAAGAAAGAT	1486
Db	1476	GGCAGAGCTTGAAGATGCGGGGACAGGGGACCCCAACGCGGA-----GACAGGGGCT	1529
OY	1487	GCCAGTGTGATGTATCAGTGAAGACCTCACCCCACTTAACCTGTCATTCAGACTA	1546
Db	1530	ACGGGAATGACTTTCATCGAATGAAACATGATGCCACCTGAAAGGCTGCATCCGACCG	1589
OY	1547	TCAGAAATTAATTCATGTTGCAAAAAGGAGTTTAAAGAAACATTAAGTTCATATG	1606

misc.feature	4646. .4735	/note="match: STS: Em:G46532"
repeat_region	5518. .5553	/note="18 copies 2 mer 9t 100% conserved"
repeat_region	5732. .3831	/note="50 copies 2 mer tt 63% conserved"
repeat_region	5769. .5828	/note="20 copies 3 mer ttc 70% conserved"
misc.feature	6079. .6504	/note="match: GSS: Em:AQ492985"
repeat_region	7839. .8140	/note="12 repeat: matches 1874. .2194 of consensus"
repeat_region	8359. .8518	/note="12 repeat: matches 2352. .2507 of consensus"
repeat_region	8896. .9177	/note="12 repeat: matches 1737. .2050 of consensus"
repeat_region	9228. .9290	/note="12 repeat: matches 2687. .2749 of consensus"
repeat_region	9294. .9811	/note="12 repeat: matches 1216. .1728 of consensus"
repeat_region	9851. .10280	/note="12 repeat: matches 2290. .2710 of consensus"
misc.feature	10257. .10653	/note="match: GSS: Em:AQ068985"
repeat_region	10443. .10519	/note="MIR repeat: matches 64. .150 of consensus"
repeat_region	10655. .10728	/note="12 repeat: matches 2065. .2122 of consensus"
repeat_region	10729. .11038	/note="AlusX repeat: matches 1. .307 of consensus"
repeat_region	11039. .11089	/note="12 repeat: matches 2122. .2177 of consensus"
repeat_region	12567. .12683	/note="12 repeat: matches 2572. .2694 of consensus"
repeat_region	12867. .13157	/note="12 repeat: matches 1995. .2283 of consensus"
repeat_region	13380. .13920	/note="12 repeat: matches 1151. .1686 of consensus"
misc.feature	13721. .14168	/note="match: GSS: Em:AQ826518"
repeat_region	13982. .14216	/note="MIR repeat: matches 3. .234 of consensus"
repeat_region	14253. .14566	/note="AluY repeat: matches 1. .310 of consensus"
repeat_region	14592. .15509	/note="11P4I6 repeat: matches 5195. .6155 of consensus"
repeat_region	15511. .16185	/note="11P4I6 repeat: matches 4481. .5165 of consensus"
repeat_region	16276. .16336	/note="12 repeat: matches 2651. .2710 of consensus"
repeat_region	16688. .16993	/note="AluSg repeat: matches 1. .305 of consensus"
repeat_region	17161. .17455	/note="AluVo repeat: matches 1. .296 of consensus"
repeat_region	17760. .17825	/note="33 copies 2 mer tt 69% conserved"
misc.feature	19429. .19831	/note="match: GSS: Em:B90569"
repeat_region	22841. .22905	/note="MIR repeat: matches 86. .155 of consensus"
repeat_region	24397. .24429	/note="11P4I13 repeat: matches 5319. .5351 of consensus"
repeat_region	24456. .24578	/note="11P4I10 repeat: matches 6042. .6163 of consensus"
repeat_region	24579. .25387	/note="11P4I13 repeat: matches 5338. .6144 of consensus"
repeat_region	25604. .25637	/note="MER6A repeat: matches 1. .232 of consensus"
repeat_region	26239. .26541	/note="MER82 repeat: matches 27. .340 of consensus"
repeat_region	26541. .26707	/note="MER82 repeat: matches 476. .647 of consensus"
repeat_region	27213. .27527	

	repeat_region	/note="AluIto repeat: matches 1..298 of consensus"	28352..28395	
	repeat_region	/note="22 copies 2 mer ta 81% conserved"	29176..29316	
	repeat_region	/note="MER5B repeat: matches 172..313 of consensus"	29553..29608	
	repeat_region	/note="28 copies 2 mer aa 78% conserved"	29624..29663	
	repeat_region	/note="20 copies 2 mer ga 82% conserved"	30427..30568	
	repeat_region	/note="LIME2 repeat: matches 5692..5945 of consensus"	34962..35055	
	repeat_region	/note="MIR repeat: matches 117..201 of consensus"	36030..36161	
	repeat_region	/note="MIR repeat: matches 123..255 of consensus"	36487..36558	
	repeat_region	/note="L2 repeat: matches 2656..2749 of consensus"	37144..37239	
	repeat_region	/note="24 copies 4 mer ttct 94% conserved"	37681..38061	
	repeat_region	/note="L2 repeat: matches 1996..2395 of consensus"	39084..39361	
	misc_feature	/note="AluIo repeat: matches 38..308 of consensus"	Complement(39593..40252)	
	repeat_region	/note="match: GSS; Em:AQ473752"	40398..40685	
	repeat_region	/note="AluSx repeat: matches 22..309 of consensus"	40705..41005	
	repeat_region	/note="AluSx repeat: matches 1..302 of consensus"	41266..41537	
	repeat_region	/note="L2 repeat: matches 1681..1894 of consensus"	41538..41940	
	repeat_region	/note="MLTIA1 repeat: matches 1..365 of consensus"	41941..42213	
	repeat_region	/note="L2 repeat: matches 1894..2176 of consensus"	42354..42480	
	repeat_region	/note="MIR repeat: matches 27..155 of consensus"	45158..45403	
	repeat_region	/note="LIPAF repeat: matches 5887..6141 of consensus"	46498..46809	
	misc_feature	/note="AluSx repeat: matches 1..310 of consensus"	Complement(46514..47037)	
	misc_feature	/note="match: GSS; Em:AQ345555"	Complement(46652..47055)	
	misc_feature	/note="match: GSS; Em:AQ767953"	14445 a 8652 c 9349 g 14611 t	
	BASE COUNT	14445 a 8652 c 9349 g 14611 t		
	ORIGIN			
OY	Query Match	14.3%; Score 396.8; DB 9; Length 47057;		
Dd	Best Local Similarity	99.5%; Pred. No. 5.8e-75;		
	Matches 398; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
OY	I ATGCCCGCCACACAGCGGGAAGAAGAGGGCGCGCGGCTTGGTGAAGAC	60		
Dd	4316 ATGCCCGCCACACAGCGGGAAGAAGAGGGCGCGCGGCTTGGTGAAGAC	43757		
OY	GGGCAGAGGGGGGGGGGGGGGGGGGGGGGGTTGGGCACGGCATTAAGATTGGAG	120		
Dd	4376 GGGCAGAGGGGGGGGGGGGGGGGGGGGGGGTTGGGCACGGCATTAAGATTGGAG	44355		
OY	121 TCGGCGCGGGGACAGGTCCTCTTAACATCGGCACCGGCACAGGGGCGAGGCGCTCTACTG	180		
Dd	4436 TCGGCGCGGGGACAGGTCCTCTTAACATCGGCACCGGCACAGGGGCGAGGCGCTCTACTG	44955		
OY	181 CTGGGCAACCCGCGGGCCACGCTTGGTGGCGGGCGGGTGGCTGAGGGAAGCCGCCGG	240		
Dd	4496 CTGGGCAACCCGCGGGCCACGCTTGGTGGCGGGCGGGTGGCTGAGGGAAGCCGCCGG	45555		
OY	241 GGCAAGACAGGGGGCCGGATAGCGCTGTGGGGAAGCGCGCTCTTACACAGTAGGCAG	300		
Dd	4556 GGCAAGACAGGGGGCCGGATAGCGCTGTGGGGAAGCGCGCTCTTACACAGTAGGCAG	46155		
OY	301 AGTGGCGGCGCAACGTCACTACCAGCGGGGTGACAGAACTACTACCAACGTCTGGAG	360		

```

Db      4616 AGCTCCGGCGCAAGCTACAGTCCGGGGTGGAGAGACTGTTACAGCTGTGTGAG 4675
Qy      361  AGACCCCGGGGCTGGGCGCTTATCTATCTACACAGCTTTGCTTT 400
Db      4676 AGACCCCGGGGCTGGGCGCTTATCTATCTACACAGCTTTGCTTT 4715

RESULT 49
AX456862 3005 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 3 from Patent W00232960.
ACCESSION AX456862
VERSION AX456862.1 GI:21715729
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Argentieri,T.M. and Sheldon,J.H.
AUTHORS Methods of selecting compounds for modulation of bladder function
TITLE Patent: WO 0232960-A 3 25-APR-2002;
JOURNAL Myeth (US)
FEATURES
Source 1.3005
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 646 a 815 c 844 g 597 t 103 others
ORIGIN
Query Match 14.1%; Score 389.6; DB 6; Length 3005;
Best Local Similarity 61.8%; Pred. No. 1.3e-73;
Matches 710; Conservative 0; Mismatches 394; Indels 44; Gaps 4;

Qy      39 CGCGGGCTCTGGGTGAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 98
Db      230 CGCAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 289
Qy      99 CAGCGCATGAAGATGTGAGTGGAGCGCGCG--GGCAGGTGTCTGTAACTCGGACGCC 156
Db      290 GCTAACCCAGCCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349
Qy      157 GCCAGGGCGGACGGCTGCTACTGTGGGACACCGCGCGCGCGCGCGCGCGCGCGCG 216
Db      350 GCGCGCGCGCGAGTGGAGCAAGTCACTTGGCGTGGCGCGCGCGCGCGCGCGCGCG 409
Qy      217 GGTGGCTTGAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276
Db      410 ACCCTGTCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATC 469
Qy      277 CCGCTCTCTTACAGAGTACAGCTGCC-----GGCGCAACGTCAAGTACCGG 327
Db      470 GGGCTCTTGGCCAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 529
Qy      328 CGGGTGCAGACTACCTGTACAACTGCTGTGAGAGACCGCGCGCGCGCGCGCGCTTCACTAC 387
Db      530 CGCATCAAAACTTGTATCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 589
Qy      388 CACGCTTTCGTTTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
Db      590 CACGCGTGTGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
Qy      448 CCTGAGCAGCAAAATTTGGCTCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 507
Db      650 AAGAGATGAGACACTGTCTGTGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
Qy      508 GTCTTTGGTTGGAGTTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 567
Db      710 ATCTTTGGAGCCGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
Qy      568 GGATGGCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 627

```

```

Db      770 GGCTGGCGGGGCCACTGAAGTTTGCAGAGAGCCCGCTGTGATGTGTGACATCTTTGTC 829
Qy      628 CTATGCTCTCAATAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 687
Db      830 CTGATTTCTCTGTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
Qy      688 GCACTCAGAGTCTCCGTTTCTTACAGATGCTCCGCTGCGCATGTGAGCGGAGGGA 747
Db      890 ---CTGGAGAGCCCTGCGCTTCTCGAGATCTGCGCATGTGCTGATGTGAGCGGAGG 946
Qy      748 GGCATCTTGAATTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 807
Db      947 GGCACCTGGAAAGCTTCTGTGGCTCAGCCATCTGTGCGCACAGCAAGAACTCATACGGCC 1006
Qy      808 TGGTACATAGAGATTTTGTCTTATTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 867
Db      1007 TGTGATCTGCTTCTTCTGACACTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1066
Qy      868 GATGCC-----AATTAAGATTTTCTACATATGCA 897
Db      1067 GAGCTCCAGAGTGTGATGCACAGAGAGAGATGAAGAGAGATTTGAGACCTATGCA 1126
Qy      898 GATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
Db      1127 GATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1186
Qy      958 CTAACTTGGCTGGGAAGATTTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 1017
Db      1187 AAAAGCTGGGAAGGCGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1246
Qy      1018 GCACTTCTCTCGCGCATTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
Db      1247 GCCCTTCAAGCGGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1306
Qy      1078 CAGAAACCTTTGAAAGAAAGAAAGAACCCACTGTGCAACCTCATCTAGTGTGTGTGTGT 1137
Db      1307 CAGAAACCTTTGAAAGAAAGAAAGAACCCACTGTGCAACCTCATCTAGTGTGTGTGTGT 1366
Qy      1138 AGTTACGC 1145
Db      1367 TATTATGC 1374

RESULT 50
AB000504 2247 bp mRNA linear ROD 23-JAN-1999
LOCUS AB000504
DEFINITION Mus musculus mRNA for alternative splicing:see accession between
ACCESSION AB000504
VERSION AB000504.1 GI:4176413
KEYWORDS mKOT2.11; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,
Sasai,H. and Nishi,Y.
TITLE KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
JOURNAL J. Biol. Chem. 273(15):10511-10518 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2247)
AUTHORS Watanabe,H.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc.,
Pharmaceutical Basic Research Lab., 6-2, Umeogakka, Aoba-ku,
Yokohama, Kanagawa 227, Japan (E-mail:watanabe@crl.jti.co.jp,
Tel:045-972-5741)
FEATURES
Source 1.2247
Location/Qualifiers
/organism="Mus musculus"

```

CDS
/db_xref="taxon:10090"
87..1103
/note="mKOT2.11"

/product="alternative splicing: see accession between
AB000494 and AB000504"
/protein_id="BAA37166.1"
/db_xref="gi:4176414"

/translation="MYOKSRNGVYPGNSGKKLVKVPVGLDPAADSTRDALLIG
SEAPKRGSVLSKPRGTGAGAGKPKRMAFYKLONFLNVLNLERPMATYHAYFL
VSCULVSPSTIKEYKSESGALYILEIVIVFVGVFVIRIMAGCCCRGWMGR
LFRKPFCEVIDIMVLASIAVLAAAGSNGFASLSRLFLQILRMIMDRRGSTW
KLGSVYAHSEKELVAMVIGFLCLILASIFLAEKENDHEDYADALIMGLTIT
TIGYDKYFQTMNGRLIATFTLIGVSEFFALPAVSPAHLPLEMLGVLEAPKAMPW
TCEL"

polyA_site

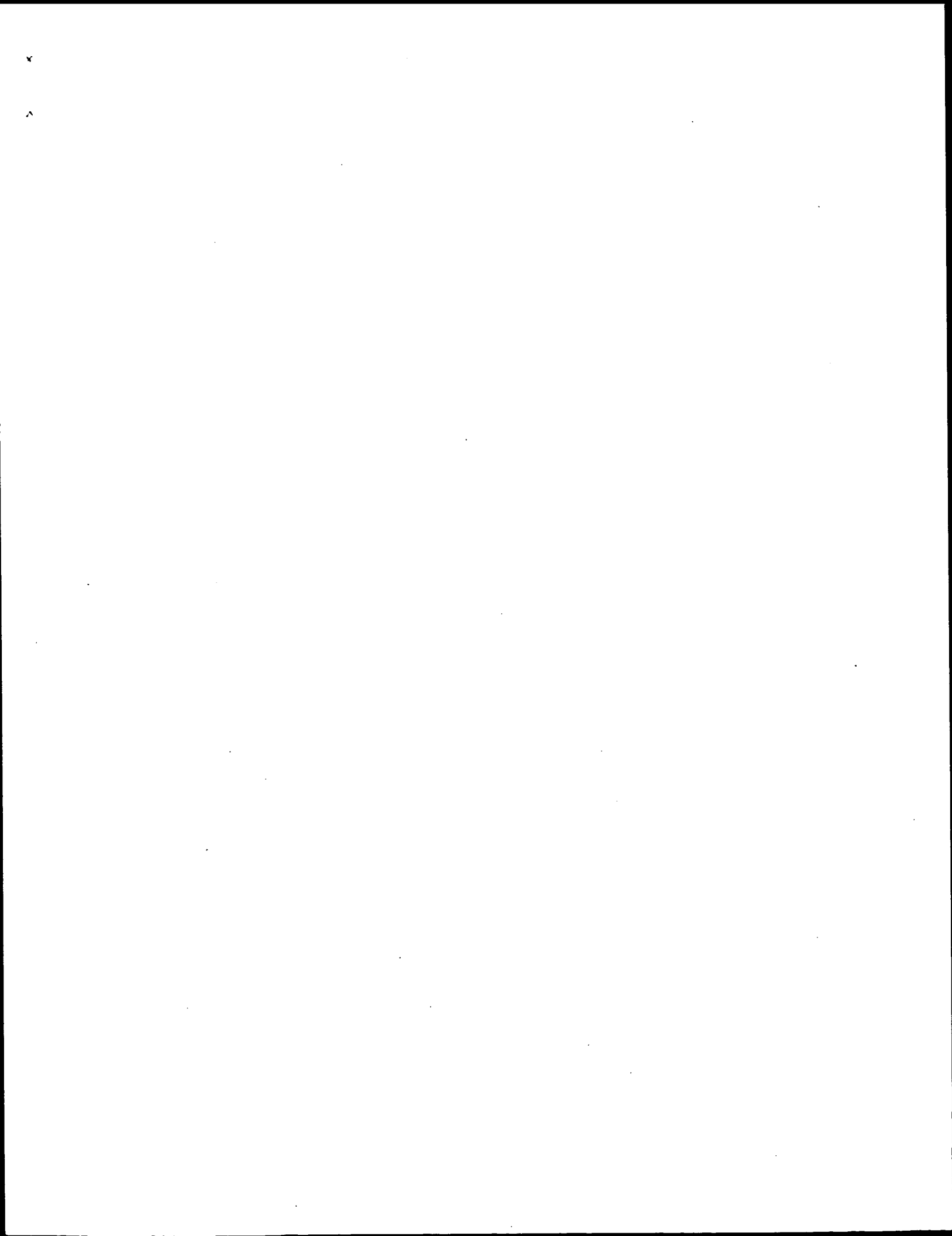
BASE COUNT 444 a 587 c 655 g 561 t
ORIGIN

Query Match 13.2%; Score 365.6; DB 10; Length 2247;
Best Local Similarity 63.8%; Pred. No. 2e-68;
Matches 554; Conservative 0; Mismatches 314; Indels 0; Gaps 0;

QY 169 GGCCTGCTACTGCTGGGACCCGCGGCCACGCTCGTGCGGCGCGGCTTGAGG 228
DB 153 GGCCTGCTGCGGTGGACCCGCGGCCGACGCTCCACACGCGAGCGCGCTACTCATT 212
QY 229 GAGAGCGCGCGGGGACAGAGCGCGCGGATGAGCCTGCTGGGAGCGCGCTCTTAC 288
DB 213 GCGGCTCCGAGGCGCCCGGAGCGCGGATTTGAGCAAAACCGCGAGCGCGCGCG 272
QY 289 ACGAGTAGCCAGAGCTGCGCGCCCAAGTAACTGCGCGGCGGTGAGACACTGCTTAC 348
DB 273 GAGCGCGGAGAGCGCCCGGAGCGCAAGCGCTTCTACCGCAAGCTGCAAAATTCCTTAC 332
QY 349 AACGCTGGAAGAGACCCCGCGGTGCGCTTCACTTACCAAGCTTCTTCTCTT 408
DB 333 AACGCTGGAAGAGCGCGCGGTGCGCTTCACTTACCAAGCTTCTTCTTCTT 392
QY 409 GTCCTTGGTGGTCTGATTTTGTGATGTTTCTACATCCCTGAGCACAAATTTGGCC 468
DB 393 GTCCTTCTCTGCTGCTGCTTCTTCTGTTTCCACCAATCAAGGATACGAGAGAGCTCT 452
QY 469 TCAAGTGCCTCTTGAATCTGAGTTCGTGATGATGCTTCTTGTGAGTTCATC 528
DB 453 GAGGCGCGCTCTTGAATCTGAGTTCGTGATGATGCTTCTTGTGAGTTCATC 512
QY 529 ATTGAATCTGCTGCGCGGTGCTGCTTGCATATAGAGATGCGCAAGAGACTGAGG 588
DB 513 GTGAGATCTGGGCTGCGAGCTGCTGCGGTATCGAGGCTGGAGCGCGCTCAAG 572
QY 589 TTTGCTCGAAAGCCCTTCTGTTATAGATACATGTTCTTATCGCTTCAATAGCAGTT 648
DB 573 TTTGCGAAGAGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATG 632
QY 649 GTTCTGCAAAACTCAGGGAATATTTTTCACGCTGCTGACAGAGTCTCGTTTC 708
DB 633 CTGGCTGCTGTTCCAGGGAATGTTTTCACATCTCGCTTCGAGCTTCGGGTTTC 692
QY 709 CTACAGATCTCCCGATGCTGCGCATGAGCCGAAGGAGGAGCACTTGAATTTACTGGGT 768
DB 693 TTGCAAAATCTTGGCATGATTCGATGAGGAGCGGAGGAGGAGCACTTGGGA 752
QY 769 TCACTGCTTATGCTACAGCAAGCAATTAATCAAGCTGATACATAGATTTTGGTT 828
DB 753 TCGGTAGCTAGCTACAGCAAGCAAGGAGCTGAGTACCTGCTGATGCTTCTCTCC 812
QY 829 CTATATTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 888
DB 813 CTCAATCCCTGAGCTCAATTTCTGATGAGCAAGGAGGAGGAGGAGGAGGAGGAG 872
QY 889 ACATATGAGATGCTCTGCTGAGGAGCAATTAATTAATTAATTAATTAATTAATTA 948

DB 873 ACCTACGAGATGACACTCTGCTGAGGCTGATACCTGAGACCATGCTACGGGGAC 932
QY 949 AAACTCCCTTAATCTTGGCTGAGAGATGCTTCTGCAAGGCTTGGCACTCTTGGCAT 1008
DB 933 AAGTACCTCAGACCTGGAAGCGGAGGCTGCTGCAAGGAGGAGGAGGAGGAGGAGG 992
QY 1009 TCTTCTTGGCACTTCTGCTGCGGAGTTC 1036
DB 993 TCGTCTTGGCTTCTGCTGCTGCTGAGTC 1020

Search completed: June 19, 2003, 10:10:13
Job time : 6994 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:57:11 ; Search time 3469 Seconds
(without alignments)
12941.450 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772

Sequence: 1 atgcccgcgcacacgcggg.....ctcatgtcaactgcaataa 2772

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 24

Total number of hits satisfying chosen parameters: 69

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hlc:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	20.9	658	10	BE158938
2	490	17.7	506	12	BF959996
3	478	17.2	734	12	BG532543
4	470	17.0	547	13	BI034993
5	466	16.8	491	12	BF959488
6	432	15.6	570	13	BI033850

C	7	419	15.1	435	12	BF943257	BF943257 QV2-NN004
C	8	359	13.0	568	14	BQ339931	BQ339931 QV2-NN004
C	9	332	12.0	517	12	BF954375	BF954375 QV2-NN004
C	10	321	11.6	508	12	BF240146	BF240146 QV2-NN004
C	11	215	7.8	267	12	BF945327	BF945327 QV2-NN004
C	12	212	7.6	266	14	BQ340178	BQ340178 QV2-NN200
C	13	179	6.5	520	17	AQ383296	AQ383296 RPT11-13
C	14	179	6.5	659	17	AQ344243	AQ344243 RPT11-13
C	15	158	5.7	224	12	BF954374	BF954374 QV2-NN004
C	16	144	5.2	297	12	BQ340041	BQ340041 QV2-NN004
C	17	129	4.7	267	14	BG185229	BG185229 RST4167 A
C	18	115	4.1	166	17	AQ019541	AQ019541 CIT-HSP-2
C	19	107	3.9	248	10	BE177584	BE177584 RCT1-HT059
C	20	106	3.8	267	12	BG185740	BG185740 RST4692 A
C	21	106	3.8	335	12	BG218030	BG218030 RST37756
C	22	102	3.7	160	12	BF959223	BF959223 QV2-NN004
C	23	102	3.7	160	12	BF959223	BF959223 QV2-NN004
C	24	56	2.0	469	10	BE103175	BE103175 QV2-NN004
C	25	56	2.0	469	10	BE103175	BE103175 QV2-NN004
C	26	48	1.7	434	13	BI290441	BI290441 QV2-NN004
C	27	48	1.7	719	17	BH307140	BH307140 CH230-10L
C	28	44	1.6	584	10	AM049888	AM049888 QV2-NN004
C	29	44	1.6	662	10	BB657491	BB657491 QV2-NN004
C	30	38	1.4	477	17	AZ443500	AZ443500 QV2-NN004
C	31	38	1.4	679	10	BE647997	BE647997 QV2-NN004
C	32	35	1.3	226	9	AI705051	AI705051 QV2-NN004
C	33	35	1.3	226	9	AI705051	AI705051 QV2-NN004
C	34	35	1.3	330	10	AW122800	AW122800 QV2-NN004
C	35	35	1.3	330	10	AW122800	AW122800 QV2-NN004
C	36	35	1.3	411	12	BF414224	BF414224 QV2-NN004
C	37	35	1.3	425	10	BE648243	BE648243 QV2-NN004
C	38	35	1.3	427	12	BF523361	BF523361 QV2-NN004
C	39	34	1.2	632	10	BB624101	BB624101 QV2-NN004
C	40	31	1.1	282	9	AI603318	AI603318 QV2-NN004
C	41	31	1.1	766	11	AK020325	AK020325 QV2-NN004
C	42	26	0.9	121	12	BE549164	BE549164 QV2-NN004
C	43	26	0.9	597	10	BE260338	BE260338 QV2-NN004
C	44	26	0.9	622	10	BE257127	BE257127 QV2-NN004
C	45	26	0.9	749	14	BQ192564	BQ192564 QV2-NN004
C	46	26	0.9	914	12	BF312386	BF312386 QV2-NN004
C	47	26	0.9	920	12	BF317072	BF317072 QV2-NN004
C	48	26	0.9	942	17	CNS04101	CNS04101 QV2-NN004
C	49	26	0.9	1019	17	AG082214	AG082214 QV2-NN004
C	50	26	0.9	1068	12	BF311176	BF311176 QV2-NN004
C	51	25	0.9	360	9	AJ473656	AJ473656 QV2-NN004
C	52	25	0.9	515	12	BF962769	BF962769 QV2-NN004
C	53	25	0.9	620	13	BI481490	BI481490 QV2-NN004
C	54	25	0.9	654	13	BQ322066	BQ322066 QV2-NN004
C	55	24	0.9	245	14	BQ743468	BQ743468 QV2-NN004
C	56	24	0.9	305	9	AL819351	AL819351 QV2-NN004
C	57	24	0.9	360	10	BE424257	BE424257 QV2-NN004
C	58	24	0.9	439	10	AV433779	AV433779 QV2-NN004
C	59	24	0.9	452	13	BI099054	BI099054 QV2-NN004
C	60	24	0.9	475	12	BF412048	BF412048 QV2-NN004
C	61	24	0.9	528	10	AW677894	AW677894 QV2-NN004
C	62	24	0.9	542	9	AL818794	AL818794 QV2-NN004
C	63	24	0.9	606	14	BQ804704	BQ804704 QV2-NN004
C	64	24	0.9	622	9	AL552285	AL552285 QV2-NN004
C	65	24	0.9	634	9	AL589812	AL589812 QV2-NN004
C	66	24	0.9	681	14	BQ744000	BQ744000 QV2-NN004
C	67	24	0.9	691	17	CNS021M5	CNS021M5 QV2-NN004
C	68	24	0.9	697	14	BQ806810	BQ806810 QV2-NN004
C	69	24	0.9	850	9	AL555639	AL555639 QV2-NN004

ALIGNMENTS

RESULT 1	BE158938	658 bp	MRNA	EST 21-JUN-2000
LOCUS	BE158938			
DEFINITION	MR0-HT0404-210200-001-c04 HT0404		Homo sapiens	CDNA, mRNA sequence.
ACCESSION	BE158938			

VERSION BE158938.1 GI:8621659
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 658)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=MR0-HT0404-210
 200-001-C046t3=2000-02-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 657.
 Location/Qualifiers
 1..658
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0404"
 /dev_stage="Adult"
 /note="Organ: head-neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 181 a 175 c 153 g 149 t
 Query Match 20.9%; Score 578; DB 10; Length 658;
 Best Local Similarity 99.8%; Pred. No. 7.6e-286;
 Matches 628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 936 TGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAGATTGCTTCTGACAGGCTTTGC 995
 Db 17 TGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAGATTGCTTCTGACAGGCTTTGC 76
 QY 996 ACTCCCTGGGATTTCTTCTTGGACTTCCGCGCGGCAATCTTGGCTGACGTTTTCATT 1055
 Db 77 ACTCCCTGGGATTTCTTCTTGGACTTCCGCGCGGCAATCTTGGCTGACGTTTTCATT 136
 QY 1056 AAAAGTACAGAACACCGCCGCAAAACATTGAGAAAAGAAAGAACCCAGCTGCCAA 1115
 Db 137 AAAAGTACAGAACACCGCCGCAAAACATTGAGAAAAGAAAGAACCCAGCTGCCAA 196
 QY 1116 CCTCATTCAGTGTGTTGGCGTACTAAGCAGCTGATGAGAAATCTGTTCCATTGCAAC 1175
 Db 197 CCTCATTCAGTGTGTTGGCGTACTAAGCAGCTGATGAGAAATCTGTTCCATTGCAAC 256
 QY 1176 CTGGAAGCCCACTTGAAGGCTTGCACACTGACAGCCCTACCATTCAGAACTTAAGTTT 1235
 Db 257 CTGGAAGCCCACTTGAAGGCTTGCACACTGACAGCCCTACCATTCAGAACTTAAGTTT 316
 QY 1236 TAAGAGCGAGTCCGATGCTAGCCCGAGGGCGAGATTTAAGAGCCGACAGCCCTC 1295
 Db 1236 TAAGAGCGAGTCCGATGCTAGCCCGAGGGCGAGATTTAAGAGCCGACAGCCCTC 1295

Db 317 TAAGAGCGAGTCCGATGCTAGCCCGAGGGCGCAAGATTTAAGAGCCGACAGCCCTC 376
 QY 1296 ACTAGTGCACAGAGAGTCCCGACACCCGACATACAGCCGAGGAGTCCACCAAGT 1355
 Db 377 ACTAGTGCACAGAGAGTCCCGACACCCGACATACAGCCGAGGAGTCCACCAAGT 436
 QY 1356 GCAGAGAGCTGAGGCTTCAACGACGACCCGCTCGGCGCTGGCGGCTGCAAAAG 1415
 Db 437 GCAGAGAGCTGAGGCTTCAACGACGACCCGCTCGGCGCTGGCGGCTGCAAAAG 496
 QY 1416 TTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATATGA 1475
 Db 497 TTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATATGA 556
 QY 1476 TGAAGAGATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1535
 Db 557 TGAAGAGATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 616
 QY 1536 CATTGAGCTATCAGATTAATGAATTC 1564
 Db 617 CATTGAGCTATCAGATTAATGAATTC 645
 RESULT 2
 BF959996/c 506 bp mRNA linear EST 22-JAN-2001
 LOCUS QV2-NN0045-051200-526-g09 NN0045 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF959996
 ACCESSION BF959996.1 GI:12377271
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 506)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 COMMENT Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-051200-526-g09&t3=2000-12-05&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 506.
 Location/Qualifiers
 1..506
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous, normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 125 a 108 c 104 g 168 t 1 others

TITLE
JOURNAL
MEDLINE
COMMENT

'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN2004-120401-621-902&t3=2001-04-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 543.

FEATURES

source

1. .547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN2004"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Location/Qualifiers
175 a 127 c 116 g 129 t

BASE COUNT 175 a 127 c 116 g 129 t
ORIGIN

Query Match 17.0%; Score 470; DB 13; Length 547;
Best Local Similarity 99.8%; Pred. No. 3e-230; Indels 0; Gaps 0;
Matches 520; Conservative 0; Mismatches 1;

1373 TCACGACCGACCGCCGCTCCGCGCTCGTCCGCTCAAAAGTTCTCAGCCAAACGAG 1432
1 TCACGACCGACCGCCGCTCCGCGCTCGTCCGCTCAAAAGTTCTCAGCCAAACGAG 60

1433 TGTATATGCTGACACAGCCCTTGCCACTGATGATGATGATGATGATGATGATGATGAT 1492
61 TGTATATGCTGACACAGCCCTTGCCACTGATGATGATGATGATGATGATGATGATGAT 120

1493 GTGATGATCAGGAGAACCTCACCACCACTTAAAGTCTATTCGAGCTATCAGAA 1552
121 GTGATGATCAGGAGAACCTCACCACCACTTAAAGTCTATTCGAGCTATCAGAA 180

1553 TTATGAAATTTTCATGTTGCAAAAGGAGTTTAAGAAACATTTAGCTCATATGATGTA 1612
181 TTATGAAATTTTCATGTTGCAAAAGGAGTTTAAGAAACATTTAGCTCATATGATGTA 240

1613 AAGATGTCATTGACAAATATTTCTGCTGATATCTGGACATTTGTGTAAGATTAAAGCC 1672
241 AAGATGTCATTGACAAATATTTCTGCTGATATCTGGACATTTGTGTAAGATTAAAGCC 300

1673 TTCAACAGCGTGTGATCAAAATCTTGGAAAGGGCAAAATCAGATCAGATAAGAGACC 1732
301 TTCAACAGCGTGTGATCAAAATCTTGGAAAGGGCAAAATCAGATCAGATAAGAGACC 360

1733 GAGAGAAATTAACAGCAGAACATGAGACACAGACATCTCAGTATGCTCGGTGGGTGG 1792
361 GAGAGAAATTAACAGCAGAACATGAGACACAGACATCTCAGTATGCTCGGTGGGTGG 420

1793 TCAAGGTTGAAAAAGAGTACAGTACATAGATTAATCCAAAGCTGAGTGCCTACTAGACATCT 1852
421 TCAAGGTTGAAAAAGAGTACAGTACATAGATTAATCCAAAGCTGAGTGCCTACTAGACATCT 480

1853 ATCAACAGGTCCTTGGAAGAGGCTTGCGTCAGCCCTCGCT 1893

Db 481 ATCAACAGGTCCTTGGAAGAGGCTTGCGTCAGCCCTCGCT 521

RESULT 5
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF959488 491 bp mRNA linear EST 22-JAN-2001
QV2-NN0045-031200-511-b03 NN0045 Homo sapiens cDNA, mRNA sequence.
BF959488
BF959488.1 GI:12376763
EST.
SOURCE
human.
Homo sapiens

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 491)
Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalhal, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.G.

TITLE
JOURNAL
MEDLINE
COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-031200-511-b03&t3=2000-12-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 491.

BASE COUNT 165 a 103 c 107 g 114 t
ORIGIN

FEATURES
source

1. .491
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Location/Qualifiers
165 a 103 c 107 g 114 t

Query Match 16.8%; Score 466; DB 12; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.4e-228; Indels 0; Gaps 0;
Matches 466; Conservative 0; Mismatches 0;

1373 TCACGACCGACCGCCGCTCCGCGCTCGTCCGCTCAAAAGTTCTCAGCCAAACGAG 1432
14 TCACGACCGACCGCCGCTCCGCGCTCGTCCGCTCAAAAGTTCTCAGCCAAACGAG 73

1433 TGTATGATGCTGACACAGCCCTTGCCACTGATGATGATGATGATGATGATGATGATGAT 1492
74 TGTATGATGCTGACACAGCCCTTGCCACTGATGATGATGATGATGATGATGATGATGAT 133

1493 GTGATGATCAGGAGAACCTCACCACCACTTAAAGTCTCATTGAGCTATCAGAA 1552
134 GTGATGATCAGGAGAACCTCACCACCACTTAAAGTCTCATTGAGCTATCAGAA 193

1553 TTATGAAATTTTCATGTTGCAAAAGGAGTTTAAGAAACATTTAGCTCATATGATGTA 1612


```

|||||
DB 194 TTATGAAATTTTCATTTGTCAAACGGAAGTTTAAAGAAACATTCCTCCATATGATGTTAA 253
OY 1613 AAGATGTCATGGAACAAATATTCCTGCTGTCATCTGACATGTTGTAGATTTAAAGCC 1672
DB 254 AAGATGTCATGGAACAAATATTCCTGCTGTCATCTGACATGTTGTAGATTTAAAGCC 313
OY 1673 TTCAAAACACGCTGTCATCAAAATTTCTTGAAAGGCAAAATCAGATCAGATTAAGAGGCC 1732
DB 314 TTCAAAACACGCTGTCATCAAAATTTCTTGAAAGGCAAAATCAGATCAGATTAAGAGGCC 373
OY 1723 GAGAGAAATATACAGACAGAAATGAGACACAGACATCTCAGTATGCTGCTGCGGTGG 1792
DB 374 GAGAGAAATATACAGACAGAAATGAGACACAGACATCTCAGTATGCTGCTGCGGTGG 433
OY 1793 TCAGGTTGAAAAACAGGTACAGTCCATAGATTCACAGCTGACTG 1838
DB 434 TCAGGTTGAAAAACAGGTACAGTCCATAGATTCACAGCTGACTG 479

```

```

RESULT 6
BI033850/c 570 bp mRNA linear EST 14-JUN-2001
LOCUS QV2-NN2003-080301-615-c03 NN2003 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI033850
VERSION BI033850.1 GI:14440476
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 570)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&tl2-QV2-NN2003-
080301-615-c03&tl3-2001-03-08&tl4-1)
Seq primer: puc 18 forward
High quality sequence stop: 570.
Location/Qualifiers
1..570
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NN2003"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site1: SmaI;
Site2: SmaI; A mini-library was made by cloning products
derived from ORFESTS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

```

BASE COUNT 135 a 122 c 131 g 182 t
ORIGIN
Query Match 15.6%; Score 432; DB 13; Length 570;

```

```

Best Local Similarity 99.6%; Pred. No. 1.le-210;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1416 TTTCACGCCAAACACAGATGATGATGATGACACAGCCCTGGCAGATGATGATATATGA 1475
DB 534 TTTCACGCCAAACACAGATGATGATGATGACACAGCCCTGGCAGATGATGATATATGA 475
OY 1476 TGAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1535
DB 474 TGAAGAAAGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
OY 1536 CATTCAGACCTATCAGAAATTTGAAATTTTCATGTTGCAAAACGAGACTTTAAGAAACATT 1595
DB 414 CATTCAGACCTATCAGAAATTTGAAATTTTCATGTTGCAAAACGAGACTTTAAGAAACATT 355
OY 1596 ACGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1655
DB 354 ACGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 255
OY 1656 GTGTAGAAATTAAGACCTTCAACACAGCTGTGATCAAAATTTCTTGAAAAAGGCAAAATCAC 1715
DB 294 GTGTAGAAATTAAGACCTTCAACACAGCTGTGATCAAAATTTCTTGAAAAAGGCAAAATCAC 235
OY 1716 ATCAGATTAAGAAAGAGCCGAGAGAAATTAACAGCAACATGAGACCAAGACATGCTCAG 1775
DB 234 ATCAGATTAAGAAAGAGCCGAGAGAAATTAACAGCAACATGAGACCAAGACATGCTCAG 175
OY 1776 TATGCTCGGTGGGGGTGATCAAGTTGAAAAACAGTACAGTCCATAGATTCACAGCTGGA 1835
DB 174 TATGCTCGGTGGGGGTGATCAAGTTGAAAAACAGTACAGTCCATAGATTCACAGCTGGA 115
OY 1836 CTGCTACTAGACATCTATCAACAGGCTCTTGGAAAAAGGCTGCTGACGCTCGCTTT 1895
DB 114 CTGCTACTAGACATCTATCAACAGGCTCTTGGAAAAAGGCTGCTGACGCTCGCTTT 55
OY 1896 GCGTTCATTCAGATCCGACCTTTTAAATGTAAGACAGACATCTGACATATCAAG 1949
DB 54 GCGTTCATTCAGATCCGACCTTTTAAATGTAAGACAGACATCTGACATATCAAG 1

```

```

RESULT 7
BF943257/c 435 bp mRNA linear EST 22-JAN-2001
LOCUS QV2-NN0045-041000-403-h12 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF943257
VERSION BF943257.1 GI:12360532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 435)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&tl2-QV2-NN0045-

```

```

TITLE
JOURNAL
MEDLINE
COMMENT

```

FEATURES

041000-403-h126t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 433.
Location/Qualifiers
1..435

BASE COUNT

110 a 94 c 89 g 142 t

ORIGIN

Query Match 15.1%; Score 419; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.3e-204;
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1533 TGTGATTCGAGCTATCGAATTAATGAAATTTGATGTCGCAAAACGAACTTTAAGGAAC 1592
|||||
DB 435 TGTGATTCGAGCTATCGAATTAATGAAATTTGATGTCGCAAAACGAACTTTAAGGAAC 376
|||||
QY 1593 ATTACGTCCTATGATGATTAAGATGTCATGACCAATATTCGTGTCATCTGACAT 1652
|||||
DB 375 ATTACGTCCTATGATGATTAAGATGTCATGACCAATATTCGTGTCATCTGACAT 316
|||||
QY 1653 GTTGTGTAGATTAAGAGCTTCAACACGCTGTGATCAATTTCTTGGAAAGGGCAAT 1712
|||||
DB 315 GTTGTGTAGATTAAGAGCTTCAACACGCTGTGATCAATTTCTTGGAAAGGGCAAT 256
|||||
QY 1713 CACATCAGATTAAGAGCGGAGAGAAATTAACAGCAATGAGACAGACAGATCT 1772
|||||
DB 255 CACATCAGATTAAGAGCGGAGAGAAATTAACAGCAATGAGACAGACAGATCT 196
|||||
QY 1773 CAGTATGCTGCGTGGGTGCTCAAGTTGAAAGAGAGTACAGTCCATAGATCCAAAGT 1832
|||||
DB 195 CAGTATGCTGCGTGGGTGCTCAAGTTGAAAGAGAGTACAGTCCATAGATCCAAAGT 136
|||||
QY 1833 GGACCTGCTACTAGACATCTATCAACAGCTCTTGGAAAGGCTCTGCTCAGCCCTGCG 1892
|||||
DB 135 GGACCTGCTACTAGACATCTATCAACAGCTCTTGGAAAGGCTCTGCTCAGCCCTGCG 76
|||||
QY 1893 TTTGGCTCATTCAGATCCACCTTTTGAATGTAAGACAGATCTGACTATCAAGCC 1951
|||||
DB 75 TTTGGCTCATTCAGATCCACCTTTTGAATGTAAGACAGATCTGACTATCAAGCC 17
|||||
RESULT 8 BQ339331 568 bp mRNA linear EST 20-MAY-2002
LOCUS QV2-NN0045-081200-535-f03 NN0045 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ339331
ACCESSION BQ339331.1 GI:21000109
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 568)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAESP/ILICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV2&t2=QV2-NN0045-
081200-535-f03&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1..568

FEATURES

Source

BASE COUNT

176 a 121 c 128 g 143 t

Query Match 13.0%; Score 359; DB 14; Length 568;
Best Local Similarity 100.0%; Pred. No. 4.5e-173;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1527 TAAACTGTCTAGTGAAGCTATCAGATTAATGAAATTTGATGTCGCAAAACGAAAGTTAA 1586
|||||
DB 180 TAAACTGTCTAGTGAAGCTATCAGATTAATGAAATTTGATGTCGCAAAACGAAAGTTAA 239
|||||
QY 1587 GGAACATTAGCTCATATGATTAAGAGTGTCAATGAAATATTCGCTGCTATCT 1646
|||||
DB 240 GGAACATTAGCTCATATGATTAAGAGTGTCAATGAAATATTCGCTGCTATCT 299
|||||
QY 1647 GGACATGTTGTGTAATTAAGAGCTTCAACAGAGTGTGATCAATTTCTTGGAAAG 1706
|||||
DB 300 GGACATGTTGTGTAATTAAGAGCTTCAACAGAGTGTGATCAATTTCTTGGAAAG 359
|||||
QY 1707 GCAATTCATCATATAAGAGAGCGGAGAGAAATTAACAGCAATGAGACACAGA 1766
|||||
DB 360 GCAATTCATCATATAAGAGAGCGGAGAGAAATTAACAGCAATGAGACACAGA 419
|||||
QY 1767 CGATCTCAGTATGCTGCGGTGCGGTCAAGGTTGAAAGAGGTACATCCATAGAATC 1826
|||||
DB 420 CGATCTCAGTATGCTGCGGTGCGGTGCAAGGTTGAAAGAGGTACATCCATAGAATC 479
|||||
QY 1827 CAAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTGGAAAGGCTCTGCTCAG 1885
|||||
DB 480 CAAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTGGAAAGGCTCTGCTCAG 538
|||||
RESULT 9 BF954375 517 bp mRNA linear EST 22-JAN-2001
LOCUS BF954375
DEFINITION QV2-NN0045-131100-414-f08 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF954375
VERSION BF954375.1 GI:12371650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 517)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE
JOURNAL
MEDLINE
COMMENT

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t2=QV2-NN0045-131100-414-f08&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 517.
Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous; normal; Vector: puc18; Site: 1; SmaI; Site: 2; SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT
169 a 106 c 123 g 119 t
ORIGIN

Query Match
Best Local Similarity 12.0%; Score 332; DB 12; Length 517;
Pred. No. 3.5e-159;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1550 GAATTTGAATTTTCATGTTGCAAAACGAGATTAAAGAAACATTCATCATATGATG 1609
186 GATTTCATTAATTTTCATGTTGCAAAACGAGATTAAAGAAACATTCATCATATGATG 245
1610 TAAAGATGTCATGTAACAAATATTCGCTGTCATGTCGACATGTTGTGTAATTAAGA 1669
246 TAAAGATGTCATGTAACAAATATTCGCTGTCATGTCGACATGTTGTGTAATTAAGA 305
1670 GCCTTAAACACGCTGTCATGTAACAAATTCCTGAAAGGCAATTCATCATTAAGAAGA 1729
306 GCCTTAAACACGCTGTCATGTAACAAATTCCTGAAAGGCAATTCATCATTAAGAAGA 365
1730 GCGAGAGAAATTAACAGCAGAAATGAGACCAAGCATCTCAGTATGCTCGGTCGGG 1789
366 GCGAGAGAAATTAACAGCAGAAATGAGACCAAGCATCTCAGTATGCTCGGTCGGG 425
1790 TGGTCAGGTTGTAAGAAACAGGTACAGTCCATAGATTCAGACTGCTACTAGACA 1849
426 TGGTCAGGTTGTAAGAAACAGGTACAGTCCATAGATTCAGACTGCTACTAGACA 485
1850 TCTATCAACAGGTCCTTCGGAAGGCTCTGCC 1881
486 TCTATCAACAGGTCCTTCGGAAGGCTCTGCC 517
DB

RESULT 10
BF240146 908 bp mRNA linear EST 14-NOV-2000
LOCUS 601905649F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133293 5',
DEFINITION mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BF240146
BF240146.1 GI:11154069
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 908)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1034 row: b column: 14
High quality sequence stop: 615.
Location/Qualifiers
1..908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4133293"
/clone_lib="NIH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccgcctcggcc); Site: 2: SfiI (ggccatcagcc)
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGGCGGAGCGGCCACATG-df(30)-NH-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT
263 a 229 c 217 g 199 t
ORIGIN

Query Match
Best Local Similarity 11.6%; Score 321; DB 12; Length 908;
Pred. No. 1.9e-153;
Matches 441; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

2103 CAGTCAGCAACACAGGTCGCAATTTAGTCAACGATGCTCAGCAGTGGCAGCCACCA 2162
1 CAGTCAGCAACACAGGTCGCAATTTAGTCAACGATGCTCAGCAGTGGCAGCCACCA 60
2163 CAGTCAGCAACACAGGTCGCAATTTAGTCAACGATGCTCAGCAGTGGCAGCCACCA 2222
61 CAGTCAGCAACACAGGTCGCAATTTAGTCAACGATGCTCAGCAGTGGCAGCCACCA 120
2223 CCACCTCTCTCCACGATCAAGATTCGCCAGGCCAGAACTCTGACACCTTAACC 2282
121 CCACCTCTCTCCACGATCAAGATTCGCCAGGCCAGAACTCTGACACCTTAACC 179
2283 TGCAGGCTTACAGGAAGCATTTCTGACGTCACACACCTGCTTGTCTCCCAAGAAA 2342
180 TGCAGGCTTACAGGAAGCATTTCTGACGTCACACACCTGCTTGTCTCCCAAGAAA 239
2343 TGTTCAGGTTGACAGTCAATCTCACCAGGACCGTTCTATGAGAAAGCTTTGACAT 2402
240 TGTTCAGGTTGACAGTCAATCTCACCAGGACCGTTCTATGAGAAAGCTTTGACAT 299
2403 GGGAGGAGAAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2462
300 GGGAGGAGAAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 359
2463 GTCTGTGCAAAACCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2522
DB

D_b 360 GTCTGTGCAAAACCTGATCAGGTCACCGACGAGAACTGAATATATACACTTTCAGGGGAGTGA 419

O_Y 2523 GTCAAGTGGCTCCAGAGGCAGC 2544

D_b 420 GTCAAGTGGCTCCAGAGGCAGC 441

RESULT	11
LOCUS	Bf945327/c
DEFINITION	Bf945327
ACCESSION	U02-NN00645-231000-425-a01 NN0045 Homo sapiens CDNA,
VERSION	Bf945327
KEYWORDS	Bf945327.1 GI:12362602
SOURCE	EST.
ORGANISM	human.
	Homo sapiens
	Homo sapiens

REFERENCE AUTHORS	TITLE
1 (pages 1 to 267) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bittencourt, M. R., Negal, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, C. H., Carvalho, A. F., Matsushima, A., Bata, G. S., Simpson, D. H., Brunslein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
Contact: Simpson A. J. G.	

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=QV2&tbl=QV2-NN0045>
 231000-425-001ct3-2000-10-23ct4-1)
 Seq primer: puc 18 forward
 High quality sequence stat: 19
 High quality sequence stop: 267.
 Location/Qualifiers
 1..267
 source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="organ: nervous normal; Vector: puc19, site_1: SmaI;
site_2: SmaI; A mini-library was made by cloning products
derived from ORESPRS PCR (U.S. Letters Patent application
No. 196,716 Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

Query Match	Best Local Similarity	7.8%;	Score 215;	DB 12;	Length 267;
		100.0%;	Pred. No. 5.4e-99;		
Matches	215;	Conservative	0;	Mismatches	0;
			Indels	0;	Gaps
1373	TCAACACCGAAGCCCGCTTCGGGCCCGGTGGGCGCCCAAAAGTTCACGCCAAACACG	1432			
1373					
267	TCACACACCGAAGCCCGCTTCGGGCCCGGTGGGCGCCCAAAAGTTCACGCCAAACACG	208			
267					
1433	TCATAGATCTGCACACAGCCCTTGGCAGCTATGATGATATGATGAAGAAAGGATGCCAGT	1492			
1433					
207	TCATAGATCTGCACACAGCCCTTGGCAGCTATGATGATATGATGAAGAAAGGATGCCAGT	148			
207					

OY 1493 TTGATGTGTGCTGGAGACCTCACCCACCACCTTTAAATCTGTATTCGAGCTATCGAA 1552
 Db 147 GTGATGTATTCAGTGGAGAACCTCACCCACCACCTTTAAATCTGTATTCGAGCTATCGAA 88
 OY 1553 TTATGAATTCATGTTGCGAAACGGAAGTTTANG 1587
 Db 87 TTATGAATTCATGTTGCGAAACGGAAGTTTANG 53

RESULT	12
LOCUS	BQ340178
DEFINITION	BQ340178 266 bp mRNA linear EST 20-MAY-2002
ACCESSION	Q9V-NN2004-040501-643-b02 NN2004 Homo sapiens cDNA, mRNA sequence.
VERSION	BQ340178
KEYWORDS	BQ340178.1 GI:21000738
SOURCE	EST.
	human.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
1 (bases 1 to 266)						
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,						
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, E.F.,						
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,						
Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare						
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and						
Simpson, A.J.						
Shotgun sequencing of the human transcriptome with ORF expressed						
sequence tags						
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
20202663						
Contact: Simpson A.J.G.						

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t2=QV2-NN2004-040501-643-b02&t3=2001-05-04&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 266.
Location/Qualifiers
1..266
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN2004"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site: 1: SmaI;
Site: 2: SmaI; A mini-library was made by cloning products
derived from OESRMS PCR (U. S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

Query Match	7.6%;	Score 212;	DB 14;	Length 266;
Best Local Similarity	99.6%;	Pred. No. 1.9e-97;		
Matches 262;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
QY	1687	GATCAATTCCTGGGAAAAAGGCCAATCATCATGATAGAGAGCCGAGAGAAATATACA	1746	
Db	4	GATCAATTCCTGGGAAAAAGGCCAATCATCATGATAGAGAGCCGAGAGAAATATACA	63	
QY	1747	GGAGAACATGAGAACCCACAGCATCTCACTATGCTCGCTGGGTGGTCAAGGTTGAAAAA	1806	
Db	64	GGAGAACATGAGAACCCACAGCATCTCACTATGCTCGCTGGGTGGTCAAGGTTGAAAAA	123	

QY 1807 CAGTACACATTCATGATGAGTGCCTACTAGACATCTATCAACAGGCTCTT 1866
 DB 124 CAGGTACATCTCATAGATCAATCCAGCTGAGTGCCTACTATCAATCAACAGGCTCTT 183
 QY 1867 CGGAAGAGCTCTGCTCCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGT 1926
 DB 184 CGGAAGAGCTCTGCTCCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGT 243
 QY 1927 GAAACAGACATCTGACTATCAAG 1949
 DB 244 GAAACAGACATCTGACTATCAAG 266

RESULT 13
 AO383296 520 bp DNA linear GSS 21-MAY-1999
 LOCUS AO383296/c
 DEFINITION RPCI11-138M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-138M5,
 DNA sequence.
 ACCESSION AO383296
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 520)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 ,J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSSs: RPCI11-138M5.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source location/Qualifiers
 1..520
 /organism="Homo sapiens"
 /db_xref="GDB:7552900"
 /db_xref="taxon:9606"
 /clone="RPCI-11-138M5"
 /clone_1bp="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 164 a 105 c 92 g 159 t
 ORIGIN

Query Match 6.5%; Score 179; DB 17; Length 520;
 Best Local Similarity 100.0%; Pred. No. 2.2e-80;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 AGATACCATGTTCTTATCGCTTCAATAGACAGTTTTCGCAAAAACCTCAGGGTAATAT 674
 DB 380 AGATACCATGTTCTTATCGCTTCAATAGACAGTTTTCGCAAAAACCTCAGGGTAATAT 321
 QY 675 TTTTGCACGCTCTGACCTCAGAGTCTCGCTTCTTACAGATCTCCGATGTCGCGCAT 734
 DB 320 TTTTGCACGCTCTGACCTCAGAGTCTCGCTTCTTACAGATCTCCGATGTCGCGCAT 261

QY 735 GGACCGAAGGGGAGGACACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCAGCAAGG 793
 DB 260 GGACCGAAGGGGAGGACACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCAGCAAGG 202

RESULT 14
 AO344243/c 659 bp DNA linear GSS 07-MAY-1999
 LOCUS AO344243
 DEFINITION RPCI11-133N24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-133N24,
 DNA sequence.
 ACCESSION AO344243
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 659)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 ,J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSSs: RPCI11-133N24.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source location/Qualifiers
 1..659
 /organism="Homo sapiens"
 /db_xref="GDB:751023"
 /db_xref="taxon:9606"
 /clone="RPCI-11-133N24"
 /clone_1bp="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 201 a 135 c 123 g 200 t
 ORIGIN

Query Match 6.5%; Score 179; DB 17; Length 659;
 Best Local Similarity 100.0%; Pred. No. 2.4e-80;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 AGATACCATGTTCTTATCGCTTCAATAGACAGTTTTCGCAAAAACCTCAGGGTAATAT 674
 DB 375 AGATACCATGTTCTTATCGCTTCAATAGACAGTTTTCGCAAAAACCTCAGGGTAATAT 316
 QY 675 TTTTGCACGCTCTGACCTCAGAGTCTCGCTTCTTACAGATCTCCGATGTCGCGCAT 734
 DB 315 TTTTGCACGCTCTGACCTCAGAGTCTCGCTTCTTACAGATCTCCGATGTCGCGCAT 256
 QY 735 GGACCGAAGGGGAGGACACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCAGCAAGG 793
 DB 255 GGACCGAAGGGGAGGACACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCAGCAAGG 197

RESULT 15
 BF954374 224 bp mRNA linear EST 22-JAN-2001
 LOCUS

DEFINITION QV2-NN0045-131100-414-c02 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE954374
VERSION BE954374.1 GI:12371649
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&t2-QV2-NN0045-131100-414-c02&t3-2000-11-13&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 224.
Location/Qualifiers
1..224
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 69 a 58 c 46 g 51 t
ORIGIN
Query Match 5.7%; Score 158; DB 12; Length 224;
Best Local Similarity 99.5%; Pred. No. 1.2e-69;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1373 TCACGACGGAACCCGCTCCGCGCTCGCTGCGCCCTCAAAAGTCTCAGCCAAACCG 1432
DB 16 TCACGACGGAACCCGCTCCGCGCTCGCTGCGCCCTCAAAAGTCTCAGCCAAACCG 75
QY 1433 TGTATATGCTGCACACAGCCCTTGCGACGTGATGATATGATGAAAAAGATGCCACT 1492
DB 76 TGTATATGCTGCACACAGCCCTTGCGACGTGATGATGATGAAAAAGATGCCACT 135
QY 1493 GTGATATATCAGTGAAGAGACCTCACCACCACTTAACACTGATTCGAGTATCAGAA 1552
DB 136 GTGATATATCAGTGAAGAGACCTCACCACCACTTAACACTGATTCGAGTATCAGAA 195
QY 1553 TTATGAAATTTTCATGTTGCAAAACGGAAG 1581
DB 196 TTATGAAATTTTCATGTTGCAAAACGGAAG 224
RESULT 16 297 bp mRNA linear EST 20-MAY-2002
BQ340041 BQ340041

DEFINITION QV2-NN0045-261200-569-b11 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ340041
VERSION BQ340041.1 GI:21000357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&t2-QV2-NN0045-261200-569-b11&t3-2000-12-26&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 50.
Location/Qualifiers
1..297
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 82 a 73 c 69 g 73 t
ORIGIN
Query Match 5.2%; Score 144; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1815 GTCCATAGATTCGAAGCTGGAGCTGCTTACATCATATCAACAGAGCTCTGGAAAG 1874
DB 148 GTCCATAGATTCGAAGCTGGAGCTGCTTACATCATATCAACAGAGCTCTGGAAAG 207
QY 1875 CTCGCGCTCAGCCCTCGCTTGCTTGCATTCAGATCCACCTTTGAATGTAAGACAG 1934
DB 208 CTCGCGCTCAGCCCTCGCTTGCTTGCATTCAGATCCACCTTTGAATGTAAGACAG 267
QY 1935 ATCTGACTATCAAAAGCCCTGTGGA 1958
DB 268 ATCTGACTATCAAAAGCCCTGTGGA 291
RESULT 17 268 bp mRNA linear EST 21-APR-2001
BQ185229 BQ185229
LOCUS BQ185229 268 bp mRNA linear EST 21-APR-2001
DEFINITION RST4167 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ185229
VERSION BQ185229.1 GI:13706916
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 268)
AUTHORS Harrington,J.J., Sherif,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Kikla,A., Hess,J., Cothran,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 268.
Location/Qualifiers
1..268
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 72 a 46 c 63 g 87 t
ORIGIN

Query Match 4.7%; Score 129; DB 12; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 488 TGAAGTTCGATGATTTGCTGTTGGAGTTCAATCTGCTGCGG 547
|||||
Db 3 TGAAGTTCGATGATTTGCTGTTGGAGTTCAATCTGCTGCGG 62
|||||

QY 548 GTTGTGTTGCGATGATGAGGATGCAAGAACTGAGTTGCTCGAAAGCCCTTC 607
|||||
Db 63 GTTGTGTTGCGATGATGAGGATGCAAGAACTGAGTTGCTCGAAAGCCCTTC 122
|||||

QY 608 GTGTTATAG 616
|||||
Db 123 GTGTTATAG 131
|||||

RESULT 18
A0019541/c 166 bp DNA linear GSS 09-JUN-1998
LOCUS CIT-HSP-2305P7.TF CIT-HSP Homo sapiens genomic clone 2305P7, DNA
DEFINITION
ACCESSION A0019541
VERSION A0019541.1 GI:3198277
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 166)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2305P7.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
Location/Qualifiers
1..166
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2305P7"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 34 a 31 c 56 g 45 t
ORIGIN

Query Match 4.1%; Score 115; DB 17; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.5e-47;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2225 CACCTCTCTCCAGCCATCAAGATGCGCCAGCCAGAAACTGACCTAACCTG 2284
|||||
Db 166 CACCTCTCTCCAGCCATCAAGATGCGCCAGCCAGAAACTGACCTAACCTG 107
|||||

QY 2285 CAGGCTTACAGGAAGCATTTCTGACGTCACACCTGCTTGTGCTCCAGGAATG 2344
|||||
Db 106 CAGGCTTACAGGAAGCATTTCTGACGTCACACCTGCTTGTGCTCCAGGAATG 47
|||||

QY 2345 TTCAGGTTGACAGTCAATCTCACCAGAACCGTTTATGAGAA 2390
|||||
Db 46 TTCAGGTTGACAGTCAATCTCACCAGAACCGTTTATGAGAA 1
|||||

RESULT 19
BE177584/c 248 bp mRNA linear EST 22-JUN-2000
LOCUS BE177584
DEFINITION RCI-HT0597-210300-011-H01 HT0597 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE177584
VERSION BE177584.1 GI:8656736
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=et2-RC1-HT0597-210
300-011-h01et3=2000-03-21et4-1)

Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 248.
Location/Qualifiers

FEATURES

Source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0597"
/dev_stage="Adult"
/note="Organ: head, neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      63 a      53 c      65 g      67 t
ORIGIN

```

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-43;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 2609 AAGAGACAGACACACTTTGATGCCGACGAGCCTGCAGAGGAGCTGCTTTG 2668
    |||||||
Db 248 AAGAGACAGACACACTTTGATGCCGACGAGCCTGCAGAGGAGCTGCTTTG 189
    |||||||
OY 2669 CATGAGACTCTTAAGACTGAGAGTGCAGATCATCTCAGAGCATT 2715
    |||||||
Db 188 CATGAGACTCTTAAGACTGAGAGTGCAGATCATCTCAGAGCATT 142
    |||||||

```

RESULT 20

BG185740

LOCUS BG185740 267 bp mRNA linear EST 21-APR-2001
DEFINITION RST4662 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG185740
VERSION BG185740.1 GI:13707427
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 267)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Kikka, A., Hess, J., Cochren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.

TITLE
JOURNAL Creation of genome-wide protein expression libraries using random
MEDLINE activation of gene expression
COMMENT Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com

FEATURES
Source High quality sequence stop: 267.
Location/Qualifiers
1..267

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation

```

method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 73 a 45 c 62 g 87 t

ORIGIN

```

OY 511 TTGGTTGGAGTTCATCATTCGATCTGTCTGCGGGTTCGTCGATATAGAGA 570
    |||||||
Db 25 TTGGTTGGAGTTCATCATTCGATCTGTCTGCGGGTTCGTCGATATAGAGA 84
    |||||||
OY 571 TGGCAAGAGAGTGTGCTGCTGCAAGCCCTTCTGTATTAG 616
    |||||||
Db 85 TGGCAAGAGAGTGTGCTGCTGCAAGCCCTTCTGTATTAG 130
    |||||||

```

RESULT 21

BG218030

LOCUS BG218030 335 bp mRNA linear EST 21-APR-2001
DEFINITION RST37756 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG218030
VERSION BG218030.1 GI:13744051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 335)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Kikka, A., Hess, J., Cochren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.

TITLE
JOURNAL Creation of genome-wide protein expression libraries using random
MEDLINE activation of gene expression
COMMENT Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com

FEATURES
Source High quality sequence stop: 335.
Location/Qualifiers
1..335

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 88 a 61 c 77 g 108 t 1 others
ORIGIN

```

Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 511 TTGGTTGGAGTTCATCATTCGATCTGTCTGCGGGTTCGTCGATATAGAGA 570
    |||||||
Db 26 TTGGTTGGAGTTCATCATTCGATCTGTCTGCGGGTTCGTCGATATAGAGA 85
    |||||||
OY 571 TGGCAAGAGAGTGTGCTGCTGCAAGCCCTTCTGTATTAG 616
    |||||||
Db 86 TGGCAAGAGAGTGTGCTGCTGCAAGCCCTTCTGTATTAG 131
    |||||||

```


RESULT 22
LOCUS BE959223 160 bp mRNA linear EST 22-JAN-2001
DEFINITION QV2-NN0045-011200-502-a05 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE959223
VERSION BE959223.1 GI:12376498
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 160)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202663
MEDLINE
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1-QV2&t2-QV2-NN0045-
011200-502-a05&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 159.
Location/Qualifiers
FEATURES
source
1..160
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTIS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 44 a 43 c 36 g 37 t
ORIGIN
Query Match 3.7%; Score 102; DB 12; Length 160;
Best Local Similarity 100.0%; Pred. No. 7.4e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1372 TTCACGACGACCGCCGCTCCGCTGCGCCCAAAAGTTCAGCAAAACCA 1431
|||||
Db 14 TTCACGACGACCGACCCGCTCCGCTGCGCCCAAAAGTTCAGCAAAACCA 73
QY 1432 GTGATAGATGCTGACACAGCCCTTGACACTGATGATATAT 1473
|||||
Db 74 GTGATAGATGCTGACACAGCCCTTGACACTGATGATATAT 115
RESULT 23
LOCUS AI576388 300 bp mRNA linear EST 05-APR-1999
DEFINITION UT-R-Y0-vm-b-07-0-UI.s1 UT-R-Y0 Rattus norvegicus cDNA clone
ACCESSION AI576388
VERSION AI576388.1 GI:4560764

KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 300)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 37-71,
>GC-rich#Low-complexity
Seq primer: M13 Forward.
Location/Qualifiers
FEATURES
source
1..300
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone_lib="UT-R-Y0-vm-b-07-0-UI"
/clone_lib="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; The UT-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dt track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)".
BASE COUNT 44 a 108 c 109 g 38 t 1 others
ORIGIN
Query Match 2.0%; Score 56; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 4.3e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 GAGAGCGCGCGGCAAGCAGGCGCGGATGAGCTGTGGGACCGGCTCTC 284
|||||
Db 78 GAGAGCGCGCGGCGGCAAGCAGGCGCGGATGAGCTGTGGGACCGGCTCTC 133
RESULT 24
LOCUS BE103175 469 bp mRNA linear EST 13-JUN-2000
DEFINITION UT-R-BT1-agx-h-11-0-UI.s1 UT-R-BT1 Rattus norvegicus cDNA clone

Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat brain pool library cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

SOURCE

Location/Qualifiers

1. 434
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-DKO-CfW-C-12-0-UI"
 /clone.lib="UI-R-DKO"
 /dev_stage="ADULT"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-DKO library is a subtracted library derived from a mixture of five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%), aorta-nRBP (20%), and placenta-nRBP (20%). Each original library was constructed from a mixture of equal amounts of RNA from seven different developmental time-points: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, and adult day 200. (Exception: the aorta pool does not contain embryonic day 17 RNA and the placenta pool contains only the three embryonic stages). Each library was normalized individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CNOs), aorta (CWOs), and placenta (CNOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CNO), aorta (CWO), and placenta (CNO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.
 TAG_LIB=UI-R-DKO
 TAG_TRISUB=rat brain pool
 TAG_SEQ=ACTTC"

BASE COUNT 82 a 97 c 109 g 145 t 1 others
 ORIGIN

Query Match 1.7%; Score 48; DB 13; Length 434;
 Best Local Similarity 100.0%; Pred. No. 6.2e-13;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1345 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 1392
 |||||||
 DB 396 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 349

RESULT 27 719 bp DNA linear GSS 30-NOV-2001
 BH307140
 LOCUS CH230-10L20-TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION

ACCESSION CH230-10L20, DNA sequence.
 VERSION BH307140
 KEYWORDS GI:17219548
 SOURCE GSS.
 ORGANISM Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 719)
 Authors Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.
 Title Rat BAC End Sequences from Library CHORI-230 ECORI segment
 Journal Unpublished (1999)
 Comment Other GSS: CH230-10L20-TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or erting information.htm). BAC end page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
 Plate: 10 row: L column: 20
 Seq primer: 17
 Class: BAC ends.

FEATURES

SOURCE

Location/Qualifiers

1. 719
 /organism="Rattus norvegicus"
 /strain="BN/SSHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-10L20"
 /clone.lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; site 1: EcoRI; site 2: EcoRI;
 CHORI-230 Rat (BN/SSHsd/MCW) BAC library produced by Pieter de Jong"

BASE COUNT 199 a 164 c 168 g 188 t
 ORIGIN

Query Match 1.7%; Score 48; DB 17; Length 719;
 Best Local Similarity 100.0%; Pred. No. 7.1e-13;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1345 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 1392
 |||||||
 DB 423 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 470

RESULT 28 584 bp mRNA linear EST 18-SEP-1999
 AM049888
 LOCUS UI-M-BH1-anr-g-09-0-UI-s1 NTH.BMAP.M52 Mus musculus cDNA clone
 DEFINITION UI-M-BH1-anr-g-09-0-UI 3', mRNA sequence.
 ACCESSION AM049888
 VERSION AM049888.1 GI:5910417
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 584)
 Authors Bonaldo, M.F., Lennon, G., and Soares, M.B.
 Title Normalization and subtraction: two approaches to facilitate gene discovery
 Journal Genome Res. 6 (9), 791-806 (1996)

MEDLINE
COMMENT
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dt track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Scores Lab clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
The following repetitive elements were found in this cDNA sequence:
37-71, >GC richflow.complexity
Seq primer: M13 Forward
POLYA-NO
FEATURES
source
1. 584
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U1-M-BH1-anr-g-09-0-U1"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI. The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB="NIH_BMAP_M_S2"
TAG_TISSUE="corpus-striatum"
TAG_SEQ="ACGGC"
BASE COUNT 107 a 151 c 174 g 152 t
ORIGIN

Query Match 1.68; Score 44; DB 10; Length 584;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 412 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 455
|||||
261 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 304
|||||
RESULT 29
LOCUS BB657491 662 bp mRNA linear EST 26-OCT-2001
DEFINITION BB657491 RIKEN full-length enriched, 12 days embryo eyeball Mus
ACCESSION BB657491
VERSION BB657491.1 GI:16491317
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 662)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Himoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

TITLE JOURNAL COMMENT

Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9222
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational analysis of full-length mouse cDNAs compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.
FEATURES
source
1. 662
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D230004A10"
/clone_lib="RIKEN full-length enriched, 12 days embryo
eyeball"
/tissue_type="eyeball"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGCGCCGACACTCGAGTGTTCACCATCCCTGAGCA 3'], cDNA was
prepared by using triethanolamine thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTCGAGTGTTCACCATCCCTGAGCA 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FIC I."

BASE COUNT 232 a 147 c 120 g 161 t 2 others
ORIGIN
Query Match 1.68; Score 44; DB 10; Length 662;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 412 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 455
|||||
205 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 248
|||||

RESULT 30
 A2443500/c 477 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M023818R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M023818 R, DNA sequence.
 A2443500
 ACCESSION A2443500.1 GI:10591541
 VERSION
 KEYWORDS
 ORGANISM house mouse.
 SOURCE Mus musculus
 house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 477)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0238 row: H column: 18
 Seq primer: CACACGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 477.
 Location/Qualifiers
 1. 477
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M023818"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 100 a 98 c 150 g 129 t
 ORIGIN

Query Match 1.4%; Score 38; DB 17; Length 477;
 Best Local Similarity 100.0%; Pred. No. 9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2188 GCACCAAGCAGACCCACACACTTACAGATCCC 2225
 |||||||||||||||||||||||||||||||||||||||
 DB 269 GCACCAAGCAGACCCACACACTTACAGATCCC 232

RESULT 31
 BE647997/c 679 bp mRNA linear EST 06-SEP-2000
 LOCUS BE647997
 DEFINITION UI-M-BH1-anr-g-09-0-UI-r1 NIH-BMAP_M.S2 Mus musculus cDNA clone
 UI-M-BH1-anr-g-09-0-UI 5', mRNA sequence.
 BE647997
 ACCESSION BE647997.1 GI:9973817
 VERSION
 KEYWORDS EST.
 ORGANISM house mouse.
 SOURCE Mus musculus
 house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 679)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chln, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 CDNA library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1. 679
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-anr-g-09-0-UI"
 /clone_1lb="NIH-BMAP_M.S2"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pTV3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH-BMAP_M.S2 library is a subtracted library derived from NIH-BMAP_M.S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH-BMAP_M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 152 a 150 c 172 g 205 t
 ORIGIN

Query Match 1.4%; Score 38; DB 10; Length 679;
 Best Local Similarity 100.0%; Pred. No. 9.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1717 TCAGATTAAGAGAGCCGAGAGAAATACAGACAGA 1754
 |||||||||||||||||||||||||||||||||||||||
 DB 429 TCAGATTAAGAGAGCCGAGAGAAATACAGACAGA 392
 |||||||||||||||||||||||||||||||||||||||
 RESULT 32
 A1705051/c 226 bp mRNA linear EST 03-JUN-1999
 LOCUS A1705051
 DEFINITION UI-R-G0-uj-d-05-0-UI.s2 UI-R-G0 Rattus norvegicus cDNA clone
 UI-R-G0-uj-d-05-0-UI 3', mRNA sequence.
 A1705051
 ACCESSION A1705051.1 GI:4992951

KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 226)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 53-210,
>GC_rich#low_complexity
Seq primer: M13 Forward
POLYA=NO.

FEATURES
source
Location/Qualifiers
1..226
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-G0-uj-d-05-0-UI"
/clone_lib="UI-R-G0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of 6 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806 (1996).
TAG_SEQ=None found"
BASE COUNT 22 a 103 c 77 g 24 t
ORIGIN

Query Match 1.3%; Score 35; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. NO. 2.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 35
|||||
Db 154 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 120
|||||

RESULT 33
AM122800/c 239 bp mRNA linear EST 22-OCT-1999
LOCUS UI-M-BH2.1-ay-f-08-0-UI.s1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
DEFINITION UI-M-BH2.1-ay-f-08-0-UI 3', mRNA sequence.
ACCESSION AM122800
VERSION AM122800.1 GI:6098330
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 239)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
COMMENT 97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7J90, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dt track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 53-102, >GC_rich#low_complexity
Seq primer: M13 Forward
POLYA=NO.

FEATURES
source
Location/Qualifiers
1..239
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-ay-f-08-0-UI"
/clone_lib="NIH_BMAP_M.S3.1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M.S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library (NIH_BMAP_M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=NIH_BMAP_M.S3.1
TAG_TISSUE=hypothalamus
TAG_SEQ=CGGTA
BASE COUNT 22 a 106 c 81 g 29 t 1 others
ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. NO. 2.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 35
|||||
Db 160 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 126
|||||

RESULT 34
AM533367/c 330 bp mRNA linear EST 06-MAR-2000
LOCUS UI-R-BU0-amb-b-01-0-UI.s1 UI-R-BU0 Rattus norvegicus cDNA clone
DEFINITION UI-R-BU0-amb-b-01-0-UI 3', mRNA sequence.

ACCESSION AM533367.1 GI:7175781
 VERSION AM533367.1
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not a site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 53-210,
 >GC_richlow_complexity 242-310, >GC_richlow_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source
 1..330
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BU0-and-b-01-0-UI"
 /clone_1db="UI-R-BU0"
 /dev_stage="adult"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BU0 library is a subtracted library derived from a mixture of eye and ganglia tissues. For a detailed description of the library from which this clone was derived, please visit our web site at ratat.eng.uiowa.edu. The subtraction has been previously described in (Ronaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_Lib-UI-R-BU0
 TAG_Tissue-Eye
 TAG_SEQ-CATTG"
 BASE COUNT 33 a 134 c 130 g 32 t 1 others
 ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 330;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCCCCGCCACGCGGAGAGAGAGGCGG 35
 ||||||||||||||||||||||||||||||||
 UI-R-BU2-bon-h-03-0-UI.s1 UI-R-BU2 Rattus norvegicus cDNA clone
 Db 154 ATGCCCCCGCCACGCGGAGAGAGAGGCGG 120

RESULT 35
 BE614224/c 411 bp mRNA linear EST 28-NOV-2000
 LOCUS BE614224
 DEFINITION UI-R-BU2-bon-h-03-0-UI.s1 UI-R-BU2 Rattus norvegicus cDNA clone
 ACCESSION BE614224
 VERSION BE614224.1 GI:11402213
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not a site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 54-211,
 >GC_richlow_complexity 243-313, >GC_richlow_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source
 1..411
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BU2-bon-h-03-0-UI"
 /clone_1db="UI-R-BU2"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BU2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratat.eng.uiowa.edu. The subtraction has been previously described in (Ronaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"
 BASE COUNT 43 a 156 c 154 g 56 t 2 others
 ORIGIN

Query Match 1.3%; Score 35; DB 12; Length 411;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCCCCGCCACGCGGAGAGAGAGGCGG 35
 ||||||||||||||||||||||||||||||||
 UI-M-BH2.1-acy-f-08-0-UI.t1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
 Db 155 ATGCCCCCGCCACGCGGAGAGAGAGGCGG 121

RESULT 36
 BE648243 425 bp mRNA linear EST 06-SEP-2000
 LOCUS BE648243
 DEFINITION UI-M-BH2.1-acy-f-08-0-UI.t1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
 ACCESSION BE648243
 VERSION BE648243.1 GI:9974064
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 425)
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chin, H
 National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements. The following repetitive elements were
found in this CDNA sequence: 172-197, >GC-rich#Low_complexity
211-242, >GC-rich#Low_complexity 275-320, >GC-rich#Low_complexity
389-438, >GC-rich#Low_complexity 275-320, >GC-rich#Low_complexity
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers
1..425
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-acy-f-08-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH-BMAP_M.S3.1 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH-BMAP_M.S3.1, NIH-BMAP_M.S2, NIH-BMAP_M.S1.
The subtracted library (NIH-BMAP_M.S3.1) was constructed
as follows: PCR amplified cDNA inserts from NIH-BMAP_M.S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH-BMAP_M.S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the
NIH-BMAP_M.S3.1 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)."

BASE COUNT

64 a 157 c 159 g 45 t

ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGCCACCGCGAGAGAGAGAGAGCGG 35
|||||
Db 282 ATGCCCCGCCACCGCGAGAGAGAGAGAGCGG 316

RESULT 37
BF523361/c 427 bp mRNA linear EST 11-DEC-2000
LOCUS
DEFINITION
UI-R-GO-ug-h-09-0-UI.r1 UI-R-GO Rattus norvegicus cDNA clone
BF523361
ACCESSION
UI-R-GO-ug-h-09-0-UI 5', mRNA sequence.
VERSION
BF523361.1 GI:11631328
KEYWORDS
EST.

SOURCE

ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
1 (bases 1 to 427)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

FEATURES

source

Location/Qualifiers
1..427
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-GO-ug-h-09-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996."

BASE COUNT

125 a 92 c 108 g 102 t

ORIGIN

Query Match 1.3%; Score 35; DB 12; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 TTGTGAAAGAGAGACCGACGTCGACACCTCAT 1121
|||||
Db 111 TTGTGAAAGAGAGACCGACGTCGACACCTCAT 77

RESULT 38

BB624101 632 bp mRNA linear EST 26-OCT-2001
LOCUS
DEFINITION
BB624101 RIKEN full-length enriched, adult male cortex Mus musculus
cDNA clone 7730402H11 5', mRNA sequence.
ACCESSION
BB624101
VERSION
BB624101.1 GI:16462710
KEYWORDS
EST.

SOURCE

ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 632)

AUTHORS

Arakawa,T., Carinich,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Matsutani,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute

TITLE

JOURNAL

COMMENT

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chih, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: MEST@mail.nih.gov
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements
 Seq primer: M13 Reverse
 Location/Qualifiers
 1. .232
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UT-M-ALI-ahk-e-04-0-UT"
 /dev_stage="27-32 days"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The
 NIH_BMAP_MCO.N library is a normalized library constructed
 from mouse cortex. The tag is a string of 5 nucleotides
 present between the Not I site and the oligo-dr track.
 The library was constructed as described by Bonaldo,
 Lennon and Soares, Genome Research 6: 791-806, 1996.
 Tissue provided by Ms. Anne Novakovich, Zivic-Miller
 Laboratories."

BASE COUNT 61 a 57 c 57 g 57 t

ORIGIN

Query Match 1.1%; Score 31; DB 12; Length 232;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2311 GTCACACCTGCTGCTGCTGCTCAAGAA 2341
 13 GTCACACCTGCTGCTGCTGCTCAAGAA 43

RESULT 41 766 bp mRNA linear HTC 19-JAN-2002
AK020325 Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
 library, clone:9230107005:VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN
 KQT-Like 5 (FRAGMENT), full insert sequence.
ACCESSION AK020325
VERSION AK020325.1 GI:12860880
KEYWORDS HTC; CAP trapper
SOURCE Mus musculus (strain:C57BL/6J) adult male epididymis cDNA to mRNA,
 clone:9230107005.
ORGANISM Mus musculus
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Mech. Enzymol. 303, 19-44 (1999)
MEDLINE 99379253
PUBMED 10349636
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493974
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Glass, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nakido, I., Pesole, G.,
 Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Rindwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.
 and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5 (bases 1 to 766)
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
 Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
 Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
 Hara, A., Hayatsu, N., Hill, D., Himoto, K., Hirooka, T., Hori, F.,
 Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Konno, H., Kozawa, M., Koya, S.,
 Kurihara, C., Matsuyama, T., Miyazaki, R., Nishi, K., Nomura, K.,
 Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shitaki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,
 Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
 Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGAGAGAGATCAAGACCTCTCTTTTTTTTTTTTTTNN 3'], cDNA was

BASE COUNT 91 a 173 c 189 g 144 t
ORIGIN

Query Match 0.9%; Score 26; DB 10; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||
DB 10 CGCGGCTGGCGCTTCATCTACACGC 35

RESULT 44
BE257127

LOCUS BE257127 622 bp mRNA linear EST 13-JUN-2000
DEFINITION 60110867F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349625 5',
ACCESSION BE257127
VERSION BE257127.1 GI:9127597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 622)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.linl.gov
Plate: LICM144 row: e column: 18
High quality sequence stop: 621.

FEATURES

Location/Qualifiers

1..622
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3349625"
/clone_1lb="NIH_MGC_16"
/tissue_type="retinodlastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 93 a 205 c 207 g 117 t
ORIGIN

Query Match 0.9%; Score 26; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||
DB 289 CGCGGCTGGCGCTTCATCTACACGC 314

RESULT 45
B0192564/c

LOCUS B0192564 749 bp mRNA linear EST 30-APR-2002
DEFINITION UI-R-DRI-ckz-b-18-0-UI s1 UI-R-DRI Rattus norvegicus cDNA clone
ACCESSION B0192564
VERSION B0192564.1 GI:20368115

KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 749)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msquares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized osteoblast library cDNA library preparation: M.B. Soares
lab clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 1-23, >AT-rich#Low-complexity
Seq primer: M13 Forward
POLYA=yes.

FEATURES

Location/Qualifiers

1..749
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DRI-ckz-b-18-0-UI"
/clone_1lb="UI-R-DRI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DRI
library is a normalized Rat Osteoblast library (mRBO)
constructed in pRT37 vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag AAGATATCAA between the Not I cloning site and
d118 stretch. The Rat Osteoblast tissue was provided by
Lian & Stein of the University of Massachusetts Medical
School.
TAG_LIB=UI-R-DRI
TAG_TISSUE=osteoblast
TAG_SEQ=AAGATATCAA"

BASE COUNT 200 a 158 c 147 g 242 t 2 others
ORIGIN

Query Match 0.9%; Score 26; DB 14; Length 749;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2569 GAATCCAAATGTTATTAACGATGA 2594
|||||
DB 699 GAATCCAAATGTTATTAACGATGA 674

RESULT 46
BF312386

LOCUS BF312386 914 bp mRNA linear EST 21-NOV-2000
DEFINITION 601896926F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127958 5',
ACCESSION BF312386
VERSION BF312386.1 GI:11260188

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1020 row: d column: 07
High quality sequence stop: 630.
Location/Qualifiers
1. 914
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4127958"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 165 a 234 c 281 g 214 t
ORIGIN

Query Match 0.9%; Score 26; DB 12; Length 914;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||
DB 31 CGCGGCTGGCGCTTCATCTACACGC 56

RESULT 47
BF317072 920 bp mRNA linear EST 21-NOV-2000
LOCUS 601903470F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4136200 5',
DEFINITION mRNA sequence.
ACCESSION BF317072
VERSION BF317072.1 GI:11265477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1041 row: k column: 17
High quality sequence stop: 714.

FEATURES
SOURCE
Location/Qualifiers
1. 920
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4136200"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 150 a 256 c 298 g 216 t
ORIGIN

Query Match 0.9%; Score 26; DB 12; Length 920;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||
DB 30 CGCGGCTGGCGCTTCATCTACACGC 55

RESULT 48
CNS04101/c 942 bp DNA linear GSS 18-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence PUC-Orl end of clone
DEFINITION 074H14 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL270459.1 GI:7992380
VERSION AL270459.1 GI:7992380
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 942)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 942)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 942)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
1. 942
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="074H14"
/clone_lib="G"
/note="Genoscope sequence ID : C0B6074BD07SP1-end :
PUC-Orl"

```

BASE COUNT      226 a      232 c      248 g      230 t      6 others
ORIGIN
Query Match      0.9%; Score 26; DB 17; Length 942;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1357 CAGAGAGCTGAGCTTCAACGACCG 1382
      |||||||
Db      118 CAGAAGAGCTGAGCTTCAACGACCG 93

RESULT 49
AG082214      1019 bp      DNA      linear      GSS 03-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-079A15.R, genomic survey sequence.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Tetok, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 1019)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Tetok, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hnp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1.1019
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-079A15.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      176 a      432 c      362 g      26 t      23 others
ORIGIN
Query Match      0.9%; Score 26; DB 17; Length 1019;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 GCGGCGGCGGCGGCGGCGGCGGCG 92
      |||||||
Db      344 GCGGCGGCGGCGGCGGCGGCGGCG 369

RESULT 50
BF311176      1068 bp      mRNA      linear      EST 21-NOV-2000
LOCUS      60189864BF1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128226 5',
DEFINITION
mRNA sequence.
ACCESSION
BF311176

```

```

VERSION      BF311176.1      GI:11258971
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1068)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LCM1020 row: c column: 11
High quality sequence stop: 696.
FEATURES
source
1.1068
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4128226"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Brain; Vector: pOTB; Site-1: XhoI; Site-2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      180 a      362 c      366 g      159 t      1 others
ORIGIN
Query Match      0.9%; Score 26; DB 12; Length 1068;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      367 GCGGCGTGGCGCTCATCTACACGCG 392
      |||||||
Db      442 GCGGCGTGGCGCTCATCTACACGCG 467

Search completed: June 19, 2003, 16:36:22
Job time : 3483 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:25:16 ; Search time 6933 Seconds

(without alignments)
11636.085 Million cell updates/sec

Title: us-09-825-147-1

Sequence: 2772 1 atgccccgcacacacgcgcggg.....ctcatgtcaactgaataa 2772

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 24

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.in:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2772	100.0	2772	6 AX268474	AX268474 Sequence
2	2772	100.0	3111	6 AX268476	AX268476 Sequence
3	1552	56.0	3074	6 AX253254	AX253254 Sequence
4	1552	56.0	3074	6 AX456864	AX456864 Sequence
5	1552	56.0	3074	6 AF249278	AF249278 Homo sapi
6	1552	56.0	3137	6 AX056817	AX056817 Sequence
7	1552	56.0	3137	6 AF202977	AF202977 Homo sapi
8	1450	52.3	2694	6 AX322509	AX322509 Sequence
9	1297	46.8	2832	9 HSA263835	AF263835 Homo sapi
10	965	34.8	1691	9 HSA272519	AJ272519 Homo sapi
11	965	34.8	120846	9 AL365232	AL365232 Human DNA
12	347	12.5	47057	9 AL445569	AL445569 Human DNA
13	293	10.6	293	9 HSA272506	AJ272506 Homo sapi
14	270	9.7	548	6 AX18576	AX18576 Sequence
15	270	9.7	548	6 AX18764	AX18764 Sequence
16	221	8.0	821	9 HSA272515	AJ272515 Homo sapi
17	179	6.5	659	11 G58300	G58300 SHGC-104174
18	179	6.5	154998	9 HSA272509	AJ272509 Homo sapi
19	179	6.5	793	9 AL360236	AL360236 Human DNA
20	135	4.9	892	9 HSA272517	AJ272517 Homo sapi
21	133	4.8	847	9 HSA272518	AJ272518 Homo sapi
22	128	4.6	460	9 HSA272510	AJ272510 Homo sapi
23	128	4.6	834	9 HSA272508	AJ272508 Homo sapi
24	112	4.0	425	9 HSA272511	AJ272511 Homo sapi
25	110	4.0	767	9 HSA272516	AJ272516 Homo sapi
26	98	3.5	748	9 HSA272513	AJ272513 Homo sapi
27	96	3.5	561	9 HSA272512	AJ272512 Homo sapi
28	92	3.3	743	9 HSA272507	AJ272507 Homo sapi
29	70	2.5	319	11 G63779	G63779 G-104174 Ra
30	63	2.3	173373	2 AC112532	AC112532 Rattus no
31	56	2.0	158119	2 AC095944	AC095944 Rattus no
32	56	2.0	179192	2 AC095904	AC095904 Rattus no
33	56	2.0	248862	2 AC091215	AC091215 Rattus no
34	47	1.7	200	10 AF525837	AF525837 Rattus no
35	44	1.6	3108	4 AF263836	AF263836 Mus muscu
36	44	1.6	185864	2 AC131088	AC131088 Mus muscu
37	38	1.4	162123	2 AC115920	AC115920 Mus muscu
38	35	1.3	162123	2 AC115920	AC115920 Mus muscu
39	35	1.3	173373	2 AC112532	AC112532 Rattus no
40	35	1.3	215256	2 AC124139	AC124139 Mus muscu
41	35	1.3	267605	2 AC125483	AC125483 Mus muscu
42	35	1.3	331447	2 AC127359	AC127359 Mus muscu
43	29	1.0	389	11 AU049631	AU049631 Rattus no
44	29	1.0	1227	10 AB000502	AB000502 Mus muscu
45	29	1.0	1689	10 AB000503	AB000503 Mus muscu
46	29	1.0	1818	10 AB000500	AB000500 Mus muscu
47	29	1.0	2014	10 AB000501	AB000501 Mus muscu
48	29	1.0	2247	10 AB000504	AB000504 Mus muscu
49	29	1.0	2382	10 AB000498	AB000498 Mus muscu
50	29	1.0	2613	10 AF490773	AF490773 Mus muscu
51	29	1.0	2613	10 AB000497	AB000497 Mus muscu
52	29	1.0	2827	10 AB000497	AB000497 Mus muscu
53	29	1.0	2899	10 AB000496	AB000496 Mus muscu
54	29	1.0	2920	10 AB000495	AB000495 Mus muscu
55	29	1.0	2935	10 AB000494	AB000494 Mus muscu
56	29	1.0	214572	10 AL450341	AL450341 Mouse DNA
57	26	0.9	1182	6 E13516	E13516 Human mRNA
58	26	0.9	1314	9 BC000699	BC000699 Homo sapi
59	26	0.9	1425	6 A94977	A94977 Sequence 4
60	26	0.9	1425	6 D82346	D82346 Homo sapien
61	26	0.9	2565	6 A94975	A94975 Sequence 2
62	26	0.9	2750	6 AX456861	AX456861 Sequence
63	26	0.9	2750	6 AF110020	AF110020 Homo sapi
64	26	0.9	3029	6 A94974	A94974 Sequence 1
65	26	0.9	3195	9 AF074247	AF074247 Homo sapi

Pred. No. is the number of results predicted by chance to have a

[illegible]

QY 541 TCTGCGGGTTCGTGTGCGATATAGAGATGCGAAGGAACTGAGTTTCTCGAAG 600
| | | | |
Db 600 TCTGCGGGTTCGTGTGCGATATAGAGATGCGAAGGAACTGAGTTTCTCGAAG 659
| | | | |
QY 601 CCTCTGTGTATATAGATACCATTTGTTCTATCCGTTCAATAGAGTTTCTCGAAG 660
| | | | |
Db 660 CCTCTGTGTATATAGATACCATTTGTTCTATCCGTTCAATAGAGTTTCTCGAAG 719
| | | | |
QY 661 ACTCAGGTAATATTTTGGCAGCTCTGACACTGAGAGTCTCCGTTCTACAGATCTC 720
| | | | |
Db 720 ACTCAGGTAATATTTTGGCAGCTCTGACACTGAGAGTCTCCGTTCTACAGATCTC 779
| | | | |
QY 721 CCGATGTCGATGACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
| | | | |
Db 780 CCGATGTCGATGACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 839
| | | | |
QY 781 GCTCAGCAGCAGAGATTAATCAGAGCTTGATAGATAGATTTTGGTTCTTATTTTTCG 840
| | | | |
Db 840 GCTCAGCAGCAGAGATTAATCAGAGCTTGATAGATAGATTTTGGTTCTTATTTTTCG 899
| | | | |
QY 841 TCTTTCCTTCTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
| | | | |
Db 900 TCTTTCCTTCTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959
| | | | |
QY 901 GCTCTGTGTGGGCGACAAATTTACATTTGACAACTATTTGGAGAGAGAGAGAGAGG 960
| | | | |
Db 960 GCTCTGTGTGGGCGACAAATTTACATTTGACAACTATTTGGAGAGAGAGAGAGG 1019
| | | | |
QY 961 ACTTGGCTGGGAGATTTGCTTTCGAGGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCG 1020
| | | | |
Db 1020 ACTTGGCTGGGAGATTTGCTTTCGAGGCTTTCGAGCTTTCGAGCTTTCGAGCTTTCG 1079
| | | | |
QY 1021 CTTCCTGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACAGAGAGAGAGAGAGG 1080
| | | | |
Db 1080 CTTCCTGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACAGAGAGAGAGAGG 1139
| | | | |
QY 1081 AAACCTTTGAG 1140
| | | | |
Db 1140 AAACCTTTGAG 1199
| | | | |
QY 1141 TACGAGCTGATAGAGAAATCTGTTTCCATTTGCAACCTGAGAGAGAGAGAGAGAG 1200
| | | | |
Db 1200 TACGAGCTGATAGAGAAATCTGTTTCCATTTGCAACCTGAGAGAGAGAGAGAGAG 1259
| | | | |
QY 1201 CACAGCTGAG 1260
| | | | |
Db 1260 CACAGCTGAG 1319
| | | | |
QY 1261 CCGAGAGGCGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
| | | | |
Db 1320 CCGAGAGGCGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
| | | | |
QY 1321 ACCGACATCAG 1380
| | | | |
Db 1380 ACCGACATCAG 1439
| | | | |
QY 1381 CGAAGCCGCTTCGAGGCTTCGAGGCTCAAAAGTTTCAGAGAGAGAGAGAGAGAGAG 1440
| | | | |
Db 1440 CGAAGCCGCTTCGAGGCTTCGAGGCTCAAAAGTTTCAGAGAGAGAGAGAGAGAG 1499
| | | | |
QY 1441 GCTGACAG 1500
| | | | |
Db 1500 GCTGACAG 1559
| | | | |
QY 1501 TCAAGTGAAG 1560
| | | | |
Db 1560 TCAAGTGAAG 1619
| | | | |
QY 1561 TTTTCAGTTTCAAAAG 1620
| | | | |
Db 1620 TTTTCAGTTTCAAAAG 1679
| | | | |
QY 1621 ATTGAACAATATTTCTGCTGATCTGACATCTGTTGTTGAATTAAGAGCTTCAAGA 1680
| | | | |
Db 1680 ATTGAACAATATTTCTGCTGATCTGACATCTGTTGTTGAATTAAGAGCTTCAAGA 1739
| | | | |
QY 1681 CGTGTGTATCAAAATTTCTTGGAAAAGGCGCAAAATCAGATTAAGAGAGAGAGAG 1740
| | | | |
Db 1740 CGTGTGTATCAAAATTTCTTGGAAAAGGCGCAAAATCAGATTAAGAGAGAGAGAG 1799
| | | | |
QY 1741 ATACAG 1800
| | | | |
Db 1800 ATACAG 1859
| | | | |
QY 1801 GAAAAACAGGTACAGTCCATAGAAATCAGAGTGAAGTCCCTACTAGACATCTTCAAG 1860
| | | | |
Db 1860 GAAAAACAGGTACAGTCCATAGAAATCAGAGTGAAGTCCCTACTAGACATCTTCAAG 1919
| | | | |
QY 1861 GTCCCTGGAGAGAGGCTGCTGCTCAGCCGCTGTTGGCTTCATTTCCAGATCCACCTTT 1920
| | | | |
Db 1920 GTCCCTGGAGAGAGGCTGCTGCTCAGCCGCTGTTGGCTTCATTTCCAGATCCACCTTT 1979
| | | | |
QY 1921 GAATGTGAACAGAGATCTGATATCAAGAGCCCTGTGATAGAGAGAGAGAGAGAG 1980
| | | | |
Db 1980 GAATGTGAACAGAGATCTGATATCAAGAGCCCTGTGATAGAGAGAGAGAGAGAG 2039
| | | | |
QY 1981 GCACAAAACAGTGGCTGCTTATCCAGATCACTAGTCCACATCTCGAGAGGCTTCAG 2040
| | | | |
Db 2040 GCACAAAACAGTGGCTGCTTATCCAGATCACTAGTCCACATCTCGAGAGGCTTCAG 2099
| | | | |
QY 2041 TTCAATCTGAGCCCAATAGATGAGTCCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 2100
| | | | |
Db 2100 TTCAATCTGAGCCCAATAGATGAGTCCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 2159
| | | | |
QY 2101 CACAGTGAACAG 2160
| | | | |
Db 2160 CACAGTGAACAG 2219
| | | | |
QY 2161 AACACATTTCAAAACCAATTAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
| | | | |
Db 2220 AACACATTTCAAAACCAATTAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2279
| | | | |
QY 2221 ATCCACCTCTCTCCAGCCATTAAGAGATCTCCAGAGAGAGAGAGAGAGAGAGAG 2280
| | | | |
Db 2280 ATCCACCTCTCTCCAGCCATTAAGAGATCTCCAGAGAGAGAGAGAGAGAGAGAG 2339
| | | | |
QY 2281 CCTGAGAGCTTAAAG 2340
| | | | |
Db 2340 CCTGAGAGCTTAAAG 2399
| | | | |
QY 2341 AATGTTGAGTTGACAGTCAAAATCTGACCAAGAGAGAGAGAGAGAGAGAGAGAG 2400
| | | | |
Db 2400 AATGTTGAGTTGACAGTCAAAATCTGACCAAGAGAGAGAGAGAGAGAGAGAGAG 2459
| | | | |
QY 2401 ATGGAG 2460
| | | | |
Db 2460 ATGGAG 2519
| | | | |
QY 2461 TTGCTGTGCAAAACCTGATCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
| | | | |
Db 2520 TTGCTGTGCAAAACCTGATCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2579
| | | | |
QY 2521 GAGTCAAGTGGCTCCAG 2580
| | | | |
Db 2580 GAGTCAAGTGGCTCCAG 2639
| | | | |
QY 2581 TTTATTAAGTGAAG 2640
| | | | |
Db 2640 TTTATTAAGTGAAG 2699
| | | | |
QY 2641 CCGAGAGCTGCGAG 2700
| | | | |
Db 2700 CCGAGAGCTGCGAG 2759
| | | | |
QY 2701 TCATCTGAGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760
| | | | |

Db	2760	TCATCTCAGACATTTGTTAAGGACAGAGAAAGTACAGATGCGCTCAGCTTCCATGTC	2819
Qy	2761	AAACTGAATAA 2772	
Db	2820	AAACTGAATAA 2831	
RESULT 3			
AX253254			
LOCUS	AX253254	3074 bp	DNA
DEFINITION	Sequence 1 from Patent WO0170811.		linear
ACCESSION	AX253254		PAT 10-OCT-2001
VERSION	AX253254.1	GI:16073802	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3074)		
TITLE	Leiche,C., Scherer,C., Seebom,G., Busch,A. and Steilmeyer,K. Potassium channel protein kcnq5, a target for diseases of central nervous system and cardiovascular system		
JOURNAL	Patent: WO 0170811-A 1 27-SEP-2001; Aventis Pharma Deutschland GmbH (DE)		
FEATURES	Location/Qualifiers		
source	1..3074		
BASE COUNT	788 a 784 c 789 g 713 t		
ORIGIN			
Query Match	56.0%; Score 1552; DB 6; Length 3074;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1552; Conservative	0; Mismatches	0; Indels	0; Gaps
Qy	1221	TCAGAGCTAAGTTTAAAGGAGCGAGTGCATGGTACGCCAGGGGCCAGATTTAA	1280
Db	1357	TCGAAGCTTAAGTTTAAAGGAGCGAGTGCATGGTACGCCAGGGGCCAGATTTAA	1416
Qy	1281	GAGCCGACAGCCTCAGTAGTGACAGAGGTCCCCAAAGCACGCATCACAGCCGAGG	1340
Db	1417	GAGCCGACAGCCTCAGTAGTGACAGAGGTCCCCAAAGCACGCATCACAGCCGAGG	1476
Qy	1341	CATCCACCAAGTGCAGAGACTGGAGGTTCAACGACGACCCTTCCGGCCCTC	1400
Db	1477	CATCCACCAAGTGCAGAGACTGGAGGTTCAACGACGACCCTTCCGGCCCTC	1536
Qy	1401	GCTGCGCTCAAAAGTCTCAGCCAAAACCAAGTATGCTGACACAGCCCTTGGCAC	1460
Db	1537	GCTGCGCTCAAAAGTCTCAGCCAAAACCAAGTATGCTGACACAGCCCTTGGCAC	1596
Qy	1461	TGATGATGTATATATGAAAAAGATGCCAGTGTATGATCAGTGAAGACCTCACCC	1520
Db	1597	TGATGATGTATATATGAAAAAGATGCCAGTGTATGATCAGTGAAGACCTCACCC	1656
Qy	1521	ACCACTTAAACCTCATTCGAGCTATCAGATTTGAATTTTCATGTTGCANAAGGAA	1580
Db	1657	ACCACTTAAACCTCATTCGAGCTATCAGATTTGAATTTTCATGTTGCANAAGGAA	1716
Qy	1581	GTTTAAAGAAACATTACCTCCATATGATGTAAAGATGTCATTAACATATTTCTGTTG	1640
Db	1717	GTTTAAAGAAACATTACCTCCATATGATGTAAAGATGTCATTAACATATTTCTGTTG	1776
Qy	1641	TCATCTGGACATGTTGTGTAGAAATTAAGCCTTCAACACGCTTGATCAAAATTTCTTG	1700
Db	1777	TCATCTGGACATGTTGTGTAGAAATTAAGCCTTCAACACGCTTGATCAAAATTTCTTG	1836
Qy	1701	AAAAAGGCAATTCACATCAGATTAAGAGAGCCGAGGAAATTAACAGCAGAAATGAGAC	1760
Db	1837	AAAAAGGCAATTCACATCAGATTAAGAGAGCCGAGGAAATTAACAGCAGAAATGAGAC	1896
Qy	1761	CACAGACATCTCAATATGCTGGTGGCTGCTCAAGTTGAAGAAACAGGTACAGTCCAT	1820

[illegible]

```

VERSION      AX456864.1  GI:21715731
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE    1
AUTHORS      Argenti, T.M. and Sheldon, J.H.
TITLE        Methods of selecting compounds for modulation of bladder function
JOURNAL      Patent: WO 0232960-A 5 25-APR-2002;
              Myeth (US)
FEATURES
  source      1. 3074
              Location/Qualifiers
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT   788 a 784 c 789 g 713 t
ORIGIN
Query Match  56.0%; Score 1552; DB 6; Length 3074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1221 TCAGAGCTAAGCTTTAAGAGAGGAGGCGCATGCTAGCCCGAGGCGCAGATTTAA 1280
    |||||
Db 1357 TCAGAGCTAAGCTTTAAGAGAGGAGGCGCATGCTAGCCCGAGGCGCAGATTTAA 1416
    |||||
QY 1281 GAGCGCAGAACCTTCAGTAGGTGACAGAGAGTCCCAAGCAGCATCAGCGAGAGG 1340
    |||||
Db 1417 GAGCGCAGAACCTTCAGTAGGTGACAGAGAGTCCCAAGCAGCATCAGCGAGAGG 1476
    |||||
QY 1341 CAGTCCCAAGAGTGCAGAGAGCTGAGCTTACGACCGAAACCGCTTCCGGCCCTC 1400
    |||||
Db 1477 CAGTCCCAAGAGTGCAGAGAGCTGAGCTTACGACCGAAACCGCTTCCGGCCCTC 1536
    |||||
QY 1401 GCTGGCCCTCAAAAAGTCTCAGCCAAAACAGATGATGATGATGATGATGATGATG 1460
    |||||
Db 1537 GCTGGCCCTCAAAAAGTCTCAGCCAAAACAGATGATGATGATGATGATGATGATG 1596
    |||||
QY 1461 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1520
    |||||
Db 1587 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1656
    |||||
QY 1521 ACCACTTAAACCTGATCGAGCTTCAGATTAATTAATTAATTAATTAATTAATTAAT 1580
    |||||
Db 1657 ACCACTTAAACCTGATCGAGCTTCAGATTAATTAATTAATTAATTAATTAATTAAT 1716
    |||||
QY 1581 GTTTAAGAGAACATTACGTCATGATGATGATGATGATGATGATGATGATGATGATG 1640
    |||||
Db 1717 GTTTAAGAGAACATTACGTCATGATGATGATGATGATGATGATGATGATGATGATG 1776
    |||||
QY 1641 TCATCTGACATGTTGTGTAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1700
    |||||
Db 1777 TCATCTGACATGTTGTGTAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1836
    |||||
QY 1701 AAAAGGGCAATTCACATCAGATTAAGAGAGCGAGAGAAATTAACAGCAGACATGAGAC 1760
    |||||
Db 1837 AAAAGGGCAATTCACATCAGATTAAGAGAGCGAGAGAAATTAACAGCAGACATGAGAC 1896
    |||||
QY 1761 CACAGAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1820
    |||||
Db 1897 CACAGAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1956
    |||||
QY 1821 AGAATCAAGCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1880
    |||||
Db 1957 AGAATCAAGCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2016
    |||||
QY 1881 CTGAGCCCTGCTTGGCTTATTCAGATCCACCTTTTGAATGATGAGACAGATCTGA 1940
    |||||
Db 2017 CTGAGCCCTGCTTGGCTTATTCAGATCCACCTTTTGAATGATGAGACAGATCTGA 2076
    |||||
QY 1941 CTATCAAGCCCTGCTGATGATCAAGATCTTGGGCTTCCGACAAAGAGTGGCTGT 2000
    |||||
Db 2077 CTATCAAGCCCTGCTGATGATCAAGATCTTGGGCTTCCGACAAAGAGTGGCTGT 2136
    |||||

```

```

QY 2001 ATCCAGATCACTAGTGCACATCTCGAGAGGCGCTGAGTCAATTCAGAGCCCAATGA 2060
    |||||
Db 2137 ATCCAGATCACTAGTGCACATCTCGAGAGGCGCTGAGTCAATTCAGAGCCCAATGA 2196
    |||||
QY 2061 GTTCAGTCCCGAGACTTTTACGCGCTTACGCTTACATGACAGTCAAGCAGACAGT 2120
    |||||
Db 2197 GTTCAGTCCCGAGACTTTTACGCGCTTACGCTTACATGACAGTCAAGCAGACAGT 2256
    |||||
QY 2121 GCCAATAGTCAAGAGATGGCTCAGAGAGTGGAGGAGCAGCAGCAGCAGTTCAGAAAT 2180
    |||||
Db 2257 GCCAATAGTCAAGAGATGGCTCAGAGAGTGGAGGAGCAGCAGCAGCAGTTCAGAAAT 2316
    |||||
QY 2181 AAATACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2240
    |||||
Db 2317 AAATACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2376
    |||||
QY 2241 CATCAGATCTGCGCCAGGCGCAGAAATCTGCAACCTTAACCTGACAGCTTACAGAAAG 2300
    |||||
Db 2377 CATCAGATCTGCGCCAGGCGCAGAAATCTGCAACCTTAACCTGACAGCTTACAGAAAG 2436
    |||||
QY 2301 CATTTGACGCTCAACCACTGCTTGTGCTCCAAAGAAATGTTACAGTTGACAGTCC 2360
    |||||
Db 2437 CATTTGACGCTCAACCACTGCTTGTGCTCCAAAGAAATGTTACAGTTGACAGTCC 2496
    |||||
QY 2361 AAATCTCAACCAAGACGCTTATGAGAGAAAGCTTTGACATGAGAGAGAAATCTGTT 2420
    |||||
Db 2497 AAATCTCAACCAAGACGCTTATGAGAGAAAGCTTTGACATGAGAGAGAAATCTGTT 2556
    |||||
QY 2421 GTCTGTCTGTCCTGATGAGGAGGAGTGGGCAATCTTGTGCTGCAAACTGAT 2480
    |||||
Db 2557 GTCTGTCTGTCCTGATGAGGAGGAGTGGGCAATCTTGTGCTGCAAACTGAT 2616
    |||||
QY 2481 CAGGTGACCGAGAGACTGAAATATACAACTTTCAGAGAGTGAATGAGTCCAGAG 2540
    |||||
Db 2617 CAGGTGACCGAGAGACTGAAATATACAACTTTCAGAGAGTGAATGAGTCCAGAG 2676
    |||||
QY 2541 CAGCAAGATTTTACCCCAATGAGAGGATCCCAATTTGTTATTAAGTGAAGAGT 2600
    |||||
Db 2677 CAGCAAGATTTTACCCCAATGAGAGGATCCCAATTTGTTATTAAGTGAAGAGT 2736
    |||||
QY 2601 GGGTCCCGAAGAGACAGAGACAGACACTTGTGATGCCAGCGAGCTGCGAGGAAAGC 2660
    |||||
Db 2737 GGGTCCCGAAGAGACAGAGACAGACACTTGTGATGCCAGCGAGCTGCGAGGAAAGC 2796
    |||||
QY 2661 TGCCCTTGATGACAGCTCTTAAGAGACTGGAAGTACAGATCATCTCAGAGCATTTGTA 2720
    |||||
Db 2797 TGCCCTTGATGACAGCTCTTAAGAGACTGGAAGTACAGATCATCTCAGAGCATTTGTA 2856
    |||||
QY 2721 GGCAGAGAGAAATGACAGATCCCTCAGCTTGCCCTCATGTCAAACTGAATAA 2772
    |||||
Db 2857 GGCAGAGAGAAATGACAGATCCCTCAGCTTGCCCTCATGTCAAACTGAATAA 2908
    |||||

RESULT 5
AF249278 3074 bp mRNA linear PRI 02-AUG-2000
DEFINITION Homo sapiens voltage-gated potassium channel (KCND5) mRNA, complete
ACCESSION AF249278
VERSION AF249278.1 GI:9651966
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Leche, C., Scherer, C.R., Seeböhm, G., Derst, C., Wei, A.D., Busch, A.E.
          and Steinhilber, K.
TITLE Molecular cloning and functional expression of KCND5, a potassium
          channel subunit that may contribute to neuronal M-current diversity
JOURNAL J. Biol. Chem. 275 (29), 22395-22400 (2000)
MEDLINE 20357367

```


Db 2857 GGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTAATAA 2908

RESULT 6
AX056817
LOCUS AX056817 3137 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 1 from Patent WO0077035.
ACCESSION AX056817
VERSION AX056817.1 GI:12309758
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Jentsch.T.J.

REFERENCE
AUTHORS Jentsch.T.J.
TITLE Novel potassium channels and genes encoding these potassium
channels
JOURNAL Patent: WO 0077035-A 1 21-DEC-2000;
NEUROSEARCH A/S (DK)

FEATURES
source location/Qualifiers
1. 3137
/organism="Homo sapiens"
/db_xref="taxon:9606"

CDS

1. 2694
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC22381.1"
/db_xref="GI:12309759"
/translation="MRDVEGRGRVILNSAARDGLILCTRAATLGGGGGLRESR
RGKGRMSLGGPLSYTSOSCRNRYKRVONYLVNLEPRGMAYIYAFVLLV
RCLILSVSTIPEHRLKASSCLILEFVAVFLEFIRIMSGCCRRYRGWGRL
RNRKPEVITVLIVLAVSAKTQGNFATLSRLQLILRMRMRGGTWK
LGSVVAHSKELITAMYLIGFLVLISSFLVLEKDNKESYADALMMGTILTT
IGYDKPTLWELGRILSAGFALIGISFPAAGLIGSGFALVQEHOKRKEPRRN
AANLLOCVRSYAADKSVSIATWPKLKLHSCSPKKEGESSSKLSEKREVM
ASPRGSIKRSQASVGRSPDITREBSPTVOKSMSEMDRTFRFSLKSSQPK
PYIDADTALGTDVYDEKQCQDVSEDLTPPLKTVIRAIRIMKFAKREKTLRP
YDKRVIEDYSHGHDMLCRINSLOTRVDLILGQVITSDKSRKETAHEHTDLS
MGRVAVKEQVQSIKSLDLIDLIQVYLRKGSASALASLFOIPEECOTSYOS
FVSDGSAVAANTIANQINTAPKPAAPTLOIPPLPAIKHLPREPLHNPAGLOE
ISIDYTCIVASKENVOVASNLTKDRSMKSPDMGENTLISCPMPKDKGKLSVO
NLIRTELENIOLGSESSGSRSDPVPKMRSKFITDEBYGFEETEDTFDAPO
PAREAPASDLSRTGRSRSSQSCKAGESTDLALPHVKLK"

BASE COUNT 865 a 749 c 745 g 778 t

Query Match 56.0%; Score 1552; DB 6; Length 3137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1221 TCAGAGCTAGTTTAAAGACGAGTGGCATGGTACCCCGAGGGCCAGAGTATTA 1280
DB 1143 TCAGAGCTAGTTTAAAGACGAGTGGCATGGTACCCCGAGGGCCAGAGTATTA 1202
QY 1281 GAGCGCAACAGCTCAGTAGTGACAGAGGTCCCAAGACCGCATCAACCGGAGG 1340
DB 1203 GAGCGCAACAGCTCAGTAGTGACAGAGGTCCCAAGACCGCATCAACCGGAGG 1262
QY 1341 CAGTCCCAACAGTGCAGAGAGCTGAGCTTCAACGACCGACCGGCTTCGGGCTC 1400
DB 1263 CAGTCCCAACAGTGCAGAGAGCTGAGCTTCAACGACCGACCGGCTTCGGGCTC 1322
QY 1401 GCTGCGCTCAAAAGTCTCGCCCAAAACAGTGTAGTGTGACACAGCCCTTGGAC 1460
DB 1323 GCTGCGCTCAAAAGTCTCGCCCAAAACAGTGTAGTGTGACACAGCCCTTGGAC 1382
QY 1461 TGATGATGATATGATGAAAAAGATGCCAGTGTATGATGATGAGGAAGACTGACCC 1520
DB 1383 TGATGATGATATGATGAAAAAGATGCCAGTGTATGATGATGAGGAAGACTGACCC 1442

QY 1521 ACCACTTAAACGTGATTCAGAGCTATCAGATTAATTAATTCATGTTGCAAAACGAA 1580
DB 1443 ACCACTTAAACGTGATTCAGAGCTATCAGATTAATTAATTCATGTTGCAAAACGAA 1502
QY 1581 GTTTAAGGAACATTAACGTTCATATGATGTAAGAGATGATGAAACAAATATTCGTGG 1640
DB 1503 GTTTAAGGAACATTAACGTTCATATGATGTAAGAGATGATGAAACAAATATTCGTGG 1562
QY 1641 TCATCTGACATGTTGTGTAGATTAATTAAGCCCTCAACCGTGTGATCAATTCCTGG 1700
DB 1563 TCATCTGACATGTTGTGTAGATTAATTAAGCCCTCAACCGTGTGATCAATTCCTGG 1622
QY 1701 AAAAGGGCAATCAGATCAGATTAAGAGAGCCGAGAGAAAATTAACAGCAGATGAGAC 1760
DB 1623 AAAAGGGCAATCAGATCAGATTAAGAGAGCCGAGAGAAAATTAACAGCAGATGAGAC 1682
QY 1761 CACAGAGCATCTCAGATGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1820
DB 1683 CACAGAGCATCTCAGATGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1742
QY 1821 AGAATCCAGCTGACCTGCTCTACTAGACATCTATCAACAGTCTCTCGAAAGCTCTGC 1880
DB 1743 AGAATCCAGCTGACCTGCTCTACTAGACATCTATCAACAGTCTCTCGAAAGCTCTGC 1802
QY 1881 CTCAGCCCTGCTTGGCTGCTTATTCAGATCCACCTTTGAATGTGAACAGACATCTGA 1940
DB 1803 CTCAGCCCTGCTTGGCTGCTTATTCAGATCCACCTTTGAATGTGAACAGACATCTGA 1862
QY 1941 CTATCAAGCCCTGTGTATGATCAAAAGATCTTGGGTTCCGACAAACAGTGGCTGT 2000
DB 1863 CTATCAAGCCCTGTGTATGATCAAAAGATCTTGGGTTCCGACAAACAGTGGCTGT 1922
QY 2001 ATCCAGATCAAGTGTGTCGCAACATCTGCAAGAGCCCTGCAAGTTCATCTGAGCCCAATGA 2060
DB 1923 ATCCAGATCAAGTGTGTCGCAACATCTGCAAGAGCCCTGCAAGTTCATCTGAGCCCAATGA 1982
QY 2061 GTTCAGTGGCCAGACTTCTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACGCGCT 2120
DB 1983 GTTCAGTGGCCAGACTTCTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACGCGCT 2042
QY 2121 GCCAATTTAGTCAAAAGCATGCTGACAGAGTGGACGACCAACACCATTTGCAACCAAT 2180
DB 2043 GCCAATTTAGTCAAAAGCATGCTGACAGAGTGGACGACCAACACCATTTGCAACCAAT 2102
QY 2181 AAATAGGCGCCAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2240
DB 2103 AAATAGGCGCCAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2162
QY 2241 CATCAAGCATCTGCCAGGCGCAGAACTGTGACCTTAACCTGAGGCTTAACAGAAAG 2300
DB 2163 CATCAAGCATCTGCCAGGCGCAGAACTGTGACCTTAACCTGAGGCTTAACAGAAAG 2222
QY 2301 CATTTCTGACGTACACACCTGCTTGTGCTCCCAAGAAATTTCAAGTGTGACACATC 2360
DB 2223 CATTTCTGACGTACACACCTGCTTGTGCTCCCAAGAAATTTCAAGTGTGACACATC 2282
QY 2361 AAATCTCACCAAGAGACGCTTCTATGAGAAAGAGTTTGACATGGAGAGAAACCTCTGT 2420
DB 2283 AAATCTCACCAAGAGACGCTTCTATGAGAAAGAGTTTGACATGGAGAGAAACCTCTGT 2342
QY 2421 GTCTGTCTGCCCATGAGTGGCGAAGACTTGGGCAATCTTGTGCTGTGCAAAACCTGAT 2480
DB 2343 GTCTGTCTGCCCATGAGTGGCGAAGACTTGGGCAATCTTGTGCTGTGCAAAACCTGAT 2402
QY 2481 CAGTTCGACCGAGAACTGAATATACACTTTAGGAGAGGAGCAAGTGGCTTCCAGAG 2540
DB 2403 CAGTTCGACCGAGAACTGAATATACACTTTAGGAGAGGAGCAAGTGGCTTCCAGAG 2462
QY 2541 CAGCCAGATTTTAAACCCAAATGAGGAGATCCAAATTTGTTATTAAGTAAAGAGT 2600
DB 2463 CAGCCAGATTTTAAACCCAAATGAGGAGATCCAAATTTGTTATTAAGTAAAGAGT 2522
QY 2601 GGGTCCCGAAGAGACAGAGACACTTTTGTATGCGGCAACCGCAGCTTCCAGGAGAGC 2660


```

|||||
2523 GGGTCCGAGAGACAGACAGACCTTTGATGCCGACCGACCTGCCGAGGAGGC 2582
OY 2661 TGCCTTCATCAGACTCTCTAAGGACGTGAGGTGACGATCTCAGAGCATTTGTAA 2720
Db 2563 TGCCCTTCATCAGACTCTCTAAGGACGTGAGGTGACGATCTCAGAGCATTTGTAA 2642
OY 2721 GGCAGAGAAAGTACAGATGCTCAGCTTGCTCATGTCAAACTGAATAA 2772
Db 2643 GGCAGAGAAAGTACAGATGCTCAGCTTGCTCATGTCAAACTGAATAA 2694

RESULT 7
AF202977 3137 bp mRNA linear PRI 01-AUG-2000
LOCUS Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
DEFINITION member 5 (KCNO5) mRNA, complete cds.
ACCESSION AF202977.1 GI:7798695
VERSION AF202977.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3137)
Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.
KCNO5, a novel potassium channel broadly expressed in brain,
mediates M-type currents
J. Biol. Chem. 275 (31), 24089-24095 (2000)
10816588
JOURNAL 20379054
MEDLINE 10816588
PUBMED 2 (bases 1 to 3137)
Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
Jentsch,T.J.
REFERENCE Direct Submission
AUTHORS Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinstrasse
85, Hamburg 20246, Germany
FEATURES
source
1..3137
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/lssue-type="brain"
1..3137
/gene="KCNO5"
1..2694
/gene="KCNO5"
/note="splice variant 1"
/codon_start=1
/product="potassium voltage-gated channel, KQT-like
subfamily, member 5"
/protein_id="AA6697.1"
/db_xref="GI:7798696"
/translaction="MKDVEGRVLLNSAARGDGLLLGTRATLGGGGGLRESR
RGKGRMSLLGKPLSTYSQSCRNVRYRYONLYLVNLRPMALFYANFVELLV
FGCLLSEVSTLPEHTKLASCLLLEFMYLFELELIRMSAGCCCRKGMQGLR
RPAKPRCVITDITVLASIAVSAKTOGNISATLSRSLFOILRMVMDRGGTAK
LIGSVYVHSHKELTANWIGLIVLIFSSFLIVLVKDKNKESTYADALMMGGITLT
IGYDKPLTWLGRLLSAGFALLGISFALPAGLIGSFALVQOQHRKHREKRRNP
AANLQICWVRSYADERSVSIATWKPRLKALHTCSPTKEGSEASSOKLSTKERYM
ASPRGQSIKSRQASVGDRRSPSTDTAGSPTRVOKSWSEFNDRTRRPSLRKSSQPK
PVIDADTALGTDDVYDEKCCQDVSEDLPLPLTVIRAIRIMKPHVARKEETLAP
YVDADTALGTDDVYDEKCCQDVSEDLPLPLTVIRAIRIMKPHVARKEETLAP
MLGRVYKQVOVSTESKLDLIDLYOOLRKGSAALALAEFOALSPFMHSGAOLVP
PVDSKDLSSGQNSCSTSRSTANTSRGLOFLITPNEFSAOFTFALSPFMHSGAOLVP
ISQSDGSAVAANTNTANOINTAPKPAFTTLDIPPLRIKHLPREBTIHPNAGLOE
SISDVTTCVLSKENVOYVAQSNLTDRSKRSFDMGEGFLISVCPWETLHPNAGLOE
NLRSTELNLIQSGSESGSGSODFYPKWRESKLFITDEEGPEPETETDITDAAPQ
PAREAPAFSDSLRTGRSRSSQISCKAGESTDALSIPHYVLIK"
BASE COUNT 865 a 749 c 745 g 778 t
ORIGIN
Query Match 56.0%; Score 1552; Db 9; Length 3137;

```

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1221 TCAGAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCCCAGGGCCAGATTTAA 1280
Db 1143 TCAGAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCCCAGGGCCAGATTTAA 1202
OY 1281 GAGCGACAGGCTCAGTAGGTGACAGAGGTCGCCAAGCAGCAGATCAGAGCGAGG 1340
Db 1203 GAGCGACAGGCTCAGTAGGTGACAGAGGTCGCCAAGCAGCAGATCAGAGCGAGG 1262
OY 1341 CAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGGCCTC 1400
Db 1263 CAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGGCCTC 1322
OY 1401 GCTGGCCCTCAAAATTCCTCAGCCCAAAACAGATAGATGCTGACAGAGCCCTGGCAC 1460
Db 1323 GCTGGCCCTCAAAAGTCTCAGCCCAAAACAGATAGATGCTGACAGAGCCCTGGCAC 1382
OY 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
Db 1383 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
OY 1521 ACCACTTAAACTGTCATTCAGACTATCAGATTTAGAAATTCATGTTCCAAAGCGAA 1580
Db 1443 ACCACTTAAACTGTCATTCAGACTATCAGATTTAGAAATTCATGTTCCAAAGCGAA 1502
OY 1581 GTTTTAAAGAAACATTCAGTCCGATGATGATGATGATGATGATGATGATGATGATGAT 1640
Db 1503 GTTTTAAAGAAACATTCAGTCCGATGATGATGATGATGATGATGATGATGATGATGAT 1562
OY 1641 TCATCTGACATGTTGTGTGAATTAAGCTTCAACACGTTGTATCAATTTCTGG 1700
Db 1563 TCATCTGACATGTTGTGTGAATTAAGCTTCAACACGTTGTATCAATTTCTGG 1622
OY 1701 AAAAGGCAATTCATCAGATTAAGAAAGACCGAGAAATTAACAGACAGATGAGAC 1760
Db 1623 AAAAGGCAATTCATCAGATTAAGAAAGACCGAGAAATTAACAGACAGATGAGAC 1682
OY 1761 CACAGACGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
Db 1683 CACAGACGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
OY 1821 AGAATCCAGCTGAGTCTCTACTAGCATCTATCAACAGTCTCTGGAAAGCTCTGC 1880
Db 1743 AGAATCCAGCTGAGTCTCTACTAGCATCTATCAACAGTCTCTGGAAAGCTCTGC 1802
OY 1881 CTCAGCCCTGCTTGGCTTCATTCAGATCCAGATCCACCTTTTGAATGTGACAGATCTGA 1940
Db 1803 CTCAGCCCTGCTTGGCTTCATTCAGATCCAGATCCACCTTTTGAATGTGACAGATCTGA 1862
OY 1941 CTATCAAAAGCCGTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTCTT 2000
Db 1863 CTATCAAAAGCCGTGTGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTCTT 1922
OY 2001 ATCCAGATCAACTAGTGCACCAATCTCGAAGGGCTCGAGTTCATTTGAGCCCAAAATGA 2060
Db 1923 ATCCAGATCAACTAGTGCACCAATCTCGAAGGGCTCGAGTTCATTTGAGCCCAAAATGA 1982
OY 2061 GTTCAGTGGCCAGACTTCTAGCGGCTTAGCCCTACTATGACAGACTCAAGCAACAGAGT 2120
Db 1983 GTTCAGTGGCCAGACTTCTAGCGGCTTAGCCCTACTATGACAGACTCAAGCAACAGAGT 2042
OY 2121 GCCAATTAAGTCAANGCGATGCTCAGAGTGGCAGCCACCAACACCATTTGCAAAACCAAT 2180
Db 2043 GCCAATTAAGTCAANGCGATGCTCAGAGTGGCAGCCACCAACACCATTTGCAAAACCAAT 2102
OY 2181 AAATAGGCGACCCCAAGAGAGAGCCCAACCAACTTAAGATCCACCTCTCTCCAGC 2240
Db 2103 AAATAGGCGACCCCAAGAGAGAGCCCAACCAACTTAAGATCCACCTCTCTCCAGC 2162
OY 2241 CATCAAGCATCTGCCAGGCGCAAGAACTCTGCACCTTAACCTGCAAGCTTACAGAAAG 2300

```

```

Db      2163  CATCAAGCTATGCTCCAGGAGGAGAACTCTGCACCTTAACCTGCAGGCTTACAGGAAG 2222
OY      2301  CATTTCTGAGTCAACACCTGCTGTTGGCTTCAAGGAAATGTCAGTTGCAAGTC 2360
Db      2223  CATTTCTGAGTCAACACCTGCTGTTGGCTTCAAGGAAATGTCAGTTGCAAGTC 2282
OY      2361  AAATCTACACCAAGACCGTCTATGAGAAAAAGCTTTGACATGGAGGAAACTGTGTT 2420
Db      2283  AAATCTACACCAAGACCGTCTATGAGAAAAAGCTTTGACATGGAGGAAACTGTGTT 2342
OY      2421  GTCTGTCTGCTCCCTGGGAGGAGGAGTGGGCAAACTTGTCTGTCTCAAACTGAT 2480
Db      2343  GTCTGTCTGCTCCCTGGGAGGAGGAGTGGGCAAACTTGTCTGTCTCAAACTGAT 2402
OY      2481  CAGCTGACCGGAGGAGTGAATATACAACTTTCAGGAGTGAAGTGAAGTCCAGAG 2540
Db      2403  CAGCTGACCGGAGGAGTGAATATACAACTTTCAGGAGTGAAGTGAAGTCCAGAG 2462
OY      2541  CAGCCAAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATTAATGATGAAGAGT 2600
Db      2463  CAGCCAAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATTAATGATGAAGAGT 2522
OY      2601  GGGTCCCGAAGAGACAGACAGACTTTTGTATGCGCAGCGAGCGTCCAGGGAAGC 2660
Db      2523  GGGTCCCGAAGAGACAGACAGACTTTTGTATGCGCAGCGAGCGTCCAGGGAAGC 2582
OY      2661  TGGCTTTGATCAGACTCTCTTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2720
Db      2583  TGGCTTTGATCAGACTCTCTTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2642
OY      2721  GGCAGAGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2772
Db      2643  GGCAGAGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2694

RESULT 8
LOCUS   AX322509                2694 bp      DNA      Linear      PAT 07-JAN-2002
DEFINITION   Sequence 1 from Patent WO0192526.
ACCESSION   AX322509
VERSION     AX322509.1   GI:18093555
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1
AUTHORS     Dorezky, S.I., Ramanathan, C.S., Trojnecki, J.T., Boissard, C.G. and
            Gribkoff, V.K.
TITLE       Human Kcnq5 potassium channel, methods and compositions thereof
JOURNAL     Patent: WO 0192526-A 1 06-DEC-2001;
            Bristol-Myers Squibb Company (US)
FEATURES
            Location/Qualifiers
            source          1..2694
                           /organism="Homo sapiens"
                           /db_xref="taxon:9606"
BASE COUNT  714 a      671 c      669 g      640 t
ORIGIN
Query Match      52.3%; Score 1450; DB 6; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Db      1263  CAGTCCACCAAAAGTGCAGAGAGCTGAGCTTCAAGACCGAACCCTCCGCGCTC 1322
OY      1401  GCTGGCCCTCAAAAAGTTCTCAGCCAAACACAGATAGATGCTGACAGAGCCCTGGAC 1460
Db      1323  GCTGGCCCTCAAAAAGTTCTCAGCCAAACACAGATAGATGCTGACAGAGCCCTGGAC 1382
OY      1461  TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
Db      1383  TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
OY      1521  ACCACTTAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
Db      1443  ACCACTTAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1502
OY      1581  GTTAAAGGAAACATTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 1640
Db      1503  GTTAAAGGAAACATTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 1562
OY      1641  TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1700
Db      1563  TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
OY      1701  AAAAGGGCAAAATCAATCAGATAGATAGAGAGCCGAGAGAAATTAACAGCAAGATGAG 1760
Db      1623  AAAAGGGCAAAATCAATCAGATAGATAGAGAGCCGAGAGAAATTAACAGCAAGATGAG 1682
OY      1761  CACAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
Db      1683  CACAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
OY      1821  AGAATCCAAAGTGGAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1880
Db      1743  AGAATCCAAAGTGGAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1802
OY      1881  CTCAGCCCTGCTGCTTGGCTTATTCAGATCCACCTTTGATGATGATGATGATGATGATGAT 1940
Db      1803  CTCAGCCCTGCTGCTTGGCTTATTCAGATCCACCTTTGATGATGATGATGATGATGATGAT 1862
OY      1941  CTATCAAAAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
Db      1863  CTATCAAAAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
OY      2001  ATCCAGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2060
Db      1923  ATCCAGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
OY      2061  GTTCAGGCGCCAGACTTTTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACG 2120
Db      1983  GTTCAGGCGCCAGACTTTTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACGCGCTTACG 2042
OY      2121  GCCAATTAAGTCAAAAGGATGCTCAGCAGTGGAGCCACCAACACATTTGCAAAACCAAT 2180
Db      2043  GCCAATTAAGTCAAAAGGATGCTCAGCAGTGGAGCCACCAACACATTTGCAAAACCAAT 2102
OY      2181  AAATAGGCAACCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2240
Db      2103  AAATAGGCAACCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2162
OY      2241  CATCAAGATCTGCGCCAGGCGCAGAACTGCAACCCCTTAACCCCTTAACCCCTTAACCCCT 2300
Db      2163  CATCAAGATCTGCGCCAGGCGCAGAACTGCAACCCCTTAACCCCTTAACCCCTTAACCCCT 2222
OY      2301  CATTTCTGACGTCACCACTGCTTGTGCTTGCCTCAAGGAAATGTTGAGTTGCAAGTC 2360
Db      2223  CATTTCTGACGTCACCACTGCTTGTGCTTGCCTCAAGGAAATGTTGAGTTGCAAGTC 2282
OY      2361  AAATCTACCAAGGAGCCGTTATGAGAAAGCTTTGATGATGATGATGATGATGATGATGAT 2420
Db      2283  AAATCTACCAAGGAGCCGTTATGAGAAAGCTTTGATGATGATGATGATGATGATGATGAT 2342
OY      2421  GTCTGTCTGCTCCCTGGGAGGAGTGGGCAAACTTGTCTGTCTCAAACTGAT 2480
Db      2343  GTCTGTCTGCTCCCTGGGAGGAGTGGGCAAACTTGTCTGTCTCAAACTGAT 2402

```


OY 2481 CAGGTCAGCCAGAGAACTGATATACACTTTCAGGAGGTGAGTCAAGTGGCTCCAGAGG 2540
 |||||||
 DB 2403 CAGGTCAGCCAGAGAACTGATATACACTTTCAGGAGGTGAGTCAAGTGGCTCCAGAGG 2462
 |||||||
 OY 2541 CAGCCAGATTTTAACTGAGGAAATTCCTGTTTATATACATGATGAAGGT 2600
 |||||||
 DB 2463 CAGCCAGATTTTAACTGAGGAAATTCCTGTTTATATACATGATGAAGGT 2522
 |||||||
 OY 2601 GGGTCCCAAGAGAGACAGACACTTTCAGGAGGTGAGTCAAGTGGCTCCAGAGG 2660
 |||||||
 DB 2533 GGGTCCCAAGAGAGACAGACACTTTCAGGAGGTGAGTCAAGTGGCTCCAGAGG 2582
 |||||||
 OY 2661 TGCCTTTCAGATGAGTCTCTAAGAGTCAAGTCAATCTCAGAGCATTTTAA 2720
 |||||||
 DB 2583 TGCCTTTCAGATGAGTCTCTAAGAGTCAAGTCAATCTCAGAGCATTTTAA 2642
 |||||||
 OY 2721 GGCAGAGAAAGTACAGATGCTCTGAGTCTGCTCATGTCGAATGAAATTA 2772
 |||||||
 DB 2643 GGCAGAGAAAGTACAGATGCTCTGAGTCTGCTCATGTCGAATGAAATTA 2694
 |||||||

RESULT 9
 AF263835 2832 bp mRNA linear PRI 01-JUN-2000
 LOCUS Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA.
 DEFINITION partial cds.
 ACCESSION AF263835
 VERSION AF263835.1 GI:8132996
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 2832)
 Kniazeva, M. and Han, M.
 A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders
 unpublished
 2 (bases 1 to 2832)
 Kniazeva, M. and Han, M.
 Direct Submission
 Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA
 Location/Qualifiers

FEATURES
 source
 1..2832
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q:D6S280"
 /tissue_type="brain; retina"
 /gene="KCNQ5"
 /note="member of the KCNQ family"
 /codon_start=1
 /product="voltage-gated potassium channel KCNQ5"
 /protein_id="AA073446.1"
 /db_xref="GI:8132997"
 /translation="GGGLRBSRKGKQAGMSLLKPLSTSSQSRNRYKRVONYL
 YNLEPRGMAFIHIAEYFLVFGCLISFSTIEPHKLAASCLIEFVAVFGL
 EETIRMSAGCCARGMGRLRFAKREPCVDITVLASIVASAKTIEFVAVFGL
 RSLPEIOLIRBMRDRGRTWKLIGSVYAKSELITAYIGELVIFSSFLYVLEK
 DAKFEFTYALALMKGTTITLTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILG
 SGAFLKVOEHRQKHEKRNPAULIOWRSYADEKSYSTATPKPLKHLNCS
 TRKQGEASSQSLSEKRVASPRGSIKRSQASVGRSSTDTIEGSPYKQK
 SMSFNDRTFRPSRLKSOPKVIDADTALGTIDVYDERGQCDVLEDFPLKTV
 IRAIRIKFEHAKRKEETLRPYDVADVEQYSAGHLMICRKSLOTVRDQILGGS
 ITSDKSRKEITAEHETDDLSMLGRVYVEKQVSIKSLCLIDLYOVLKGSAS
 ALALASRPIPEECBOTSDYOSPSKDSGSAONGCISRSNANISRLQPLIPN
 EFSADTFALSTFTHMSQATQVPISSDSGSAVAVATNINAIINAPAPAPATITQIDPP
 LPAIKHLRPEFTLHPNAGLQPSISDVTTCLVAASKENVOVQASNLKDKSMKRSFDMG

CDS
 gene
 CDS

BASE COUNT 783 a 685 c 663 g 701 t
 ORIGIN
 GCTLLSYCPWPKDLGKSLSVONILRSTEEINLOLSGSSGSRGRDFFPKRESKL
 FIDPEEYGEETETEDTFDAAPQAREAFASDILRTGRSSQSSQISICKAGESTDALSLP
 HVKIK"

Query Match 46.8%; Score 1297; DB 9; Length 2832;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1547; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1221 TCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTACGCCAGGGGCCAGAGTTTAA 1280
 |||||||
 DB 1035 TCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTACGCCAGGGGCCAGAGTTTAA 1094
 |||||||
 OY 1281 CAGCCGACAAAGCTTCAGTGAAGTGAAGAGGTCGCCAACACGACGATCAGACCGAGG 1340
 |||||||
 DB 1095 GAGCCGACAAAGCTTCAGTGAAGTGAAGAGGTCGCCAACACGACGATCAGACCGAGG 1154
 |||||||
 OY 1341 CAGTCCACCAAGTGCAGAGAGTGGAGCTTCAACGACCGACCGCTCCGCCCTC 1400
 |||||||
 DB 1155 CAGTCCACCAAGTGCAGAGAGTGGAGCTTCAACGACCGACCGCTCCGCCCTC 1214
 |||||||
 OY 1401 GCTGCGCTCAAAAGTTCAGCCCAAAACGAGATGATGCTGACACAGCCCTGGCAC 1460
 |||||||
 DB 1215 GCTGCGCTCAAAAGTTCAGCCCAAAACGAGATGATGCTGACACAGCCCTGGCAC 1274
 |||||||
 OY 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 |||||||
 DB 1275 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1334
 |||||||
 OY 1521 ACCACTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
 |||||||
 DB 1335 ACCACTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394
 |||||||
 OY 1581 GTTTAAGGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 |||||||
 DB 1395 GTTTAAGGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1454
 |||||||
 OY 1641 TCATCTGACATGTTGTGTGAATTAAGCCTTCAACAGTGTGATCAATTTCTGG 1700
 |||||||
 DB 1455 TCATCTGACATGTTGTGTGAATTAAGCCTTCAACAGTGTGATCAATTTCTGG 1514
 |||||||
 OY 1701 AAAAGGCAATATACATCAATTAAGAGCCGAGAAATATACAGAGAACTGAGAC 1760
 |||||||
 DB 1515 AAAAGGCAATATACATCAATTAAGAGCCGAGAAATATACAGAGAACTGAGAC 1574
 |||||||
 OY 1761 CACAGAGATCTAGTGTGCTCGGTGGGTGTCAGGTTGAAAAACAGTACAGTCCAT 1820
 |||||||
 DB 1575 CACAGAGATCTAGTGTGCTCGGTGGGTGTCAGGTTGAAAAACAGTACAGTCCAT 1634
 |||||||
 OY 1821 AGAATCCAGCTGACCTGCTACTAGACATCTATCAACAGTCCCTCGGAAAGGCTGCG 1880
 |||||||
 DB 1635 AGAATCCAGCTGACCTGCTACTAGACATCTATCAACAGTCCCTCGGAAAGGCTGCG 1694
 |||||||
 OY 1881 CTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1940
 |||||||
 DB 1695 CTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1754
 |||||||
 OY 1941 CTATCAAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
 |||||||
 DB 1755 CTATCAAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1814
 |||||||
 OY 2001 ATCCAGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2060
 |||||||
 DB 1815 ATCCAGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1874
 |||||||
 OY 2061 GTTAGAGCCAGACTTCTAGGCGCTTACTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2120
 |||||||
 DB 1875 GTTAGAGCCAGACTTCTAGGCGCTTACTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1934
 |||||||
 OY 2121 GCCAATTAAGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAG 2180
 |||||||
 DB 1935 GCCAATTAAGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAGGCGTCAAG 1994
 |||||||

OY		2181	AAATTCGGCAGCCACCGCCAGGACGCCCAACAACATTTCAGATGCCACTCTCTCCAGC	2240
Db		1995	AAATTCGGCAGCCACCGCCAGGACGCCCAACAACATTTCAGATGCCACTCTCTCCAGC	2054
OY		2241	CATCAAGCATCTGCCAGGCSCAAGAACTGTGCACCCTTAACCCGCGAGGCTTACGGAAG	2300
Db		2055	CATCAAGCATCTGCCAGGCSCAAGAACTGTGCACCCTTAACCCGCGAGGCTTACGGAAG	2114
OY		2301	CATTCTCAAGCTCACCACTTGCCCTTTGTTGCCCTCCAAAGAAAATGTTGAGGTTGCACATC	2360
Db		2115	CATTCTCAAGCTCACCACTTGCCCTTTGTTGCCCTCCAAAGAAAATGTTGAGGTTGCACATC	2174
OY		2361	AAATCTCAAGGACCGTTCATGAGGAAAAAGCTTGACATGGGAGAGAATACTCTGTT	2420
Db		2175	AAATCTCAAGGACCGTTCATGAGGAAAAAGCTTGACATGGGAGAGAATACTCTGTT	2234
OY		2421	GTCGTCTGTCTCCATGTGTCCGAAAGACTTGGGCAAACTTTGCTGTGCAAAACCGAT	2480
Db		2235	GTCGTCTGTCTCCATGTGTCCGAAAGACTTGGGCAAACTTTGCTGTGCAAAACCGAT	2294
OY		2481	CAGTTCGACCGAGGAACGAAATATCAACTTTTCAGGAGTAGTCAAGTGGCTCCAGAG	2540
Db		2295	CAGTTCGACCGAGGAACGAAATATCAACTTTTCAGGAGTAGTCAAGTGGCTCCAGAG	2354
OY		2541	CAGCCAAGATTTTTAACCCCAATGGAGGAAATCCAAATGTTTATTAACGTGANAAGGT	2600
Db		2355	CAGCCAAGATTTTTAACCCCAATGGAGGAAATCCAAATGTTTATTAACGTGANAAGGT	2414
OY		2601	GGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCCGACCGCAGCCCTGCCAGGGAAG	2660
Db		2415	GGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCCGACCGCAGCCCTGCCAGGGAAG	2474
OY		2661	TGCGTTTGATCAGACTCTCTAAGAGACTGGAAGGTACAGATCATCTCAGAGATTTGTA	2720
Db		2475	TGCGTTTGATCAGACTCTCTAAGAGACTGGAAGGTACAGATCATCTCAGAGATTTGTA	2534
OY		2721	GGCAGGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAATAA	2772
Db		2535	GGCAGGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAATAA	2586
RESULT 10				
LOCUS		HSA272519		
DEFINITION		Homo sapiens partial KCNQ5 gene, exon 14.		
ACCESSION		AJ272519		
VERSION		AJ272519.1		
KEYWORDS		KCNQ5 gene; KCNQ5 protein.		
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammlia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		1 Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and Steinlein,O.K. The new voltage gated potassium channel KCNQ5 and earlyinfantile convulsions Unpublished 2 (bases 1 to 1691) Steinlein,O.K. Direct Submission Submitted (22-FEB-2000) Steinlein O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY Location/Qualifiers 1..1691 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="q14" 286..1248 /gene="KCNQ5"		
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
SOURCE				
gene				
exon				

Query Match	Best Local Similarity	Matches	95%; Conservative	34.8%;	Score 965;	DB 9;	Length 1691;
Query	1808	AGGTACAGTCCATATGATATCCAAAGCTGAGTCCCTACTAGACATCTATCAACAGGCTCCTC	1867				
Db	284	AGGTACAGTCCATATGATATCCAAAGCTGAGTCCCTACTAGACATCTATCAACAGGCTCCTC	343				
QY	1868	GGAAGGCTCTGCTCCAGCCGCTCGCTTGGCTTCATTCGAGATCCCAACCTTTGAAATGTG	1927				
Db	344	GGAAGGCTCTGCTCCAGCCGCTCGCTTGGCTTCATTCGAGATCCCAACCTTTGAAATGTG	403				
QY	1928	AACAGACATCTGACATATCAAGCCCTGTGGATAGCAAGAATCTTTCGGTTCGGCACAA	1987				
Db	404	AACAGACATCTGACATATCAAGCCCTGTGGATAGCAAGAATCTTTCGGTTCGGCACAA	463				
QY	1988	ACAGTGGCTGCTTATCCAGATACATAGTGGCCAAACATCTTCGAGAGGCTCAGTTCATTC	2047				
Db	464	ACAGTGGCTGCTTATCCAGATACATAGTGGCCAAACATCTTCGAGAGGCTCAGTTCATTC	523				
QY	2048	TGACGCCAATAGATTAGTTCAGTGGCCAGACTTTCTACGCGCTTACGCCCTACTATGACAGTGC	2107				
Db	524	TGACGCCAATAGATTAGTTCAGTGGCCAGACTTTCTACGCGCTTACGCCCTACTATGACAGTGC	583				
QY	2108	AAGCAACAGAGTGGCCAAATTTAGTCAAGCGATAGGCTCAGACATGGCAGCCACCAACCA	2167				
Db	584	AAGCAACAGAGTGGCCAAATTTAGTCAAGCGATAGGCTCAGACATGGCAGCCACCAACCA	643				
QY	2168	TTGCAAAACCAATTAATACGCGACCCCAAGCCAGCCCAACATTTATAGATGCCAC	2227				
Db	644	TTGCAAAACCAATTAATACGCGACCCCAAGCCAGCCCAACATTTATAGATGCCAC	703				
QY	2228	CTCCTCTCCAGCCATCAGCATCTGCCAGGCCGAAGACTCTGCAACCCCTAGCGAG	2287				
Db	704	CTCCTCTCCAGCCATCAGCATCTGCCAGGCCGAAGACTCTGCAACCCCTAGCGAG	763				
QY	2288	GCTTACAGGAAGCATTTCTGACGTCAACACCTGCTTGTGGCCGCAAGGAATGTC	2347				
Db	764	GCTTACAGGAAGCATTTCTGACGTCAACACCTGCTTGTGGCCGCAAGGAATGTC	823				
QY	2348	AGGTGCACAGTCAATCTCAACCAAGGACGCTTATAGGAGAAAGCTTTGACATGGGAG	2407				
Db	824	AGGTGCACAGTCAATCTCAACCAAGGACGCTTATAGGAGAAAGCTTTGACATGGGAG	883				
QY	2408	GAGAAACTCTGTTGTCTGTCTGTCTGCCAATGGTGGCCGAAGGACTTGGGCAATCTTTGTCTG	2467				
Db	884	GAGAAACTCTGTTGTCTGTCTGTCTGCCAATGGTGGCCGAAGGACTTGGGCAATCTTTGTCTG	943				
QY	2468	TGCAAAACCTGATCAGGTGACCGAGAGACATGAATATACAATCTTCAGGAGTGAATCA	2527				
Db	944	TGCAAAACCTGATCAGGTGACCGAGAGACATGAATATACAATCTTCAGGAGTGAATCA	1003				
QY	2528	GTTGGCTCCAGAGCAGCCAAAGATTTTACCCTAAATGAGGGAATCCAAATGTTTATTA	2587				
Db	1004	GTTGGCTCCAGAGCAGCCAAAGATTTTACCCTAAATGAGGGAATCCAAATGTTTATTA	1063				
QY	2588	CTGATGAAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTGATAGCCGACCCGACG	2647				
Db	1064	CTGATGAAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTGATAGCCGACCCGACG	1123				
QY	2648	CTGCCAAGGAGAGCTGCTTTGATCAGACTCTTAAAGGACTGGAAGGTCAAGATCATCTC	2707				
Db	1124	CTGCCAAGGAGAGCTGCTTTGATCAGACTCTTAAAGGACTGGAAGGTCAAGATCATCTC	1183				
QY	2708	AGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAAGTGA	2767				
Db	1184	AGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAAGTGA	1243				

OY 2768 AATAA 2772
 11111
 Db 1244 AATAA 1248

RESULT 11
 AL365232
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-257K9 on chromosome 6, complete sequence.
 ACCESSION AL365232
 KEYWORDS AL365232.24 GI:13234949
 SOURCE HTG.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 120846)
 REFERENCE
 AUTHORS Williams, S.
 TITLE Direct Submision
 JOURNAL Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Mar 5, 2001 this sequence version replaced gi:13160293.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-257K9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-257K9 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true left end of clone RP11-257K9 is at 1 in this sequence. The true left end of clone RP1-319022 is at 120747 in this sequence. The true right end of clone RP11-380M3 is at 18652 in this sequence.

FEATURES
 SOURCE
 Location/Qualifiers
 1..120846
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-257K9"
 /clone_1id="RPCI-11.1"
 2592..2964
 /note="MULTI repeat: matches 4..390 of consensus"
 repeat_region
 4469..4695
 /note="MIR repeat: matches 28..261 of consensus"
 repeat_region
 7930..8258
 /note="MULTI repeat: matches 1..365 of consensus"
 repeat_region
 8713..9200
 /note="MULTI repeat: matches 1..568 of consensus"
 repeat_region

repeat_region
 9523..9826
 /note="AluSg repeat: matches 1..304 of consensus"
 repeat_region
 11404..11893
 /note="MULTI repeat: matches 72..536 of consensus"
 repeat_region
 12067..12277
 /note="MIR repeat: matches 8..245 of consensus"
 repeat_region
 12626..12979
 /note="H3C repeat: matches 1..371 of consensus"
 repeat_region
 13234..13542
 /note="AluB repeat: matches 3..309 of consensus"
 repeat_region
 13931..14179
 /note="MIR repeat: matches 21..262 of consensus"
 repeat_region
 14522..14579
 /note="L2 repeat: matches 2655..2710 of consensus"
 repeat_region
 16405..16696
 /note="AluSg repeat: matches 1..295 of consensus"
 repeat_region
 16697..16722
 /note="13 copies 2 mer ga 928 conserved"
 repeat_region
 16801..17320
 /note="L1MD1 repeat: matches 5188..5745 of consensus"
 repeat_region
 17437..17496
 /note="L1MC/D repeat: matches 5751..5810 of consensus"
 repeat_region
 17506..17660
 /note="L1MD1 repeat: matches 5753..5906 of consensus"
 repeat_region
 17738..18052
 /note="L1MD1 repeat: matches 5908..6223 of consensus"
 repeat_region
 18473..18730
 /note="HAI1 repeat: matches 890..1179 of consensus"
 repeat_region
 18829..19080
 /note="HAI1 repeat: matches 797..1052 of consensus"
 repeat_region
 19213..19412
 /note="HAI1 repeat: matches 161..360 of consensus"
 repeat_region
 19507..19632
 /note="HAI1 repeat: matches 2..133 of consensus"
 repeat_region
 21835..21924
 /note="L2 repeat: matches 2542..2634 of consensus"
 repeat_region
 23241..23537
 /note="AluSg repeat: matches 1..308 of consensus"
 repeat_region
 24751..25402
 /note="CpG Island"
 /evidence="not experimental"
 repeat_region
 25146..25454
 /note="AluSg repeat: matches 1..312 of consensus"
 repeat_region
 25963..26384
 /note="L1PA13 repeat: matches 5719..6156 of consensus"
 repeat_region
 26891..27204
 /note="AluY repeat: matches 1..311 of consensus"
 repeat_region
 27647..27824
 /note="MER5B repeat: matches 1..178 of consensus"
 repeat_region
 27854..28504
 /note="L1MA4A repeat: matches 5646..6295 of consensus"
 repeat_region
 28796..29115
 /note="AluSg repeat: matches 1..310 of consensus"
 repeat_region
 29598..29996
 /note="MER6 repeat: matches 2..404 of consensus"
 repeat_region
 29997..30290
 /note="AluB repeat: matches 1..288 of consensus"
 repeat_region
 30291..30303
 /note="MER6 repeat: matches 404..415 of consensus"
 repeat_region
 30340..30353
 /note="MER6 repeat: matches 384..396 of consensus"
 repeat_region
 30354..30668
 /note="AluSg repeat: matches 1..312 of consensus"
 repeat_region
 30669..31120
 /note="MER6 repeat: matches 396..861 of consensus"
 repeat_region
 31872..32173
 /note="AluB repeat: matches 1..294 of consensus"
 repeat_region
 32560..32851
 /note="AluSg repeat: matches 9..311 of consensus"
 repeat_region
 32905..33039
 /note="MIR repeat: matches 31..159 of consensus"
 repeat_region
 33040..33341
 /note="AluY repeat: matches 1..298 of consensus"
 repeat_region

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS 1 (bases 1 to 47057)
 TITLE Direct Submission
 JOURNAL Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/Help/Chr6>

RP11-135M8 is from the library RPCR-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-135M8. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true right end of clone RP3-474615 is at 100 in this sequence.
 The true right end of clone RP11-135M8 is at 47057 in this sequence.

FEATURES

source location/Qualifiers
 1..47057
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-135M8"
 /clone_lib="RPC1-11.1"
 943..1075
 /note="Alu/FLAM repeat: matches 1..133 of consensus"
 3341..5507
 /note="CpG island"
 /evidence="not_experimental"
 4646..4735
 /note="match: STS: Em:G46532"
 5518..5553
 /note="18 copies 2 mer gt 100% conserved"
 5732..5831
 /note="50 copies 2 mer tt 63% conserved"
 5769..5828
 /note="20 copies 3 mer ttc 70% conserved"
 6079..6504
 /note="match: GSS: Em:AQ492985"
 7839..8140
 /note="L2 repeat: matches 1874..2194 of consensus"
 8359..8518
 /note="L2 repeat: matches 2352..2507 of consensus"
 8896..9177
 /note="L2 repeat: matches 1737..2050 of consensus"
 9228..9290
 /note="L2 repeat: matches 2687..2749 of consensus"
 9294..9811
 /note="L2 repeat: matches 1216..1728 of consensus"
 9851..10280
 /note="L2 repeat: matches 2290..2710 of consensus"

misc_feature 10257..10653
 /note="match: GSS: Em:AQ068985"
 10443..10519
 /note="MIR repeat: matches 64..150 of consensus"
 repeat_region 10655..10728
 /note="L2 repeat: matches 2065..2122 of consensus"
 repeat_region 10729..11038
 /note="AluX repeat: matches 1..307 of consensus"
 repeat_region 11039..11089
 /note="L2 repeat: matches 2122..2177 of consensus"
 repeat_region 12567..12683
 /note="L2 repeat: matches 2572..2694 of consensus"
 repeat_region 12867..13157
 /note="L2 repeat: matches 1995..2283 of consensus"
 repeat_region 13380..13920
 /note="L2 repeat: matches 1151..1686 of consensus"
 misc_feature 13721..14158
 /note="match: GSS: Em:AQ826518"
 13982..14216
 /note="MIR repeat: matches 3..234 of consensus"
 repeat_region 14253..14566
 /note="AluY repeat: matches 1..310 of consensus"
 repeat_region 14592..15509
 /note="L1PA16 repeat: matches 5195..6155 of consensus"
 repeat_region 15511..16185
 /note="L1PA16 repeat: matches 4481..5165 of consensus"
 repeat_region 16276..16336
 /note="L2 repeat: matches 2651..2710 of consensus"
 repeat_region 16688..16993
 /note="AluSg repeat: matches 1..305 of consensus"
 repeat_region 17161..17455
 /note="AluJo repeat: matches 1..296 of consensus"
 repeat_region 17760..17825
 /note="33 copies 2 mer tt 69% conserved"
 19429..19831
 /note="match: GSS: Em:B90569"
 22841..22905
 /note="MIR repeat: matches 86..155 of consensus"
 repeat_region 24397..24429
 /note="L1PA13 repeat: matches 5319..5351 of consensus"
 repeat_region 24456..24578
 /note="L1PA10 repeat: matches 6042..6163 of consensus"
 repeat_region 24579..25387
 /note="L1PA13 repeat: matches 5338..6144 of consensus"
 repeat_region 25604..25837
 /note="MER46A repeat: matches 1..232 of consensus"
 repeat_region 26239..26541
 /note="MER82 repeat: matches 27..340 of consensus"
 repeat_region 26541..26707
 /note="MER82 repeat: matches 476..647 of consensus"
 repeat_region 27213..27527
 /note="AluJo repeat: matches 1..298 of consensus"
 repeat_region 28352..28395
 /note="22 copies 2 mer ta 81% conserved"
 repeat_region 29176..29316
 /note="MER58B repeat: matches 172..313 of consensus"
 repeat_region 29553..29608
 /note="28 copies 2 mer aa 78% conserved"
 repeat_region 29624..29663
 /note="20 copies 2 mer ga 82% conserved"
 repeat_region 30427..30668
 /note="LINE2 repeat: matches 5692..5945 of consensus"
 repeat_region 34982..35055
 /note="MIR repeat: matches 117..201 of consensus"
 repeat_region 36030..36161
 /note="MIR repeat: matches 123..255 of consensus"
 repeat_region 36487..36558
 /note="L2 repeat: matches 2656..2749 of consensus"
 repeat_region 37144..37239
 /note="24 copies 4 mer ttct 94% conserved"
 repeat_region 37681..38061
 /note="L2 repeat: matches 1996..2395 of consensus"
 repeat_region 39084..39361


```

Db      181 TACAGAGTACGACAGGCTGGCGGCAACGTCACCGGGGGTGGAGAACTACCTG 240
QY      346 TACAACTGCTGAGAGAGACCCCGGCTGGCTTATCTACACGCTTTCGT 398
Db      241 TACAACTGCTGAGAGAGACCCCGGCTGGCTTATCTACACGCTTTCGT 293

RESULT 14
LOCUS   AX318576                      548 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 81 from Patent WO0177155.
ACCESSION AX318576
VERSION   AX318576.2 GI:21713342
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Fernandes, E., Vernet, C.A., Mishnu, V.S., Leach, M.D., Shinkets, R.A.,
          Zerhusen, B.D. and Kekuda, R.
          Orfx polynucleotides and polypeptides
          Patent: WO 0177155-A 81 18-OCT-2001;
          Curgan Corporation (US)
          On Jul 8, 2002 this sequence version replaced gi:17900990.
FEATURES
source    1. 548
          /organism="Homo sapiens"
          /db_xref="taxon:9606"

BASE COUNT      83 a      152 c      194 g      119 t

Query Match
Best Local Similarity 100.0%; Score 270; DB 6; Length 548;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      158 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCGCGGGCCAGCGTGGGGGGGCG 217
Db      95 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCGCGGGCCAGCGTGGGGGGGCG 154
QY      218 GTGGCGCTGAGGAGAGCGCGCGGGGCAAGGAGGGGCGCGGATGAGCTGCTGGGGAAGC 277
Db      155 GTGGCGCTGAGGAGAGCGCGCGGGGCAAGGAGGGGCGCGGATGAGCTGCTGGGGAAGC 214
QY      278 CGCTCTCTTACAGAGTAGAGCGAGCTGCGCGGCAACGTAAGTACCGGGGGTGCAGA 337
Db      215 CGCTCTCTTACAGAGTAGAGCGAGCTGCGCGGCAACGTAAGTACCGGGGGTGCAGA 274
QY      338 ACACACCTGACACAGCTGCTGGAGAGACCCCGGCGTGGCGTTCATCTACACGCTTTCG 397
Db      275 ACTACCTGTACAAAGCTGCTGGAGAGACCCCGGCGTGGCGTTCATCTACACGCTTTCG 334
QY      398 TTTTTCCTCTGCTTGTGTTGTTGTTGATT 427
Db      335 TTTTTCCTCTGCTTGTGTTGTTGTTGATT 364

RESULT 15
LOCUS   AX318764                      548 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 269 from Patent WO0177155.
ACCESSION AX318764
VERSION   AX318764.1 GI:17901084
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Fernandes, E., Vernet, C.A., Mishnu, V.S., Leach, M.D., Shinkets, R.A.,
          Zerhusen, B.D. and Kekuda, R.
          Orfx polynucleotides and polypeptides

```

```

JOURNAL Patent: WO 0177155-A 269 18-OCT-2001;
          Curgan Corporation (US)
FEATURES
source    1. 548
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /note="Expressed in Bone, Osteosarcoma, Lymphoid
          tissue, Lymph node-internal ID: FLC:2498 -
          accnos=11755212/11755212 correct-Encodes a protein in
          sequence listing 270 that is 47% similar to gi14758632
          potassium voltage-gated channel, KQT-like subfamily,
          member 4"

BASE COUNT      83 a      152 c      194 g      119 t

Query Match
Best Local Similarity 100.0%; Score 270; DB 6; Length 548;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      158 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCGCGGGCCAGCGTGGGGGGGCG 217
Db      95 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCGCGGGCCAGCGTGGGGGGGCG 154
QY      218 GTGGCGCTGAGGAGAGCGCGCGGGGCAAGGAGGGGCGCGGATGAGCTGCTGGGGAAGC 277
Db      155 GTGGCGCTGAGGAGAGCGCGCGGGGCAAGGAGGGGCGCGGATGAGCTGCTGGGGAAGC 214
QY      278 CGCTCTCTTACAGAGTAGAGCTGCGCGGGGCAACGTAAGTACCGGGGGTGCAGA 337
Db      215 CGCTCTCTTACAGAGTAGAGCTGCGCGGGGCAACGTAAGTACCGGGGGTGCAGA 274
QY      338 ACTACCTGTACAAAGCTGCTGGAGAGACCCCGGCGTGGCGTTCATCTACACGCTTTCG 397
Db      275 ACTACCTGTACAAAGCTGCTGGAGAGACCCCGGCGTGGCGTTCATCTACACGCTTTCG 334
QY      398 TTTTTCCTCTGCTTGTGTTGTTGTTGATT 427
Db      335 TTTTTCCTCTGCTTGTGTTGTTGTTGATT 364

RESULT 16
LOCUS   HSA272515                      821 bp      DNA      linear      PRI 21-FEB-2002
DEFINITION Homo sapiens partial KCNO5 gene, exon 10.
ACCESSION AJ272515
VERSION   AJ272515.1 GI:18873686
KEYWORDS  KCNO5 gene; KCNO5 protein.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Kananura, C., Bliervert, B., Hechenberger, M., Engels, H. and
          Steinlein, O.K.
          The new voltage gated potassium channel KCNO5 and early infantile
          convulsions
          Unpublished
          Steinlein, O.K.
          Direct Submission
          Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
          Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
FEATURES
source    1. 821
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /chromosome="6"
          /map="q14"
          /gene="KCNO5"
          /gene="KCNO5"
          /gene="KCNO5"
          /number=10

```


OY		675	TTTTGGCAGCTCTGCACCTACGAAAGTCCGTCCGTTTCACAGATCCCTCCGATGGCGCAT	734
Db		412	TTTTGGCACGCTGCGACCTACGAAGTCTCCGTTCTACAGATCTCCGATGGCGCAT	471
OY		735	GGACCGAAGGGGAGGACACTTGAAATTACTGGGGTTCAGTGGTTTATGCTACAGCAAG	793
Db		472	GGACCGAAGGGGAGGACACTTGAAATTACTGGGTTCAGTGGTTTATGCTACAGCAAG	530
	RESULT 19			
	AL360236			
	LOCUS			
	DEFINITION			
	Human DNA sequence from clone RP11-380M3 on chromosome 6, complete			
	sequence.			
	ACCESSION	AL360236		
	VERSION	AL360236.26	GI:13398790	
	KEYWORDS	HTG.		
	SOURCE	human.		
	ORGANISM	Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 15498)		
AUTHORS		Clark,G.		
TITLE		Direct Submission		
JOURNAL		Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,		
		CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone		
		requests: clonerequest@sanger.ac.uk		
COMMENT		On Mar 21, 2001 this sequence version replaced g1:13161652.		
		This sequence was controlled from overlapping clones		

AL360236 154998 bp DNA linear PRI 19-MAR-2001
 Human DNA sequence from clone RP11-380M3 on chromosome 6, complete
 sequence.
 AL360236
 AL360236.26 GI:13398790
 HTG.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 154998).
 Clark, G.
 Direct Submission
 Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Mar 21, 2001 this sequence version replaced gi:13161652.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30): an attempt was made to resolve all sequencing problems, such
 as compressions and repeats: all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; Sw,
 SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence
 was generated from part of bacterial clone conf1s of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/MGP/chr6>
 RP11-380M3 is from the library RPCI-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-380M3. It may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true left end of clone RP11-380M3 is at 1 in this sequence. The
 true left end of clone RP11-257K9 is at 154899 in this sequence.
 The true right end of clone RP11-374I18 is at 51132 in this
 sequence.

FEATURES
source

```
misc_feature      7. .188
                  /note="match: GSS: Em:AQ219858
misc_feature      9. .707
                  /note="match: GSS: Em:AQ534723
```

```
misc_feature      112..513
                  /note="match: GSS: Em:AQ0101949"
misc_feature      192..421
                  /note="match: GSS: Em:AQ219858"
repeat_region     476..6116
                  /note="L1P45 repeat: matches 476..6143 of consensus"
repeat_region     6117..6162
                  /note="L1P45 repeat: matches 6117..6162 of consensus"
repeat_region     6163..6630
                  /note="L1P45 repeat: matches 6163..6630 of consensus"
repeat_region     6713..7014
                  /note="L1P45 repeat: matches 6713..7014 of consensus"
repeat_region     7371..7733
                  /note="L1P45 repeat: matches 7371..7733 of consensus"
repeat_region     7733..8033
                  /note="L1P45 repeat: matches 7733..8033 of consensus"
repeat_region     8034..8085
                  /note="L1P45 repeat: matches 8034..8085 of consensus"
misc_feature      8164..8330
                  /note="match: GSS: Em:A2576083"
repeat_region     9583..9713
                  /note="MER85 repeat: matches 9583..9713 of consensus"
repeat_region     9935..10102
                  /note="MIR repeat: matches 9935..10102 of consensus"
repeat_region     10115..10415
                  /note="L1P46 repeat: matches 10115..10415 of consensus"
repeat_region     10431..13637
                  /note="L1H8 repeat: matches 10431..13637 of consensus"
repeat_region     15693..16473
                  /note="L1H8 repeat: matches 15693..16473 of consensus"
misc_feature      16027..16453
                  /note="Cpg island"
                  /evidence="not_experimental"
repeat_region     16874..17172
                  /note="AluSg repeat: matches 16874..17172 of consensus"
repeat_region     19281..19598
                  /note="AluY repeat: matches 19281..19598 of consensus"
repeat_region     20241..20537
                  /note="AluY repeat: matches 20241..20537 of consensus"
repeat_region     21391..21727
                  /note="Char1a1e4 repeat: matches 21391..21727 of consensus"
repeat_region     22440..22724
                  /note="L2 repeat: matches 22440..22724 of consensus"
repeat_region     23659..23944
                  /note="AluJo repeat: matches 23659..23944 of consensus"
repeat_region     24150..24363
                  /note="MIR repeat: matches 24150..24363 of consensus"
repeat_region     24466..24636
                  /note="MER58A repeat: matches 24466..24636 of consensus"
repeat_region     28159..28463
                  /note="AluX repeat: matches 28159..28463 of consensus"
repeat_region     29064..29193
                  /note="MIR repeat: matches 29064..29193 of consensus"
repeat_region     29195..29713
                  /note="L1M4C repeat: matches 29195..29713 of consensus"
repeat_region     29699..30773
                  /note="L1M3 repeat: matches 29699..30773 of consensus"
repeat_region     30774..31078
                  /note="AluX repeat: matches 30774..31078 of consensus"
repeat_region     31079..34443
                  /note="L1M3 repeat: matches 31079..34443 of consensus"
repeat_region     34472..34614
                  /note="L1P40 repeat: matches 34472..34614 of consensus"
misc_feature      complement(35198..35733)
                  /note="match: GSS: Em:AD670983"
repeat_region     37733..38172
                  /note="L2 repeat: matches 37733..38172 of consensus"
misc_feature      38963..39395
                  /note="match: GSS: Em:AQ769788"
misc_feature      complement(39752..40160)
                  /note="match: GSS: Em:AD044057"
misc_feature      complement(39755..40159)
                  /note="match: GSS: Em:AD044057"
misc_feature      complement(39755..40159)
                  /note="match: GSS: Em:AD044057"
```

```
misc_feature      complement(40907..41433)
                  /note="match: GSS: Em:A0724407"
misc_feature      41084..41545
                  /note="match: GSS: Em:A0144356"
repeat_region    41812..42593
                  /note="MER21B repeat: matches 2..790 of consensus"
repeat_region    42775..42937
                  /note="L2 repeat: matches 2360..2521 of consensus"
repeat_region    43050..43155
                  /note="L2 repeat: matches 2624..2736 of consensus"
repeat_region    43165..43441
                  /note="L2 repeat: matches 2487..2710 of consensus"
repeat_region    44149..44406
                  /note="AluJo repeat: matches 3..293 of consensus"
misc_feature      complement(44409..44930)
                  /note="match: GSS: Em:A0316119
match: STS: Em:g59247"
repeat_region    44717..45220
                  /note="L2 repeat: matches 1686..2222 of consensus"
misc_feature      complement(46056..46280)
                  /note="match: GSS: Em:A2340331"
misc_feature      46107..46212
                  /note="match: STS: Em:G07820"
misc_feature      complement(46107..46212)
                  /note="match: STS: Em:G27286"
misc_feature      46113..46222
                  /note="match: GSS: Em:A0307337"
misc_feature      complement(46125..46222)
                  /note="match: STS: Em:G08746"
misc_feature      46125..46222
                  /note="match: STS: Em:L30635"
misc_feature      complement(46129..46222,85430..85560)
                  /note="match: GSS: Em:A0056687"
misc_feature      join(46140..46204,85438..85547)
                  /note="match: STS: Em:G08877"
misc_feature      46140..46227
                  /note="match: GSS: Em:A2327331"
misc_feature      complement(46141..46204,85460..85563)
                  /note="match: STS: Em:G10403"
misc_feature      join(46142..46204,85460..85553)
                  /note="match: STS: Em:L30467"
misc_feature      complement(46144..46204,85445..85569)
                  /note="match: STS: Em:G08112"
misc_feature      complement(46145..46222,85432..85552)
                  /note="match: STS: Em:G10066"
misc_feature      join(46147..46222,85403..85552)
                  /note="match: STS: Em:L18516"
misc_feature      complement(46150..46222,85236..85570)
                  /note="match: GSS: Em:A278393"
misc_feature      join(46150..46216,85380..85568)
                  /note="match: GSS: Em:A243673"
misc_feature      complement(46150..46235,85455..85567)
                  /note="match: GSS: Em:A2005602"
misc_feature      complement(46150..46222,85432..85560)
                  /note="match: GSS: Em:A2035523"
misc_feature      complement(46150..46275,85289..85560)
                  /note="match: GSS: Em:A269644"
misc_feature      join(46150..46216,85368..85556)
                  /note="match: GSS: Em:A012275"
misc_feature      complement(46150..46216,75487..75764,85371..85531)
                  /note="match: GSS: Em:A2593167"
misc_feature      join(46150..46216,85434..85558)
                  /note="match: GSS: Em:A2850525"
misc_feature      join(46150..46216,85369..85504)
                  /note="match: GSS: Em:A0921614"
misc_feature      join(46150..46216,85358..85401)
```

ary Match	6.5%;	Score 179;	DB 9;	Length 15498;
Local Similarity	100.0%;	Pred. No. 7.2e-93;		
Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

615 AGATACCATTTGTTCTATCGCTTCATAGCACTTGTTCCTGCAAAACACGAGGTAAAT 674

Db	99107	AGATACCAATGTCTTATTCGCTTCATATAGCAAGTTTCTTCTGAAAAACTCAGGGTAATAT	99166
Qy	675	TTTGGCCACGCTGTGCACTCAGAAAGTCTCCGTTTCTTCTACAGATCTCCGATGGTCCGAT	734
Db	99167	TTTTGGCCACGCTGTGCACTCAGAAAGTCTCCGTTTCTTCTACAGATCTCCGATGGTCCGAT	99226
Qy	735	GGACCGAAGGGAGGAGCACTTGAATATCTGGGTTCACTGGTTATATGCTACACAGAAG	793
Db	99227	GGACCGAAGGGAGGAGCACTTGAATATCTGGGTTCACTGGTTATATGCTACACAGAAG	99285
RESULT 20			
LOCUS	HSA272517	892 bp	DNA
DEFINITION	Homo sapiens partial KCNQ5 gene, exon 12.		linear
ACCESSION	AJ272517.1		
VERSION	AJ272517.1		GI:18873688
KEYWORDS	KCNQ5 gene; KCNQ5 protein.		human.
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Kanamura, C., Bievvert, B., Hechenberger, M., Engels, H. and Steinlehn, O. K.		
TITLE	The new voltage gated potassium channel KCNQ5 and early infantile convulsions		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 892)		
AUTHORS	Steinlehn, O. K.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-FEB-2000) Steinlehn O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY		
FEATURES	Location/Qualifiers		
source	1..892		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="6"		
gene	/map="6q14"		
	343..474		
exon	/gene="KCNQ5"		
	343..474		
	/gene="KCNQ5"		
	/number=12		
BASE COUNT	/usedin=AJ272506:KCNQ5_cds		
ORIGIN	276 a 138 c 154 g 324 t		
Query Match	4.9%; Score 135; DB 9; Length 892;		
Best Local Similarity	100.0%; Pred. No. 6.1e-67;		
Matches 135; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1548	CAGAAATATGAAATTCATGTTGCAAAAGGAAGTTTAAGAAACATTACGTCATATGA	1607
Db	340	CAGAAATATGAAATTCATGTTGCAAAAGGAAGTTTAAGAAACATTACGTCATATGA	399
Qy	1608	TGTAAACATGTCATTAAGCAATATTCGCTGGTCATCTGACATGTTGTGTAGAATTAA	1667
Db	400	TGTAAACATGTCATTAAGCAATATTCGCTGGTCATCTGACATGTTGTGTAGAATTAA	459
Qy	1668	AAGCCTTCAACACG 1682	
Db	460	AAGCCTTCAACACG 474	
RESULT 21			
LOCUS	HSA272518	847 bp	DNA
DEFINITION	Homo sapiens partial KCNQ5 gene, exon 13.		linear
ACCESSION	AJ272518		
VERSION	AJ272518.1		GI:18873689
KEYWORDS	KCNQ5 gene; KCNQ5 protein.		human.
SOURCE	human.		

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bievvert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 847)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .847
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6q14"
391. .517
/gene="KCNO5"
391. .517
/gene="KCNO5"
/number=13
/usedin=AJ272506:KCNO5_cds

BASE COUNT 286 a 135 c 128 g 297 t 1 others

ORIGIN

Query Match 4.8%; Score 133; DB 9; Length 847;
Best Local Similarity 100.0%; Pred. No. 9.2e-66;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1682 GTGTTGATCAATTTCTGGAAAAAGGCCAATCATCATCATAGAGAGCCGAGAGAAA 1741
|||||
DB 330 GTTGTGATCAATTTCTGGAAAAAGGCCAATCATCATCATAGAGAGCCGAGAGAAA 449
|||||

OY 1742 TAACAGCAGACATGAGACACAGACATCATGATGTCGGTGGGTCAAGGTTG 1801
|||||
DB 450 TAACAGCAGACATGAGACACAGACATCATGATGTCGGTGGGTCAAGGTTG 509
|||||

OY 1802 AAAAACAGGTACA 1814
|||||
DB 510 AAAAACAGGTACA 522
|||||

RESULT 22
HSA272510 460 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens partial KCNO5 gene, exon 5.
DEFINITION AJ272510
ACCESSION AJ272510.1 GI:18873681
VERSION KCNO5 gene; KCNO5 protein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bievvert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 460)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"

gene /map="6q14"
202. .327
/gene="KCNO5"
202. .327
exon /gene="KCNO5"
/number=5
/usedin=AJ272506:KCNO5_cds

BASE COUNT 153 a 63 c 76 g 168 t

ORIGIN

Query Match 4.8%; Score 128; DB 9; Length 460;
Best Local Similarity 100.0%; Pred. No. 8.1e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 791 AGGAATTAATACAGCTGTGTACATAGAGATTTTGTCTTATTTTTCGTTCCCTTG 850
|||||
DB 200 AGGAATTAATACAGCTGTGTACATAGAGATTTTGTCTTATTTTTCGTTCCCTTG 259
|||||

OY 851 TCTATCTGTGGAAAAAGATGCCAATTAAGAGTTTCTACATATGACATGCTCTGCT 910
|||||
DB 260 TCTATCTGTGGAAAAAGATGCCAATTAAGAGTTTCTACATATGACATGCTCTGCT 319
|||||

OY 911 GGGGCACA 918
|||||
DB 320 GGGGCACA 327
|||||

RESULT 23
HSA272508 834 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens partial KCNO5 gene, exon 3.
DEFINITION AJ272508
ACCESSION AJ272508.1 GI:18873679
VERSION KCNO5 gene; KCNO5 protein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bievvert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 834)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .834
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6q14"
355. .481
/gene="KCNO5"
355. .481
/gene="KCNO5"
/number=3
/usedin=AJ272506:KCNO5_cds

BASE COUNT 244 a 144 c 167 g 279 t

ORIGIN

Query Match 4.8%; Score 128; DB 9; Length 834;
Best Local Similarity 100.0%; Pred. No. 8.2e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 489 GGAGTTCGATGATGTTGCTGCTTGTGATGATTCATTCGAATCTGTCGCGG 548
|||||
DB 354 GGAGTTCGATGATGTTGCTGCTTGTGATGATTCATTCGAATCTGTCGCGG 413
|||||

OY 549 TTGCTGTTGATATATAGAGATGGCAAGAACTGAGTTTGTCTGCAAGCCCTTCTG 608
|||||

```

Db      414 TTGCTGTTCGATATAGAGATGCAAGAGACTGAGTTTCGCGAAGCCCTTCG 473
QY      609 TGTATAG 616
      474 TGTATAG 481

RESULT 24
HSA272511      HSA272511      425 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 6.
ACCESSION     AJ272511
VERSION       AJ272511.1 GI:18873682
KEYWORDS      KCNQ5 gene; KCNQ5 protein.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Biervert,B., Hechenberger,M., Engels,H. and
               Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
               convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 425)
AUTHORS        Steinlein,O.K.
TITLE         Direct Submission
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
               Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
FEATURES
source         1..425
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6q14"
               /gene="KCNQ5"
               /number="6"
               /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    124 a      80 c      70 g      151 t
ORIGIN
Query Match   4.0%; Score 112; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-53;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      919 ATTACATTGACAACTATTGGCTATGAGACAACCTCCCTTAAGTGGTGGAGAGATTG 978
      151 ATTACATTGACAACTATTGGCTATGAGACAACCTCCCTTAAGTGGTGGAGAGATTG 210
Db      979 CTTTCTGAGGCTTTGACACTCCTTGGCAATTTCTTTTGGCACTTCCTGCCG 1030
      211 CTTTCTGAGGCTTTGACACTCCTTGGCAATTTCTTTTGGCACTTCCTGCCG 262

RESULT 25
HSA272516      HSA272516      767 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 11.
ACCESSION     AJ272516
VERSION       AJ272516.1 GI:18873687
KEYWORDS      KCNQ5 gene; KCNQ5 protein.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Biervert,B., Hechenberger,M., Engels,H. and
               Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
               convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 767)
AUTHORS        Steinlein,O.K.
TITLE         Direct Submission
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
               Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
FEATURES
source         1..767
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6q14"
               /gene="KCNQ5"
               /number="8"
               /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    229 a      155 c      134 g      230 t
ORIGIN

```

```

JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 767)
AUTHORS        Steinlein,O.K.
TITLE         Direct Submission
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
               Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
FEATURES
source         1..767
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6q14"
               /gene="KCNQ5"
               /number="11"
               /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    227 a      134 c      156 g      250 t
ORIGIN
Query Match   4.0%; Score 110; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1441 GCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGTA 1500
      294 GCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGAAAAAGATGCCAGTGTGATGTA 353
Db      1501 TCAGTGAAGACCTCACCACCACTTAACCTGCATTCGAGCTATCAG 1550
      354 TCAGTGAAGACCTCACCACCACTTAACCTGCATTCGAGCTATCAG 403

RESULT 26
HSA272513      HSA272513      748 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 8.
ACCESSION     AJ272513
VERSION       AJ272513.1 GI:18873684
KEYWORDS      KCNQ5 gene; KCNQ5 protein.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Biervert,B., Hechenberger,M., Engels,H. and
               Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
               convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 748)
AUTHORS        Steinlein,O.K.
TITLE         Direct Submission
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
               Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
REMARK        Revised by author 08-MAR-2000
FEATURES
source         1..748
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6q14"
               /gene="KCNQ5"
               /number="8"
               /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    229 a      155 c      134 g      230 t
ORIGIN

```

Query Match 3.5%; Score 98; DB 9; Length 748;
 Best Local Similarity 100.0%; Pred. No. 4.2e-45;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1123 CAGTGTGTTGGGCTGTTACGACGCTGAGAGAAATCTTCCATTGCAACCTGGAG 1182
 |||||||
 DB 361 CAGTGTGTTGGGCTGTTACGACGCTGAGAGAAATCTTCCATTGCAACCTGGAG 420
 |||||||

QY 1183 CCACACTTGAGGCTTGGACACCTGACGCTTACCAA 1220
 |||||||
 DB 421 CCACACTTGAGGCTTGGACACCTGACGCTTACCAA 458
 |||||||

RESULT 27
 HSA272512 561 bp DNA linear PRI 21-FEB-2002
 LOCUS Homo sapiens partial KCNQ5 gene, exon 7.
 DEFINITION AJ272512 GI:18873683
 ACCESSION
 VERSION AJ272512.1 GI:18873678
 KEYWORDS KCNQ5 gene; KCNQ5 protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and
 Steinlein, O.K.
 The new voltage gated potassium channel KCNQ5 and early infantile
 convulsions
 unpublished

TITLE 2 (bases 1 to 561)
 Steinlein, O.K.
 Direct Submission
 Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
 Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
 source
 1..561
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q14"
 149..244
 /gene="KCNQ5"
 149..244
 /gene="KCNQ5"
 /number=7
 /usedin="AJ272506:KCNQ5_cds"

BASE COUNT 154 a 100 c 106 g 201 t
 ORIGIN

Query Match 3.5%; Score 96; DB 9; Length 561;
 Best Local Similarity 100.0%; Pred. No. 6.3e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1030 GGCATTTCTGGCTGCTTTTGCATTAAAGTACAAACACGCGGAGAACTTT 1089
 |||||||
 DB 149 GGCATTTCTGGCTGCTTTTGCATTAAAGTACAAACACGCGGAGAACTTT 208
 |||||||

QY 1090 GAGAAAAGAGAACCCAGCTGCCAACCTCATTCAG 1125
 |||||||
 DB 209 GAGAAAAGAGAACCCAGCTGCCAACCTCATTCAG 244
 |||||||

RESULT 28
 HSA272507 743 bp DNA linear PRI 21-FEB-2002
 LOCUS Homo sapiens partial KCNQ5 gene, exon 2.
 DEFINITION AJ272507
 ACCESSION AJ272507.1 GI:18873678
 VERSION
 KEYWORDS KCNQ5 gene; KCNQ5 protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
 Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and
 Steinlein, O.K.
 The new voltage gated potassium channel KCNQ5 and early infantile
 convulsions
 unpublished

TITLE 2 (bases 1 to 743)
 Steinlein, O.K.
 Direct Submission
 Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
 Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
 source
 1..743
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q14"
 293..383
 /gene="KCNQ5"
 293..383
 /gene="KCNQ5"
 /number=2
 /usedin="AJ272506:KCNQ5_cds"

BASE COUNT 243 a 129 c 124 g 247 t
 ORIGIN

Query Match 3.3%; Score 92; DB 9; Length 743;
 Best Local Similarity 100.0%; Pred. No. 1.4e-41;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 TTTTCCTGCTGCTTTGGTGGTTCATTTGTCAGTGTCTTACCATCCTGAGCACAC 458
 |||||||
 DB 293 TTTTCCTGCTGCTTTGGTGGTTCATTTGTCAGTGTCTTACCATCCTGAGCACAC 352
 |||||||

QY 459 AAAATTGGCCTCAAGTTGCTTGTGATCTTGG 490
 |||||||
 DB 353 AAAATTGGCCTCAAGTTGCTTGTGATCTTGG 384
 |||||||

RESULT 29
 G63779 319 bp DNA linear STS 20-DEC-1999
 LOCUS G-104174 Random genomic STS Homo sapiens STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION G63779
 VERSION G63779.1 GI:6606596
 KEYWORDS STS.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 319)
 Oefner, P.J.
 Human random genomic STS survey, unpublished data
 unpublished (1999)

TITLE JOURNAL
 COMMENT

Contact: Peter Oefner
 Stanford Genome Center
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 6508121926
 Fax: 6508121975
 Email: Oefner@genome.stanford.edu
 Primer A: CGTGGCAAAATATATACCTGAG
 Primer B: AATTGCATAGTAAGCGCAGAA
 STS size: 319
 PCR Profile:
 Initial denaturing step of 95 degrees C for 10 min to activate
 AmpliTaq Gold (1
 min for AmpliTaq);
 14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
 min at 63

Correll, J. H., Gue

```
* * * * *
```

```
Center Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu/  
-----  
Project Information  
Center project name: GYJB  
Center Clone name: CH230-20N15  
-----  
Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 109188 bases at least Q40  
Consensus quality: 114200 bases at least Q30  
Consensus quality: 117733 bases at least Q20  
-----
```

```
* NOTE: Estimated insert size may differ from sequence length  
      (see http://www.hgsc.bcm.tmc.edu/docs/genbank_diff.txt.html),  
* NOTE: This is a "working draft" sequence. It currently  
* consists of 76 contigs. The true order of the pieces  
* is not known and their order in this sequence record is  
* arbitrary. Gaps between the contigs are represented as  
* runs of N, but the exact sizes of the gaps are unknown.  
* This record will be updated with the finished sequence,  
* as soon as it is available and the accession number will  
* be preserved.
```

```
* * * * *
```

```
1          1111: contig of 1111 bp in length  
*         1211: gap of unknown length  
*         1212: contig of 1084 bp in length  
*         2296: gap of unknown length  
*         2395: contig of 1486 bp in length  
*         3882: gap of unknown length  
*         3981: gap of unknown length  
*         5359: contig of 1358 bp in length  
*         3982:
```

5340 5439: gap of unknown length
 5440 6514: contig of 1075 bp in length
 6515 6614: gap of unknown length
 6615 7965: contig of 1351 bp in length
 7966 8065: gap of unknown length
 8066 9109: contig of 1043 bp in length
 9109 9208: gap of unknown length
 9209 10720: contig of 1512 bp in length
 10721 10820: gap of unknown length
 10821 11983: contig of 1163 bp in length
 11984 12083: gap of unknown length
 12084 13248: contig of 1165 bp in length
 13249 13348: gap of unknown length
 13349 14622: contig of 1274 bp in length
 14623 14722: gap of unknown length
 14723 16124: contig of 1402 bp in length
 16125 16224: gap of unknown length
 16225 17807: contig of 1583 bp in length
 17808 17907: gap of unknown length
 17908 19351: contig of 1444 bp in length
 19352 19451: gap of unknown length
 19452 20521: contig of 1070 bp in length
 20522 20621: gap of unknown length
 20622 22110: contig of 1489 bp in length
 22111 22211: gap of unknown length
 22212 23544: contig of 1334 bp in length
 23545 23644: gap of unknown length
 23645 24936: contig of 1292 bp in length
 24937 25036: gap of unknown length
 25037 26075: contig of 1039 bp in length
 26076 26175: gap of unknown length
 26176 27870: contig of 1695 bp in length
 27871 27970: gap of unknown length
 27971 29509: contig of 1539 bp in length
 29510 29609: gap of unknown length
 29610 30869: contig of 1260 bp in length
 30870 30969: gap of unknown length
 30970 32526: contig of 1557 bp in length
 32527 32626: gap of unknown length
 32627 33967: contig of 1341 bp in length
 33968 34067: gap of unknown length
 34068 35486: contig of 1419 bp in length
 35487 35586: gap of unknown length
 35587 37661: contig of 2075 bp in length
 37662 37761: gap of unknown length
 37762 38921: contig of 1160 bp in length
 38922 39021: gap of unknown length
 39022 40306: contig of 1285 bp in length
 40307 40406: gap of unknown length
 40407 42337: contig of 1931 bp in length
 42338 42437: gap of unknown length
 42438 43989: contig of 1352 bp in length
 43990 44089: gap of unknown length
 44090 46170: contig of 2081 bp in length
 46171 46270: gap of unknown length
 46272 47616: contig of 1346 bp in length
 47617 47716: gap of unknown length
 47717 50211: contig of 2495 bp in length
 50212 50311: gap of unknown length
 50312 52092: contig of 1781 bp in length
 52093 52192: gap of unknown length
 52193 54673: contig of 2481 bp in length
 54674 54773: gap of unknown length
 54774 57487: contig of 2714 bp in length
 57488 57587: gap of unknown length
 57588 59243: contig of 1656 bp in length
 59244 59343: gap of unknown length
 59344 60913: contig of 1570 bp in length
 60914 61013: gap of unknown length
 61014 62444: contig of 1431 bp in length
 62445 62544: gap of unknown length
 62545 64889: contig of 2345 bp in length
 64890 64989: gap of unknown length

64990 67253: contig of 2264 bp in length
 67254 67353: gap of unknown length
 67354 68768: contig of 1415 bp in length
 68769 68868: gap of unknown length
 68869 71347: contig of 2479 bp in length
 71348 71447: gap of unknown length
 71448 74130: contig of 2683 bp in length
 74131 74231: gap of unknown length
 74232 75896: contig of 1666 bp in length
 75897 75996: gap of unknown length
 75997 78359: contig of 2363 bp in length
 78360 78459: gap of unknown length
 80708 80708: contig of 2249 bp in length
 80808 80808: gap of unknown length
 83004 83004: contig of 2196 bp in length
 83104 83104: gap of unknown length
 83105 84918: contig of 1814 bp in length
 84919 85018: gap of unknown length
 85019 86508: contig of 1490 bp in length
 86509 86608: gap of unknown length
 89116 89116: contig of 2508 bp in length
 89217 89217: gap of unknown length
 92114 92114: contig of 2898 bp in length
 92214 92214: gap of unknown length
 94791 94791: contig of 2577 bp in length
 94891 94891: gap of unknown length
 94892 96527: contig of 1636 bp in length

Query Match 2.38: Score 63; DB 2; Length 173373;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 AGATACCATGTTCTTATCGCTTCATATGACGATGTTTCGCAAAACATCAGGTAATAT 674
 Db 67618 AGATACCATGTTCTTATCGCTTCATATGACGATGTTTCGCAAAACATCAGGTAATAT 67677
 QY 675 TTT 677
 Db 67678 TTT 67680

RESULT 31
 AC095944 158119 bp DNA linear HTG 12-JUL-2002
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-10P24, *** SEQUENCING IN PROGRESS
 AC095944
 VERSION
 KEYWORDS
 HTG: HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS
 1 (bases 1 to 158119)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbara,J., Benton,J., Blinagge,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowler,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhaq,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,L., Dathorne,S.R., David,R.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthett,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabrill,A., Gao,U., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J., H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hughes,M., Holloway,C., Hollins,B.,
 Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,

```

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Licherage, O., Liew, C., Liu, J., Liu, W., Louieged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheswari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Moser, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Nwabakwo, S., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenko, S., Ogun, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Saverly, G.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, Y., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Unpublished
2 (bases 1 to 158119)
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 158119)
Worley, K.C.

Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:20975970.

--- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
--- Project Information
Center project name: GDxz
Center clone name: CH230-10B24
--- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 81413 bases at least Q40
Consensus quality: 88089 bases at least Q30
Consensus quality: 93014 bases at least Q20

--- NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 80 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1015: contig of 1015 bp in length
* 1016 1115: gap of unknown length
* 1116 2566: contig of 1451 bp in length
* 2567 2666: gap of unknown length
* 2667 4281: contig of 1615 bp in length
* 4282 4382: gap of unknown length
* 4383 6207: contig of 1826 bp in length
* 6208 6308: gap of unknown length
* 6309 8110: contig of 1803 bp in length
* 8111 8210: gap of unknown length

* 8211 9571: contig of 1361 bp in length
* 9572 9671: gap of unknown length
* 9672 10707: contig of 1036 bp in length
* 10708 10807: gap of unknown length
* 10808 12352: contig of 1545 bp in length
* 12353 12453: gap of unknown length
* 12454 13960: contig of 1508 bp in length
* 13961 14060: gap of unknown length
* 14061 15413: contig of 1353 bp in length
* 15414 15513: gap of unknown length
* 15514 16664: contig of 1151 bp in length
* 16665 16764: gap of unknown length
* 16765 17828: contig of 1063 bp in length
* 17829 17927: gap of unknown length
* 17928 19247: contig of 1300 bp in length
* 19248 19347: gap of unknown length
* 19348 20517: contig of 1170 bp in length
* 20518 21780: gap of unknown length
* 21781 21880: contig of 1163 bp in length
* 21881 23057: gap of unknown length
* 23058 23157: contig of 1177 bp in length
* 23158 24853: gap of unknown length
* 24854 24953: contig of 1696 bp in length
* 24954 26344: gap of unknown length
* 26345 26444: contig of 1391 bp in length
* 26445 27983: gap of unknown length
* 27984 28083: contig of 1359 bp in length
* 28084 29735: gap of unknown length
* 29736 31482: contig of 1652 bp in length
* 31483 31582: gap of unknown length
* 31583 32711: contig of 1647 bp in length
* 32712 32712: gap of unknown length
* 32713 32713: contig of 1129 bp in length
* 32714 34521: gap of unknown length
* 34522 34621: contig of 1710 bp in length
* 34622 36147: gap of unknown length
* 36148 36247: contig of 1526 bp in length
* 36247 37311: gap of unknown length
* 37311 37411: contig of 1064 bp in length
* 37412 39031: gap of unknown length
* 39032 39131: contig of 1620 bp in length
* 39132 41285: gap of unknown length
* 41286 41385: contig of 2154 bp in length
* 41386 42767: gap of unknown length
* 42767 42867: contig of 1382 bp in length
* 42867 44682: gap of unknown length
* 44683 44782: contig of 1815 bp in length
* 44783 46866: gap of unknown length
* 46867 46966: contig of 2084 bp in length
* 46967 47976: gap of unknown length
* 47977 48076: contig of 1010 bp in length
* 48077 49547: gap of unknown length
* 49548 49647: contig of 1471 bp in length
* 49648 51218: gap of unknown length
* 51219 51318: contig of 1571 bp in length
* 51319 52918: gap of unknown length
* 52919 53018: contig of 1600 bp in length
* 53019 54334: gap of unknown length
* 54340 54534: contig of 1416 bp in length
* 54535 54535: gap of unknown length
* 54536 56268: contig of 1734 bp in length
* 56269 56368: gap of unknown length
* 56369 57621: contig of 1253 bp in length
* 57622 57721: gap of unknown length
* 57722 60195: contig of 2474 bp in length
* 60196 60295: gap of unknown length
* 60296 61598: gap of unknown length
* 61599 61698: contig of 1303 bp in length
* 61699 63335: gap of unknown length
* 63336 63435: contig of 1637 bp in length
* 63436 64830: gap of unknown length
* 64831 64930: contig of 1395 bp in length
* 64931 66934: gap of unknown length
* 66934 66934: contig of 2004 bp in length

```


11959 12058: gap of unknown length
 12059 14026: contig of 1968 bp in length
 14027 14126: gap of unknown length
 14127 15405: contig of 1279 bp in length
 15406 15505: gap of unknown length
 15506 17122: contig of 1617 bp in length
 17123 17222: gap of unknown length
 17223 18873: contig of 1651 bp in length
 18874 18973: gap of unknown length
 18974 20601: contig of 1628 bp in length
 20602 20701: gap of unknown length
 20702 22055: contig of 1353 bp in length
 22055 22134: gap of unknown length
 22135 24851: contig of 2697 bp in length
 24852 24951: gap of unknown length
 24952 26610: contig of 1659 bp in length
 26611 26710: gap of unknown length
 26711 28802: contig of 2092 bp in length
 28803 28902: gap of unknown length
 28903 30766: contig of 1864 bp in length
 30767 30866: gap of unknown length
 30867 32306: contig of 1440 bp in length
 32307 32406: gap of unknown length
 32407 33966: contig of 1560 bp in length
 33967 34066: gap of unknown length
 34067 36679: contig of 2613 bp in length
 36680 36779: gap of unknown length
 36780 38635: contig of 1856 bp in length
 38636 38735: gap of unknown length
 38736 42068: contig of 3333 bp in length
 42069 42168: gap of unknown length
 42169 44566: contig of 2488 bp in length
 44567 44756: gap of unknown length
 44757 47767: contig of 3011 bp in length
 47768 49678: gap of unknown length
 49679 49778: gap of unknown length
 49779 52158: contig of 2380 bp in length
 52159 52258: gap of unknown length
 52259 54343: contig of 2085 bp in length
 54344 54443: gap of unknown length
 54444 56895: contig of 2452 bp in length
 56896 56995: gap of unknown length
 56996 59424: contig of 2429 bp in length
 59425 59525: gap of unknown length
 59526 62014: contig of 2490 bp in length
 62015 62114: gap of unknown length
 62115 64865: contig of 2751 bp in length
 64866 64965: gap of unknown length
 64966 67928: contig of 2963 bp in length
 67929 68028: gap of unknown length
 68029 71255: contig of 3226 bp in length
 71255 71354: gap of unknown length
 71355 74111: contig of 2757 bp in length
 74112 76361: gap of unknown length
 76362 76461: gap of unknown length
 76462 78822: contig of 2361 bp in length
 78823 78922: gap of unknown length
 78923 82697: contig of 3775 bp in length
 82698 82797: gap of unknown length
 82798 86666: contig of 3869 bp in length
 86667 90137: gap of unknown length
 90138 90237: gap of unknown length
 90238 95859: contig of 5622 bp in length
 95860 95959: gap of unknown length
 95960 100305: contig of 4346 bp in length
 100306 100405: gap of unknown length
 100406 103336: contig of 2931 bp in length
 103337 103436: gap of unknown length
 103437 108501: contig of 5065 bp in length
 108502 108601: gap of unknown length

Query Match
 Best Local Similarity 100.0%; Score 56; DB 2; Length 179192;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 ACGCCAAATGAGTTCAGTCCAGACTTCTACGGCGCTTACGCTTACTATGCACAG 2105
 DB 177125 ACGCCAAATGAGTTCAGTCCAGACTTCTACGGCGCTTACGCTTACTATGCACAG 177070

RESULT 33
 AC091215/C
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-1A4, *** SEQUENCING IN PROGRESS ***
 AC091215 248862 bp DNA linear HMG 24-AUG-2002
 51 unordered pieces.
 AC091215 16 GI:22203886
 VERSION
 KEYWORDS HMG: HMG_PPHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 248862)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayala,M., Banks,T.,
 Barbarella,J., Benton,J., Bimarge,K., Blankenburg,K., Bonini,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Burch,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,X., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gottrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C., Hollins,B.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,U.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mauniny,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabdal,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokwenko,S., Oguh,M., Okunomi,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Prims,E., Pu,L.L., Qulles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojudoxan,I., Rolfe,M., Ruiz,S., Saverly,G.,
 Scherer,S., Scott,G., Shen,H., Shooshbari,N., Sisson,I.,

REFERENCE AUTHORS

Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, O.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 248862)
 Worley, K.C.

Direct Submission
 Submitted (04-APR-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 248862)
 Worley, K.C.

Direct Submission
 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 11, 2002 this sequence version replaced gi:21953790.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: TVAL
 Center clone name: CH230-1A4
 Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 3.1
 Chemistry: Dye-terminator Big Dye 3.1
 Assembly program: Phrap
 Consensus quality: 219010 bases at least Q40
 Consensus quality: 221770 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 51 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1140: contig of 1140 bp in length
 1141: gap of unknown length
 1241: contig of 1115 bp in length
 2356: gap of unknown length
 2456: contig of 1303 bp in length
 3758: gap of unknown length
 3859: contig of 1173 bp in length
 5031: gap of unknown length
 5131: gap of unknown length
 5132: contig of 1226 bp in length
 6357: gap of unknown length
 6457: contig of 1191 bp in length
 7648: gap of unknown length
 7748: contig of 1499 bp in length
 9247: gap of unknown length
 9347: contig of 1670 bp in length
 9348: gap of unknown length
 11018: contig of 1511 bp in length
 12628: gap of unknown length
 12728: contig of 1617 bp in length
 14345: gap of unknown length
 14445: contig of 1342 bp in length
 15787: gap of unknown length
 15887: gap of unknown length

15888: contig of 1843 bp in length
 17731: gap of unknown length
 17830: contig of 2067 bp in length
 19897: gap of unknown length
 19997: contig of 1654 bp in length
 21691: gap of unknown length
 21792: contig of 1038 bp in length
 22829: gap of unknown length
 22929: contig of 1456 bp in length
 24385: gap of unknown length
 2486: contig of 1334 bp in length
 25819: gap of unknown length
 25920: contig of 2260 bp in length
 28180: gap of unknown length
 28280: contig of 1751 bp in length
 30031: gap of unknown length
 30131: contig of 2190 bp in length
 32321: gap of unknown length
 32421: contig of 2131 bp in length
 34551: gap of unknown length
 34552: contig of 1645 bp in length
 36297: gap of unknown length
 36297: contig of 2283 bp in length
 38779: gap of unknown length
 38780: contig of 3599 bp in length
 42378: gap of unknown length
 42478: contig of 3054 bp in length
 45532: gap of unknown length
 45533: contig of 3701 bp in length
 45633: gap of unknown length
 49334: contig of 4455 bp in length
 49434: gap of unknown length
 53988: contig of 4106 bp in length
 58094: gap of unknown length
 58194: contig of 4339 bp in length
 62533: gap of unknown length
 62534: contig of 4873 bp in length
 67505: gap of unknown length
 67606: contig of 3996 bp in length
 67607: gap of unknown length
 71602: contig of 4167 bp in length
 71703: gap of unknown length
 75869: contig of 3650 bp in length
 75870: gap of unknown length
 79719: gap of unknown length
 79720: contig of 5179 bp in length
 84898: gap of unknown length
 84899: contig of 4505 bp in length
 85003: gap of unknown length
 85004: contig of 5374 bp in length
 89604: gap of unknown length
 94977: contig of 5065 bp in length
 95078: gap of unknown length
 100142: contig of 5279 bp in length
 100143: gap of unknown length
 105521: contig of 7158 bp in length
 105621: gap of unknown length
 112779: contig of 6151 bp in length
 112879: gap of unknown length
 119030: contig of 7702 bp in length
 119130: gap of unknown length
 126832: contig of 5812 bp in length
 126833: gap of unknown length
 132744: contig of 6700 bp in length
 132745: gap of unknown length
 132844: contig of 10475 bp in length
 139544: gap of unknown length
 150119: contig of 6048 bp in length
 150219: gap of unknown length
 156267: contig of 9107 bp in length
 156367: gap of unknown length
 165474: contig of 11023 bp in length
 165574: gap of unknown length
 176597: contig of 15650 bp in length
 176697: gap of unknown length
 192347: contig of 15650 bp in length

FEATURES

Source

1. 248862
/organism="Rattus norvegicus"
/db_xref="taxon:10116"

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 248862;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 GAGAGCCGCGGCGGAGGAGGCGGCGGATGAGCCTGCTGGGAGCCGCTTC 284
Db 77612 GAGAGCCGCGGCGGAGGAGGCGGCGGATGAGCCTGCTGGGAGCCGCTTC 77557

RESULT 34
AF525937 200 bp mRNA linear ROD 29-JUL-2002
LOCUS Rattus norvegicus potassium voltage-gated channel KQT-like
DEFINITION subfamily member 5 (Kcnq5) mRNA, partial cds.
ACCESSION AF525937
VERSION AF525937.1 GI:22001346
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 200)
Liang, G., Ulfendahl, M., Jin, Z. and Jarleback, L.
Direct Submission
Submitted (01-JUL-2002) Center for Hearing and Communication
Research, Karolinska Institute, Bldg. M1 - ENT Research Laboratory,
Stockholm SE-171 76, Sweden
Location/Qualifiers
1..200

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

1. 200
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="cochlea"
/dev_stage="adult"
/gene="Kcnq5"
/note="Kcnq5"
/product="potassium voltage-gated channel KQT-like
subfamily member 5"
/protein_id="AA088403.1"
/db_xref="GI:22001347"
/translation="TVLSTAVYSAKQGNFATSLRLFLQLLRVMDRRGCT
WKLGSVYVANSKELTAWYTG"

gene

CDS

BASE COUNT

ORIGIN

47 a 48 c 53 g 52 t

Query Match

Best Local Similarity 100.0%; Score 47; DB 10; Length 200;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 631 ATGCTTCATAGAGTGTGTTTCGCAAAAACAGGGTAATATTTT 677
Db 12 ATGCTTCATAGAGTGTGTTTCGCAAAAACAGGGTAATATTTT 58

RESULT 35
AF263836

LOCUS AF263836 3108 bp mRNA linear ROD 01-JUN-2000
DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
partial cds.
ACCESSION AF263836
VERSION AF263836.1 GI:8132998
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3108)
Knazeva, M. and Han, M.
A new gene of the voltage-gated potassium channel KCNQ family,
KCNQ5, is a candidate gene for retinal disorders
Unpublished
2 (bases 1 to 3108)
Knazeva, M. and Han, M.
Direct Submission
Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
Porter Biosciences Bldg., Boulder, CO 80309, USA
Location/Qualifiers
1..3108
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="brain"
/dev_stage="9-11 weeks"
/gene="Kcnq5"
/note="Kcnq5"
/product="similar to the Homo sapiens voltage-gated potassium
channel KCNQ5; member of the KCNQ family"
/protein_id="AA73447.1"
/db_xref="GI:8132999"

FEATURES

Source

1. 3108
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="brain"
/dev_stage="9-11 weeks"
/gene="Kcnq5"
/note="Kcnq5"
/product="similar to the Homo sapiens voltage-gated potassium
channel KCNQ5; member of the KCNQ family"
/protein_id="AA73447.1"
/db_xref="GI:8132999"

gene

CDS

BASE COUNT

ORIGIN

830 a 779 c 748 g 743 t 8 others

Query Match

Best Local Similarity 100.0%; Score 44; DB 10; Length 3108;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 TTGGTGTGCTGATTTTGTGAGTGTGTTTACACATCCCTGAGCA 455
Db 251 TTGGTGTGCTGATTTTGTGAGTGTGTTTACACATCCCTGAGCA 254

RESULT 36
AC131088 185864 bp DNA linear HTG 16-AUG-2002
LOCUS Mus musculus clone RP24-87K23, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
ACCESSION AC131088
VERSION AC131088.1 GI:22267867

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 185864)

AUTHORS Birren, B., Nusbaum, C., and Lander, E.

TITLE Mus musculus, clone RP24-87K23

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 185864)

AUTHORS Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, V., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gaidyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrum, J., Menes, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.

TITLE Direct Submission

COMMENT Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

ALL repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L24326

Center clone name: 87_K_23

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap, version 0.960731

Consensus quality: 183988 bases at least Q40

Consensus quality: 185137 bases at least Q30

Consensus quality: 185352 bases at least Q20

Insert size: 185000; agarose-ff

Insert size: 185464; sum-of-contigs

Quality coverage: 7.9 in Q20 bases; agarose-ff

Quality coverage: 7.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 54926: contig of 54926 bp in length

* 54927 55026: gap of 100 bp

* 55027 78783: contig of 23757 bp in length

* 78784 78883: gap of 100 bp

* 78884 106460: contig of 27577 bp in length

* 106461 106560: gap of 100 bp

* 106561 155796: contig of 49336 bp in length

* 155797 155896: gap of 100 bp

* 155897 185864: contig of 29968 bp in length.

* Location/Qualifiers

1..185864

BASE COUNT 55121 a 35889 c 35889 g 58565 t 400 others

ORIGIN

Query Match 1.6% Score 44; DB 2; Length 185864;

Best Local Similarity 100.0%; Pred. No. 3.4e-13;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 TTTGGTGGCTGATTGTTGTCAGTGTGTTTACCATCCGAGCA 455

DB 149433 TTTGGTGGCTGATTGTTGTCAGTGTGTTTACCATCCGAGCA 149476

RESULT 37

AC115920/C

LOCUS

DEFINITION

AC115920

AC115920.3 GI:21536151

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 162123)

Mus musculus, clone RP24-496H1

Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gaidyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazars, R., Landers, T., Lehoczký, J., Levine, R., Marquis, N., Mathews, C., Maclean, C., Macdonald, P., Major, J., Marquis, N., Menes, L., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menes, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, K., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Travers, M., Travers, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.

TITLE

JOURNAL

REFERENCE

3 (bases 1 to 162123)

Direct Submission

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., Lacroque, R., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnpack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL

COMMENT

Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2002 this sequence version replaced g1:21431285.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L24884

Center clone name: 496_H.1

Summary Statistics

Sequencing vector: Plasmid/n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159226 bases at least Q40
Consensus quality: 160353 bases at least Q30
Consensus quality: 160941 bases at least Q20
Insert size: 160000; agarose-fp

Insert size: 161323; sum-of-coverage

Quality coverage: 8.7 in Q20 bases; agarose-fp

Quality coverage: 8.6 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and the accession number will be preserved.

1 617: contig of 617 bp in length
718 717: gap of 100 bp
718 2736: contig of 2019 bp in length
2737 2836: gap of 100 bp
2837 5807: contig of 2971 bp in length
5808 5907: gap of 100 bp
5908 19603: contig of 13696 bp in length
19604 19703: gap of 100 bp
19704 34958: contig of 15255 bp in length
34959 35036: gap of 100 bp
35037 52976: contig of 17918 bp in length
52977 53076: gap of 100 bp
53077 84088: contig of 31012 bp in length
84089 84188: gap of 100 bp
84189 121220: contig of 37032 bp in length

FEATURES
* 121221 121320: gap of 100 bp
121321 162123: contig of 40803 bp in length.
Location/Qualifiers

source

1.162123
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-496H1"
/clone_lib="RPCI-24 Male Mouse BAC"
1.617

misc_feature
/note="assembly-fragment"
718..2736

misc_feature
/note="assembly-fragment"
2837..5807

misc_feature
/note="assembly-fragment"
5908..19603

misc_feature
/note="assembly-fragment"
19704..34958

misc_feature
/note="assembly-fragment"
35059..52976

misc_feature
/note="assembly-fragment"
53077..84088

misc_feature
/note="assembly-fragment"
84189..121220

misc_feature
/note="assembly-fragment"
121321..162123

BASE COUNT 47823 a 32956 c 33003 g 47530 t 811 others

ORIGIN

Query Match 1.4% Score 38; DB 2; Length 162123;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 TCAGTATAGAGAGCCGAGAGAAATTAACAGAGACA 1754
Db 138219 TCAGTATAGAGAGCCGAGAGAAATTAACAGAGACA 138182

RESULT 38

AC115920

LOCUS

DEFINITION

AC115920

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

TITLE
JOURNAL
REFERENCE
AUTHORS

Strauss, N., Subramaniam, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trillio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (phases 1 to 162123)

3 (bases 1 to 162123)

3 (bases 1 to 162123)

3 (bases 1 to 162123)

Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgeson, A., Hogues, M., Hollaway, C., Hollins, B.,
Horn, F., Howard, S., Huber, J., Hult, S., Hume, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, O., King, L., Korvah, J., Kovar, C.,
Kratochvil, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Liu, C., Liu, J., Liu, Y., Louised, H.,
Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Mageshwar, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhinney, E., McLeod, M. P., Meador, M., Mei, G., Metker, M.,
Miner, G., Miner, Z., Mitchell, T., Monabadi, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S.,
Umanil, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, S.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 173373)
Worley, K. C.

Direct Submission
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173373)
Worley, K. C.

Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:18860118.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJYB
Center clone name: CH230-20N15
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 109188 bases at least Q40
Consensus quality: 114200 bases at least Q30
Consensus quality: 117733 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1111: contig of 1111 bp in length
* 1112 1211: gap of unknown length
* 1212 2295: contig of 1084 bp in length
* 2296 2396: gap of unknown length
* 2396 3881: contig of 1486 bp in length

3882 3981: gap of unknown length
* 3982 5339: contig of 1358 bp in length
* 5340 5439: gap of unknown length
* 5440 6514: contig of 1075 bp in length
* 6515 6614: gap of unknown length
* 6615 7965: contig of 1351 bp in length
* 7966 8065: gap of unknown length
* 8066 9108: contig of 1043 bp in length
* 9109 9208: gap of unknown length
* 9209 10720: contig of 1512 bp in length
* 10721 10820: gap of unknown length
* 10821 11984: contig of 1163 bp in length
* 11985 12083: gap of unknown length
* 12084 13248: contig of 1165 bp in length
* 13249 13348: gap of unknown length
* 13349 14622: contig of 1274 bp in length
* 14623 14722: gap of unknown length
* 14723 16124: contig of 1402 bp in length
* 16125 16224: gap of unknown length
* 16225 17807: contig of 1583 bp in length
* 17808 17907: gap of unknown length
* 17908 19351: contig of 1444 bp in length
* 19352 19451: gap of unknown length
* 19452 20521: contig of 1070 bp in length
* 20522 20621: gap of unknown length
* 20622 22110: contig of 1489 bp in length
* 22111 22210: gap of unknown length
* 22211 23544: contig of 1334 bp in length
* 23545 23644: gap of unknown length
* 23645 24936: contig of 1292 bp in length
* 24937 25036: gap of unknown length
* 25037 26075: contig of 1039 bp in length
* 26076 26175: gap of unknown length
* 26176 27870: contig of 1695 bp in length
* 27871 27970: gap of unknown length
* 27971 29508: contig of 1539 bp in length
* 29509 29609: gap of unknown length
* 29610 30869: contig of 1260 bp in length
* 30870 30969: gap of unknown length
* 30970 32526: contig of 1557 bp in length
* 32527 32626: gap of unknown length
* 32627 33967: contig of 1341 bp in length
* 33968 34067: gap of unknown length
* 34068 35486: contig of 1419 bp in length
* 35487 35586: gap of unknown length
* 35587 37651: contig of 2075 bp in length
* 37652 37761: gap of unknown length
* 37762 38921: contig of 1160 bp in length
* 38922 39021: gap of unknown length
* 39022 40306: contig of 1285 bp in length
* 40307 40406: gap of unknown length
* 40407 42337: contig of 1931 bp in length
* 42338 42437: gap of unknown length
* 42439 43989: contig of 1552 bp in length
* 43990 44089: gap of unknown length
* 44090 46170: contig of 2081 bp in length
* 46171 46270: gap of unknown length
* 46271 47716: contig of 1346 bp in length
* 47717 47716: gap of unknown length
* 47718 50211: contig of 2495 bp in length
* 50212 50311: gap of unknown length
* 50312 52092: contig of 1781 bp in length
* 52093 52192: gap of unknown length
* 52193 54673: contig of 2481 bp in length
* 54674 54773: gap of unknown length
* 54774 57487: contig of 2714 bp in length
* 57488 57587: gap of unknown length
* 57588 59243: contig of 1556 bp in length
* 59244 59343: gap of unknown length
* 59344 60913: contig of 1570 bp in length
* 60914 61013: gap of unknown length
* 61014 62444: contig of 1431 bp in length
* 62445 62544: gap of unknown length


```

* 62545 64889: contig of 2345 bp in length
* 64890 64889: gap of unknown length
* 64990 67253: contig of 2264 bp in length
* 67254 67353: gap of unknown length
* 67354 67353: contig of 1415 bp in length
* 68769 68768: gap of unknown length
* 68869 71347: contig of 2479 bp in length
* 71348 71347: gap of unknown length
* 71448 71430: contig of 2683 bp in length
* 74131 74230: gap of unknown length
* 74231 74231: contig of 1666 bp in length
* 75896 75896: gap of unknown length
* 75997 78359: contig of 2363 bp in length
* 78360 78359: gap of unknown length
* 78460 80708: contig of 2249 bp in length
* 80709 80808: gap of unknown length
* 80809 83004: contig of 2196 bp in length
* 83005 83104: gap of unknown length
* 83105 84918: contig of 1814 bp in length
* 84919 85018: gap of unknown length
* 85019 86508: contig of 1490 bp in length
* 86509 86608: gap of unknown length
* 86609 89116: contig of 2508 bp in length
* 89117 89216: gap of unknown length
* 89217 92114: contig of 2898 bp in length
* 92115 92214: gap of unknown length
* 92215 94791: contig of 2577 bp in length
* 94792 94891: gap of unknown length
* 94892 96527: contig of 1636 bp in length

```

Query Match Similarity 1.3% Score 35; DB 2; Length 173373;

Best Local 100.0%; Pred. No. 7e-08; 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1087 TTGTGAGAAAGAGAACCCAGCTGCCAACCTCAT 1121

Db 168064 TTGTGAGAAAGAGAACCCAGCTGCCAACCTCAT 168030

RESULT 40 AC124139 215256 bp DNA linear HTG 10-JUN-2002

LOCUS AC124139 215256 bp DNA linear HTG 10-JUN-2002

DEFINITION Mus musculus clone RP24-78G8, WORKING DRAFT SEQUENCE, 16 ordered

ACCESSION AC124139 215256 bp DNA linear HTG 10-JUN-2002

VERSION AC124139.1 GI:21362202

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Mus musculus house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE 1 (bases 1 to 215256)

JOURNAL Mus musculus, clone RP24-78G8

REFERENCE 2 (bases 1 to 215256)

AUTHORS Bliren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

Boukhalil, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,

Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collymore, A.,

Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,

Galagan, J., Gardina, S., Glende, S., Gord, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamet, A., Karatas, A., Kells, C., Laroque, K.,

Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,

Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,

Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Melidim, J.,

Meunier, L., Milova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,

Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Risse, C.,

Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

TITLE JOURNAL

COMMENT

Schuback, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testa, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viet, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L24309
Center clone name: 78_G-8

Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960721

Consensus quality: 209693 bases at least Q40
Consensus quality: 212534 bases at least Q30
Consensus quality: 213305 bases at least Q20

Insert size: 194000; agarose-gel
Insert size: 213756; sum-of-contigs
Quality coverage: 6.5 in Q20 bases; agarose-gel
Quality coverage: 5.9 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 1419: contig of 1419 bp in length

1420 1519: gap of 100 bp

1520 2936: contig of 1417 bp in length

2937 3036: gap of 100 bp

3037 5429: contig of 2393 bp in length

5430 5529: gap of 100 bp

5530 8541: contig of 3012 bp in length

8542 8641: gap of 100 bp

8642 12670: contig of 4029 bp in length

12671 12770: gap of 100 bp

12771 17587: contig of 4817 bp in length

17588 17687: gap of 100 bp

17688 21987: contig of 4300 bp in length

21988 22087: gap of 100 bp

22088 27908: contig of 5821 bp in length

27909 28008: gap of 100 bp

28009 34487: contig of 6479 bp in length

34488 34587: gap of 100 bp

34588 42749: contig of 8162 bp in length

42750 42849: gap of 100 bp

42850 62665: contig of 19816 bp in length

62666 62765: gap of 100 bp

62766 90524: contig of 27759 bp in length

90525 90624: gap of 100 bp

90625 114652: contig of 24028 bp in length

114653 114752: gap of 100 bp

114753 143778: contig of 28026 bp in length

143779 143878: gap of 100 bp

143879 176366: contig of 32488 bp in length

176367 176466: gap of 100 bp

176467 215256: contig of 38790 bp in length.

FEATURES source

1. 215256

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-78G8"
/clone_lib="RPCI-24 Male Mouse BAC"
1.1419
misc_feature
/note="assembly-fragment"
1520..2936
/note="assembly-fragment"
3037..5429
/note="assembly-fragment"
5530..8541
/note="assembly-fragment"
8642..12670
/note="assembly-fragment"
12771..17587
/note="assembly-fragment"
17688..21987
/note="assembly-fragment"
22088..27908
/note="assembly-fragment"
28009..34487
/note="assembly-fragment"
34588..42749
/note="assembly-fragment"
42850..62665
/note="assembly-fragment"
62766..90524
/note="assembly-fragment"
90625..114652
/note="assembly-fragment"
114753..143778
/note="assembly-fragment"
143879..176366
/note="assembly-fragment"
176467..215256
/note="assembly-fragment"
misc_feature
BASE COUNT 64851 a 42308 c 42660 g 63922 t 1515 others
ORIGIN
Query Match 1.3%: Score 35; DB 2; Length 215256;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCCCGCCACGCGGAGAGAGAGAGCGG 35
|||||
Db 103522 ATGCCCGCCACGCGGAGAGAGAGAGCGG 103556
|||||
RESULT 41
AC125483/c 267605 bp DNA linear HTG 02-JUL-2002
LOCUS
DEFINITION
Mus musculus chromosome UNK clone RP23-10919, WORKING DRAFT
AC125483
ACCESSION
VERSION
AC125483.2 GI:21672246
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
The sequence of Mus musculus clone
JOURNAL
Unpublished
2 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (27-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUL-2002) Genome Sequencing Center, 4444 Forest Park

```

```

COMMENT
Parkway, St. Louis, MO 63108, USA
On Jul 2, 2002 this sequence version replaced gi:21617556.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project Information
Center project name: M8A0109109
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 265605 bases at least Q40
Consensus quality: 266280 bases at least Q20
Insert size: 225000; agarose-fp
Insert size: 267105; sum-of-ctiggs
Quality coverage: 13.62 in Q20 bases; agarose-fp
Quality coverage: 11.39 in Q20 bases; sum-of-ctiggs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 17494: contig of 17494 bp in length
* 17495 17594: gap of unknown length
* 17595 42777: contig of 25183 bp in length
* 42778 42877: gap of unknown length
* 42878 113213: contig of 70336 bp in length
* 113214 113314: gap of unknown length
* 113314 246944: contig of 133631 bp in length
* 246945 247044: gap of unknown length
* 247045 253029: contig of 5985 bp in length
* 253030 253129: gap of unknown length
* 253130 267605: contig of 14476 bp in length.
FEATURES
Location/Qualifiers
source
1.267605
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-10919"
1.17494
/note="assembly_name:Contig10"
17595..42777
/note="assembly_name:Contig11"
42878..113213
/note="assembly_name:Contig12"
113314..246944
/note="assembly_name:Contig13"
247045..253029
/note="assembly_name:Contig18"
253130..267605
/note="assembly_name:Contig19"
BASE COUNT 83559 a 51673 c 50947 g 80915 t 511 others
ORIGIN
Query Match 1.3%: Score 35; DB 2; Length 267605;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCGCCACGCGGAGAGAGAGAGCGG 35
|||||
Db 201645 ATGCCCGCCACGCGGAGAGAGAGAGCGG 201611
|||||

```


RESULT 44
AB000502
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000502
VERSION AB000502.1 GI:4176409
KEYWORDS mKQT2.9; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1227
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1136
/note="mKQT2.9"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37164.1"
/db_xref="GI:4176410"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1227
/note="19 a nucleotides"
BASE COUNT 220 a 346 c 378 g 283 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1227;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||
RESULT 45
AB000503
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000503
VERSION AB000503.1 GI:4176411
KEYWORDS mKQT2.10; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||
RESULT 46
AB000500
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000500
VERSION AB000500.1 GI:4176405
KEYWORDS mKQT2.7; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||
RESULT 46
AB000500
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000500
VERSION AB000500.1 GI:4176405
KEYWORDS mKQT2.7; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||

Sasai,H. and Nishi,Y.
KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||
RESULT 46
AB000500
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000500
VERSION AB000500.1 GI:4176405
KEYWORDS mKQT2.7; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||
RESULT 46
AB000500
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000500
VERSION AB000500.1 GI:4176405
KEYWORDS mKQT2.7; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
Location/Qualifiers
FEATURES
source
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVYPTSGEKKLVGVGLDGPADSTRDGALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNMFYRLQNFYLVLERGMVAFIHAAYFLL VFSCLVSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRMAAGCCCRYGMRGR LKFAKRPFCVIDIMVLASIAVLAAGSGNVAFSAISRFLQILRMIDRNGGTW KLGSVVVAHSEKELVTAWYIGFLCIILASFLVLAEGKNDHEDPTADALMCLITLT TIGYDKYPTQWNGRLAATFTLLIGVSFALPAGILGSAFLAKVQEOHQRHKEKRRN PAAGLIQVSLSPC"
polyA_site
1689
/note="21 a nucleotides"
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGGCGGCTTCATCTACACGC 392
|||||
Db 348 CCCCCGGCGGCGGCTTCATCTACACGC 376
|||||

source
1. .1818
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1508
/note="mKOT2.7"
/codon_start=1
/product="alternative splicing:see accession between
AB000494 and AB000504"
/protein_id="BAA37162.1"
/db_xref="GI:4176406"
/translation="MWKSRNGGVPGTSGEKKIKYGVGLDPGAPDSTRDGLIAG
SEAPKRGSVLSKPTGAGAKPRKNAFRLQNLVNLERPGMAFLYHAYVFL
VFCVLSVSTIKETKESSEGLIETITVVEYEVRIYMAACCCRYRGR
LKFARPCVIDIMVLASIAVLAAGSOGVAFSAISLRLFLQILMIRDRGSTM
KLGSVVAHSEKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNRLLATFLIGVSEFALPAGIISGFLAYOEGRHKHFKERN
PAGILOSAMRFRATLSRDLSTWYERVTVPMSYSGOTGYGASRLIPLNQLE
LIRNLSKSGILFRKPEPRSPRSPASRGVCTHALLSLCIHIVSMGRATMG
PCVCFVQVQVCEGIPRYTSOL"

BASE COUNT 340 a 539 c 525 g 414 t

ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 CCCCCGGGCTGGCTTCATCTACACGC 392
|||||
348 CCCCCGGGCTGGCTTCATCTACACGC 376

RESULT 47
AB000501 2014 bp mRNA linear ROD 23-JAN-1999
LOCUS Mus musculus mRNA for alternative splicing:see accession between
DEFINITION AB000494 and AB000504, complete cds.
ACCESSION AB000501
VERSION AB000501.1 GI:4176407
KEYWORDS mKOT2.8; alternative splicing.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
AUTHORS Sasai, H. and Nishi, Y.
TITLE KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
JOURNAL Received Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2014)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
REFERENCE Pharmaceutical Basic Research Lab., 6-2, Umeagoka, Aoba-ku,
AUTHORS Yokohama, Kanagawa 227, Japan (E-mail:watanabectrl.jti.co.jp,
JOURNAL Tel:045-972-5741)
FEATURES
source
1. .2014
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1478
/note="mKOT2.8"
/codon_start=1
/product="alternative splicing:see accession between
AB000494 and AB000504"
/protein_id="BAA37163.1"
/db_xref="GI:4176408"
/translation="MWKSRNGGVPGTSGEKKIKYGVGLDPGAPDSTRDGLIAG
SEAPKRGSVLSKPTGAGAKPRKNAFRLQNLVNLERPGMAFLYHAYVFL
VFCVLSVSTIKETKESSEGLIETITVVEYEVRIYMAACCCRYRGR
LKFARPCVIDIMVLASIAVLAAGSOGVAFSAISLRLFLQILMIRDRGSTM
KLGSVVAHSEKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNRLLATFLIGVSEFALPAGIISGFLAYOEGRHKHFKERN
PAGILOSAMRFRATLSRDLSTWYERVTVPMSYSGOTGYGASRLIPLNQLE
LIRNLSKSGILFRKPEPRSPRSPASRGVCTHALLSLCIHIVSMGRATMG
PCVCFVQVQVCEGIPRYTSOL"

KLGSVVAHSEKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNRLLATFLIGVSEFALPAGIISGFLAYOEGRHKHFKERN
PAGILOSAMRFRATLSRDLSTWYERVTVPMSYSGOTGYGASRLIPLNQLE
LIRNLSKSGILFRKPEPRSPRSPASRGVCTHALLSLCIHIVSMGRATMGPCVCFVQVQV
TVCPEPRVTSOL"

BASE COUNT 379 a 584 c 576 g 475 t

ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2014;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 CCCCCGGGCTGGCTTCATCTACACGC 392
|||||
348 CCCCCGGGCTGGCTTCATCTACACGC 376

RESULT 48
AB000504 2247 bp mRNA linear ROD 23-JAN-1999
LOCUS Mus musculus mRNA for alternative splicing:see accession between
DEFINITION AB000494 and AB000504, complete cds.
ACCESSION AB000504
VERSION AB000504.1 GI:4176413
KEYWORDS mKOT2.11; alternative splicing.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (sites)
Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
Sasai, H. and Nishi, Y.
TITLE KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
JOURNAL Received Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2247)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
REFERENCE Pharmaceutical Basic Research Lab., 6-2, Umeagoka, Aoba-ku,
AUTHORS Yokohama, Kanagawa 227, Japan (E-mail:watanabectrl.jti.co.jp,
JOURNAL Tel:045-972-5741)
FEATURES
source
1. .2247
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1103
/note="mKOT2.11"
/codon_start=1
/product="alternative splicing:see accession between
AB000494 and AB000504"
/protein_id="BAA37166.1"
/db_xref="GI:4176414"
/translation="MWKSRNGGVPGTSGEKKIKYGVGLDPGAPDSTRDGLIAG
SEAPKRGSVLSKPTGAGAKPRKNAFRLQNLVNLERPGMAFLYHAYVFL
VFCVLSVSTIKETKESSEGLIETITVVEYEVRIYMAACCCRYRGR
LKFARPCVIDIMVLASIAVLAAGSOGVAFSAISLRLFLQILMIRDRGSTM
KLGSVVAHSEKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNRLLATFLIGVSEFALPAGIISGFLAYOEGRHKHFKERN
PAGILOSAMRFRATLSRDLSTWYERVTVPMSYSGOTGYGASRLIPLNQLE
LIRNLSKSGILFRKPEPRSPRSPASRGVCTHALLSLCIHIVSMGRATMGPCVCFVQVQV
TVCPEPRVTSOL"

polyA_site
2247
/note="21 a nucleotides"

BASE COUNT 444 a 587 c 655 g 561 t

ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2247;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 CCCCCGGGCTGGCTTCATCTACACGC 392
|||||

Db 348 CCCCCGGCTGGCGCTCATCTACCACGC 376

RESULT 49
LOCUS AB000498
DEFINITION Mus musculus mRNA for alternative splicing: see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000498
VERSION AB000498.1 GI:4176401
KEYWORDS mKOT2.5; alternative splicing.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T., Sasai, H. and Nishi, Y.
TITLE KOT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Recept. Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2382)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umegakka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail: watanabe@crl.jti.co.jp, Tel: 045-972-5741)

FEATURES
source location/Qualifiers
1..2382
/organism="Mus musculus"
/db_xref="taxon:10090"
87..1799
/note="mKOT2.5"
/product="alternative splicing: see accession between AB000494 and AB000504"
/protein_id="BA057160.1"
/db_xref="GI:4176402"
/translation="MVKSRNGGVYPTGSGEKKLVGFVGLDPAQDSTRDGALLIAG SEAPKRGSVLSKPRGTGAGAGKPKRNAPYKLNFLYNVLEPRGMAPIYHAYFLL VFSCILVSTIKKEYKSESGALYILEVTIVYFVEFVRIMAGCCCRIGMGR KLGSVYVAHSEKELVTAWYIGFLCLILASQGNFVATSLNLFLOILIMIMDRGGTW TIGYGDKYPTQWNGRLAATFTLIGVSEFALPAIGSFALKEVQEHOROKHFERRN PAAGLIOSAMRFYATNLSRTDLSTWQYERTVVPYRLLPPLNOLRLKSKSG LTFKREPOPEPSPKQVSLKDRVSSPGMAKSGSPQACTVRRSPADSLDPS KVPKSMSPGDRSRTROAFRIKGAASRONSSEASLPGEDIDNKSCEFEVTEDLTPG LKVSIRAVCMRLVSKRKRESLRPIVDVILEOYSAGHDLMSRLKSLDSRSCDWR CYLA"
2382
polyA_site /note="20 a nucleotides"
BASE COUNT 477 a 684 c 692 g 529 t
ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2382;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCTGGCGCTCATCTACCACGC 392
|||||
Db 348 CCCCCGGCTGGCGCTCATCTACCACGC 376

RESULT 50
AF490773 2613 bp mRNA linear ROD 08-APR-2002
LOCUS AF490773
DEFINITION Mus musculus potassium channel KCNQ2 mRNA, complete cds.
ACCESSION AF490773
VERSION AF490773.1 GI:20069140
KEYWORDS

SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Men, H. and Levitan, I. B.
TITLE Calmodulin is an auxiliary subunit of KCNQ channels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2613)
AUTHORS Men, H. and Levitan, I. B.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Neuroscience, University of Pennsylvania, 3450 Hamilton Walk, Philadelphia, PA 19104, USA

FEATURES
source location/Qualifiers
1..2613
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="2"
/map="between Chnra4 and Befia2"
1..2613
/codon_start=1
/product="potassium channel KCNQ2"
/protein_id="AA009696.1"
/db_xref="GI:20069141"
/translation="MVKSRNGGVYPTGSGEKKLVGFVGLDPAQDSTRDGALLIAG SEAPKRGSVLSKPRGTGAGAGKPKRNAPYKLNFLYNVLEPRGMAPIYHAYFLL VFSCILVSTIKKEYKSESGALYILEVTIVYFVEFVRIMAGCCCRIGMGR KLGSVYVAHSEKELVTAWYIGFLCLILASQGNFVATSLNLFLOILIMIMDRGGTW TIGYGDKYPTQWNGRLAATFTLIGVSEFALPAIGSFALKEVQEHOROKHFERRN PAAGLIOSAMRFYATNLSRTDLSTWQYERTVVPYRLLPPLNOLRLKSKSG LTFKREPOPEPSPKQVSLKDRVSSPGMAKSGSPQACTVRRSPADSLDPS KVPKSMSPGDRSRTROAFRIKGAASRONSSEASLPGEDIDNKSCEFEVTEDLTPG LKVSIRAVCMRLVSKRKRESLRPIVDVILEOYSAGHDLMSRLKSLDSRSCDWR CYLA"
EGPFGDVAAMAPRK"
BASE COUNT 553 a 770 c 766 g 524 t
ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2613;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCTGGCGCTCATCTACCACGC 392
|||||
Db 262 CCCCCGGCTGGCGCTCATCTACCACGC 290

Search completed: June 19, 2003, 15:38:11
Job time : 6939 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:07:46 ; Search time 597 Seconds
(without alignments)
10456.515 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772
Sequence: 1 atgccccgcacacgcgcgg.....ctcatgtcaactgaataa 2772

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 24

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database :

N.Geneseq.101002:*
1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2772	100.0	2772	AAH43633	Human ion-channel
2	2772	100.0	3111	AAH43634	Human ion-channel
3	2514	90.7	2667	AAH43635	Human ion-channel
4	1552	56.0	3074	AAH49499	Human KCNQ5 DNA
5	1552	54.1	3137	AAC85414	Human KCNQ5 potass
6	1501	52.3	3718	AAC64371	Human KCNQ5 (KCN6g
7	1450	52.3	2694	AAH43632	Human CDNA encodin
8	1450	52.3	2694	AAH27192	Human potassium ch
9	1450	52.3	3071	AAH43631	Human CDNA for vol

10	965	34.8	125910	21	AAC64370	Human KCNQ5 (KCN6g
11	312	11.3	414	24	ABN24166	Human ORFX polynuc
12	270	9.7	548	24	ABN50234	Human ORF41 coding
13	60	2.2	60	24	ABN5212	Human spliced tran
14	29	1.0	2169	20	AAH26588	Nucleotide sequenc
15	28	1.0	28	21	AAC64379	Human KCNQ5 (KCN6g
16	26	0.9	26	21	AAC64381	Human KCNQ5 (KCN6g
17	26	0.9	26	21	AAC64383	Human KCNQ5 (KCN6g
18	26	0.9	26	22	AAH43635	Human voltage-gate
19	26	0.9	26	22	AAH43637	Human voltage-gate
20	26	0.9	26	22	AAH43639	Human voltage-gate
21	26	0.9	1182	18	AAH85964	Human K+ channel g
22	26	0.9	1425	24	ABK64418	Human benign prost
23	26	0.9	2565	20	AAH81548	Human brain-derive
24	26	0.9	3029	20	AAH81547	DNA encoding novel
25	26	0.9	3195	23	AAH7831	Human KCNQ2 CDNA
26	26	0.9	3232	20	AAH7830	DNA encoding novel
27	26	0.9	3232	23	AAH7830	Human mutant KCNQ2
28	26	0.9	3237	20	AAH7145	Nucleotide sequenc
29	26	0.9	3287	20	AAH26587	DNA encoding novel
30	26	0.9	7413	23	AAH74832	Human KCNQ5 (KCN6g
31	25	0.9	25	21	AAH43634	Human voltage-gate
32	25	0.9	25	22	AAH43635	Human voltage-gate
33	25	0.9	25	22	AAH43636	Human voltage-gate
34	24	0.9	24	21	AAH43634	Human KCNQ5 (KCN6g

ALIGNMENTS

RESULT 1
AAH43633
ID AAH43633 standard; CDNA; 2772 BP.
AC AAH43633;
DT 21-JAN-2002 (first entry)
DE Human ion-channel forming protein ORF.
KW Ion-channel forming protein; voltage-gated potassium channel;
KW fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.
OS Homo sapiens.
PN WO200175108-A1.
PD 11-OCT-2001.
XX 03-APR-2001; 2001WO-US10875.
XX 03-APR-2000; 2000US-194255P.
PR 03-APR-2000; 2000US-194255P.
XX (LEXI-) LEXICON GENETICS INC.
PA
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI: 2001-656987/75.
DR P-PSDB: AAB47678.
XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosis or treating diseases, in drug screening, and in
PT clinical trial monitoring
XX
XX Claim 1: Page 34-35; 43p; English.
XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
XX The protein shares structural similarity with mammalian ion channel
XX proteins, particularly voltage-gated potassium channel proteins. The
XX proteins is expressed in many human cell lines including fetal brain,
XX brain, thymus/prostate, heart and skeletal muscle. The novel protein
XX can be used in the diagnosis or treatment of diseases, in drug

1

Db 300 GGCAGAGCGGGGGCCCGGATGAGCTGCTGGGGAGCCGCTCTTACACGAGTACCCAG 359
QY 301 AGCTGCGGGCCCAACGTCAAGTACCGGGGGGTGCGAGAACTACTGTACACGCTGTGAG 360
Db 360 AGCTGCGGGCCCAACGTCAAGTACCGGGGGGTGCGAGAACTACTGTACACGCTGTGAG 419
QY 361 AGACCCCGGGGCGGCTTCATCCACGCTTCGTTTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 420 AGACCCCGGGGCGGCTTCATCCACGCTTCGTTTCTCTCTCTCTCTCTCTCTCTCTCT 479
QY 421 TTGATTTTGTAGTGTCTTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCCTC 480
Db 480 TTGATTTTGTAGTGTCTTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCCTC 539
QY 481 TTGATCTGAGTTCGTGATGATTTGCTCTTTGGTTGGAGTTATCATTCGAAATCCG 540
Db 540 TTGATCTGAGTTCGTGATGATTTGCTCTTTGGTTGGAGTTATCATTCGAAATCCG 599
QY 541 TCTGCGGGTTCGTCTTCATATAGAGATGCGAAGAGACGTGAGTTGCTCGAAG 600
Db 600 TCTGCGGGTTCGTCTTCATATAGAGATGCGAAGAGACGTGAGTTGCTCGAAG 659
QY 601 CCTCTCTGTATATAGATACATGTTCTTATGCTTCAATAGCACTGTTTCTGCAAA 660
Db 660 CCTCTCTGTATATAGATACATGTTCTTATGCTTCAATAGCACTGTTTCTGCAAA 719
QY 661 ACTCAGGGTAATATTTTGGCAGCTGCACTCAGAGTCCGTTTCTCAGATCCCTC 720
Db 720 ACTCAGGGTAATATTTTGGCAGCTGCACTCAGAGTCCGTTTCTCAGATCCCTC 779
QY 721 CCGATGTCGGGCGGAGCGGAGGGGAGGCACTTGGAAATTTAGTGGTTCAGTGGTTAT 780
Db 780 CCGATGTCGGGCGGAGCGGAGGGGAGGCACTTGGAAATTTAGTGGTTCAGTGGTTAT 839
QY 781 GCTCAGAGCAAGAAATTAATCAGAGTGTGTACATAGATTTTGGTCTATATTTTTCG 840
Db 840 GCTCAGAGCAAGAAATTAATCAGAGTGTGTACATAGATTTTGGTCTATATTTTTCG 899
QY 841 TCTTTCCTGTCTATCTGTGTGAAAAAGATGCCAATTAAGATTTTCTACATATGAGAT 900
Db 900 TCTTTCCTGTCTATCTGTGTGAAAAAGATGCCAATTAAGATTTTCTACATATGAGAT 959
QY 901 GCTCTCTGTGTGGGCGCAATTAATGACATGACAACTATTGGGTATGAGAGCAAACTCCCTTA 960
Db 960 GCTCTCTGTGTGGGCGCAATTAATGACATGACAACTATTGGGTATGAGAGCAAACTCCCTTA 1019
QY 961 ACTTGGCTGGGAAGATGCTTCTCTGAGGCTTTGCACTCCTTGGCAATTTCTTTTGA 1020
Db 1020 ACTTGGCTGGGAAGATGCTTCTCTGAGGCTTTGCACTCCTTGGCAATTTCTTTTGA 1079
QY 1021 CTTCCTGCGGCGATCTTGGGCTCAGGTTTTCATTAAGATTAAGAAACACACCGCCAG 1080
Db 1080 CTTCCTGCGGCGATCTTGGGCTCAGGTTTTCATTAAGATTAAGAAACACACCGCCAG 1139
QY 1081 AAACACTTTGAGAAAAAGAGAAACCAGTGCACACTTACAGTGTGTTGGGCTAG 1140
Db 1140 AAACACTTTGAGAAAAAGAGAAACCAGTGCACACTTACAGTGTGTTGGGCTAG 1199
QY 1141 TACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACCTTGAAGGCTTG 1200
Db 1200 TACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACCTTGAAGGCTTG 1259
QY 1201 CACACCTGCAACCTTACCAATCAGAACTAAGTTTAAGAGAGGAGTGGGCAATGTAGC 1260
Db 1260 CACACCTGCAACCTTACCAATCAGAACTAAGTTTAAGAGAGGAGTGGGCAATGTAGC 1319
QY 1261 CCCAGGGGCGCAATATTAAGAGCGACAGACCTCAGTAGTGACAGAGAGTCCCAAGC 1320
Db 1320 CCCAGGGGCGCAATATTAAGAGCGACAGACCTCAGTAGTGACAGAGAGTCCCAAGC 1379
QY 1321 ACCGACATCAGAGCGGAGGAGTCCCAAAAGTGCAGAAAGTGAAGCTTCAAGAC 1380
Db 1380 ACCGACATCAGAGCGGAGGAGTCCCAAAAGTGCAGAAAGTGAAGCTTCAAGAC 1439
QY 1381 CGAACCCGCTTCCGGCCCTCGCTCGGCTCAAAAGTTCTCGAGCAAAACCGATATAT 1440
Db 1440 CGAACCCGCTTCCGGCCCTCGCTCGGCTCAAAAGTTCTCGAGCAAAACCGATATAT 1499
QY 1441 GCTGACACAGCCCTTGGCACTGATGATATATGATGAAAAAGATGCGACTGATGTA 1500
Db 1500 GCTGACACAGCCCTTGGCACTGATGATATATGATGAAAAAGATGCGACTGATGTA 1559
QY 1501 TCAGTGAAGACCTCAACCCACCACTTAAACGTCATTCGAGTATTCAGATTAAGAA 1560
Db 1560 TCAGTGAAGACCTCAACCCACCACTTAAACGTCATTCGAGTATTCAGATTAAGAA 1619
QY 1561 TTTTCATGTTGCAAAAGGGAAGTTTAAGAAACATTTACGTCATTTGATGTAAGATGTC 1620
Db 1620 TTTTCATGTTGCAAAAGGGAAGTTTAAGAAACATTTACGTCATTTGATGTAAGATGTC 1679
QY 1621 ATTGAACAAATTTCTGCTGTCATCTGACATGTTGTGTAATTAAGCCTTCAACA 1680
Db 1680 ATTGAACAAATTTCTGCTGTCATCTGACATGTTGTGTAATTAAGCCTTCAACA 1739
QY 1681 CGTGTGATCAAAATTTTGGAAAAAGGCAAAATGACATCAGATTAAGAAAGCCGCAAAA 1740
Db 1740 CGTGTGATCAAAATTTTGGAAAAAGGCAAAATGACATCAGATTAAGAAAGCCGCAAAA 1799
QY 1741 ATTAACAGCAAAACATGAGACCAACAGATCTCAGATGCTCGGTGGGTGTCAGAGTT 1800
Db 1800 ATTAACAGCAAAACATGAGACCAACAGATCTCAGATGCTCGGTGGGTGTCAGAGTT 1859
QY 1801 GAAAAACAGGTACAGTCCATAGAAATGCAAGCTGAGTCTACTATACATCTATCAACAG 1860
Db 1860 GAAAAACAGGTACAGTCCATAGAAATGCAAGCTGAGTCTACTATACATCTATCAACAG 1919
QY 1861 GTCTTTCGAAAGGCTTCGCTCAGGCTTCGTTGGTTCATTCAGATTCGACCTTTT 1920
Db 1920 GTCTTTCGAAAGGCTTCGCTCAGGCTTCGTTGGTTCATTCAGATTCGACCTTTT 1979
QY 1921 GAATGTGAAGCAAGCAATGCAATATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 1980
Db 1980 GAATGTGAAGCAAGCAATGCAATATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 2039
QY 1981 GCACAAAACAGTGGCTGCTTATCCAGATCAATAGTCCCAATCTCGAGAGCCCTGACG 2040
Db 2040 GCACAAAACAGTGGCTGCTTATCCAGATCAATAGTCCCAATCTCGAGAGCCCTGACG 2099
QY 2041 TTTCAATTCGAGCCCAATTAAGATTCAGTCCCAAGACTTCTTACGCGCTTAAGCCCTATAG 2100
Db 2100 TTTCAATTCGAGCCCAATTAAGATTCAGTCCCAAGACTTCTTACGCGCTTAAGCCCTATAG 2159
QY 2101 CACAGTCAAGCAACAGAGTGCCTAATTAAGTCAAAAGCGATGGCTGAGGAGCCAGC 2160
Db 2160 CACAGTCAAGCAACAGAGTGCCTAATTAAGTCAAAAGCGATGGCTGAGGAGCCAGC 2219
QY 2161 AACACCTTTGCAAAACCAATTAATTAAGGACCCAGCAGCAGGCCCCAACCACTTTAGAG 2220
Db 2220 AACACCTTTGCAAAACCAATTAATTAAGGACCCAGCAGCAGGCCCCAACCACTTTAGAG 2279
QY 2221 ATCCCACTCTCTTCCAGGCGATCAAGATTCGCGAGGCGCAGAAACTCTGACCCCTTAC 2280
Db 2280 ATCCCACTCTCTTCCAGGCGATCAAGATTCGCGAGGCGCAGAAACTCTGACCCCTTAC 2339
QY 2281 CTTGCAAGGCTTACAGAAACATTTTCAGGTCACCACTGCTTGTGCTCCAGAGAA 2340
Db 2340 CTTGCAAGGCTTACAGAAACATTTTCAGGTCACCACTGCTTGTGCTCCAGAGAA 2399
QY 2341 AATGTCAGTTCACAGATCAATCTACCAAGGACGTTCTATAGAGAAAAAGCTTTGAC 2400
Db 2400 AATGTCAGTTCACAGATCAATCTACCAAGGACGTTCTATAGAGAAAAAGCTTTGAC 2459
QY 2401 ATGGGAGGAAACTCTGTTGCTGTCATGTCATGTCGAGAGGAGGAGGAGGAGGAGGAGG 2460
Db 2460 ATGGGAGGAAACTCTGTTGCTGTCATGTCATGTCGAGAGGAGGAGGAGGAGGAGGAGG 2519

QY 2461 TTGCTGTGCAAAACCTGATCAGCGAGCAAGTAAATATCACTTTCAGGAGT 2520
 Db 2520 TTGCTGTGCAAAACCTGATCAGCGAGCAAGTAAATATCACTTTCAGGAGT 2579
 QY 2521 GAGTCAGTGGCTCCAGAGCGAGCAAGATTTTACCCCAATGAGGAGATCCAAATTG 2580
 Db 2580 GAGTCAGTGGCTCCAGAGCGAGCAAGATTTTACCCCAATGAGGAGATCCAAATTG 2639
 QY 2581 TTTATATGATGAAAGAGTGGTCCCAAGAGAGAGAGACACTTTGATGCGCA 2640
 Db 2640 TTTATATGATGAAAGAGTGGTCCCAAGAGAGAGAGACACTTTGATGCGCA 2699
 QY 2641 CCGAGCGCTGCGAGGAGTGCCTTTGATCAGACTCTTAAGACTGGAAGTCAAGA 2700
 Db 2700 CCGAGCGCTGCGAGGAGTGCCTTTGATCAGACTCTTAAGACTGGAAGTCAAGA 2759
 QY 2701 TCATCTCAGACATTTGTAAGCGAGAGAAATACAGATGCCCTCAGCTTGCCTCATGTC 2760
 Db 2760 TCATCTCAGACATTTGTAAGCGAGAGAAATACAGATGCCCTCAGCTTGCCTCATGTC 2819
 QY 2761 AAACGAAATTA 2772
 Db 2820 AAACGAAATTA 2831
 RESULT 3
 AAS14653 standard; cDNA; 2667 BP.
 AAS14653:
 18-DEC-2001 (first entry)
 Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
 Human; ss; voltage-gated potassium channel; KCNQ5-2; nontoxic;
 cerebroprotective; neurotropic; analgesic; vision disorder;
 central nervous system disorder; epilepsy; migraine; hearing disorder;
 psychotic disorder; seizure; learning disorder; memory disorder;
 stroke; pain; gene therapy; splice variant.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 1..2967
 /*tag-a
 /product- "hKCNQ5-2"
 W0200170759-A1.
 27-SEP-2001.
 20-MAR-2001; 2001WO-US09328.
 21-MAR-2000; 2000US-190954P.
 (ICAG-) ICAGEN INC.
 Jegla TJ;
 WPI: 2001-611467/70.
 P-PSDB; AAU09021.
 Polyptides and polynucleotides of potassium channel KCNQ5 for
 identifying a compound modulating ion flux in eukaryotic cell or cell
 membrane expressing the protein, comprises KCNQ alpha
 subunits
 Claim 5; Page 63-64; 78pp; English.
 The invention relates to an isolated polypeptide comprising an
 alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-2.
 CC
 XX Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 other;
 XX
 QY 106 ATGAAGATGTGAGATCGCGCGGCGAGGCTGCTGACCTGCGAGCCGCGAGGCGG 165
 Db 1 ATGAAGATGTGAGATCGCGCGGCGAGGCTGCTGACCTGCGAGCCGCGAGGCGG 60
 QY 166 GACGCGCTGCTACTGCTGCGGACCCGCGGCGACCGCTGCTGCGGCGGCTGCTG 225
 Db 61 GACGCGCTGCTACTGCTGCGGACCCGCGGCGACCGCTGCTGCGGCGGCTGCTG 120
 QY 226 AGGAGAGCGCGCGGCGGCAAGAGCGGCGCGGATGAGCTGCTGCGGAGAGCGCTCT 285
 Db 121 AGGAGAGCGCGCGGCGGCAAGAGCGGCGCGGATGAGCTGCTGCGGAGAGCGCTCT 180
 QY 286 TACAGAGTAGGAGAGAGAGCGCGGCGCAAGTACAGCGGCGGCTGCAAGTACCTG 345
 Db 181 TACAGAGTAGGAGAGAGAGCGCGGCGCAAGTACAGCGGCGGCTGCAAGTACCTG 240
 QY 346 TACAGAGTAGGAGAGAGAGCGCGGCGGCTGCAAGTACAGCGGCGGCTGCTGCTC 405
 Db 241 TACAGAGTAGGAGAGAGAGCGCGGCGGCTGCAAGTACAGCGGCGGCTGCTGCTC 300
 QY 406 CTGTGCTTGTGCTGCTGATTTTGTGAGTCTTCTACATCCCTGAGACACAAATTG 465
 Db 301 CTGTGCTTGTGCTGCTGATTTTGTGAGTCTTCTACATCCCTGAGACACAAATTG 360
 QY 466 GCTCAAGTGTGCTGCTGATCTGAGTCTGATGATGATGCTGCTTGTGAGTCTG 525
 Db 361 GCTCAAGTGTGCTGCTGATCTGAGTCTGATGATGATGCTGCTTGTGAGTCTG 420
 QY 526 ATCATTCGAATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
 Db 421 ATCATTCGAATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 586 AGGTTGCTGGAAGCGCTTCTGTTATATATATATATATATATATATATATATAT 645
 Db 481 AGGTTGCTGGAAGCGCTTCTGTTATATATATATATATATATATATATATATAT 540
 QY 646 GTTGTTCGCAAAACTGAGGATATATTTTGTGCAAGTCTGCAAGTCTGCTGCT 705
 Db 541 GTTGTTCGCAAAACTGAGGATATATTTTGTGCAAGTCTGCAAGTCTGCTGCTGCT 600
 QY 706 TTCTTACAGATCTCCGATGCTGCGATGAGACGAGGAGGAGGAGGAGGAGGAGT 765
 Db 601 TTCTTACAGATCTCCGATGCTGCGATGAGACGAGGAGGAGGAGGAGGAGGAGT 660
 QY 766 GGTTCAGTGTATATGCTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 825

Db 2737 GGGTCCGGAAGACAGACAGACACTTTTGATGCCGACCGACGCTTGCAGGGAAGC 2796
 QY 2661 TGCCTTGCATCAGACTCTTAAAGAGTGAAGTACAGATCATCTCAGAGCATTTGTA 2720
 Db 2797 TGCCTTGCATCAGACTCTTAAAGAGTGAAGTACAGATCATCTCAGAGCATTTGTA 2856
 QY 2721 GGAAGGGAAGTACAGATGCTTCAAGTTCGCTTCAATCTCAAACTGAATAA 2772
 Db 2857 GGAAGGGAAGTACAGATGCTTCAAGTTCGCTTCAATCTCAAACTGAATAA 2908

RESULT 5

AAC85414
 ID AAC85414 standard; cDNA; 3137 BP.
 AC AAC85414;

XX 20-APR-2001 (first entry)

DE Human KCNQ5 potassium channel subunit coding sequence.

KM Human: KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
 KM central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
 KM CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
 KM compulsive behaviour; dementia; depression; Huntington's disease;
 KM mania; memory impairment; memory dysfunction; spinal cord damage;
 KM phobia; Pick's disease; psychosis; stroke; tremor; seizure; convulsion;
 KM epilepsy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..2694 /tag= a
 FT /product= "KCNQ5 subunit"

XX MO200077035-A2.

XX 21-DEC-2000.

XX 29-MAY-2000; 2000MO-DK00289.

XX 11-JUN-1999; 99DK-0000828.

XX (NEUR-) NEUROSEARCH AS.

XX Jentsch TJ;

XX WPI: 2001-080678/09.

XX P-PSDB; AAB47046.

XX Novel genes encoding KCNQ5 potassium channel subunits, useful for
 PT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
 PT depression, Huntington's disease, schizophrenia and Parkinson's disease

XX Claim 2; Page 44-48; 50pp; English.

XX This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
 CC heteromeric channels with other KCNQ channel subunits. In particular
 CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
 CC chromosome 6 (6p44). Chemicals which have the ability to bind to
 CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
 CC of diseases related to diseases or adverse conditions of the central
 CC nervous system (CNS), including affective disorders, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders, memory dysfunction, motion disorders, motor
 CC disorders, neurodegenerative diseases, Parkinson's disease and
 CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
 CC convulsions and epilepsy.

XX Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 other;
 SQ Query Match 56.0%; Score 1552; DB 22; Length 3137;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1221 TCAGAGCTAAGTTTAAAGAGGAGTGGCCATGCTAGCCCGAGGGCCAGAGTATTA 1280
 Db 1143 TCAGAGCTAAGTTTAAAGAGGAGTGGCCATGCTAGCCCGAGGGCCAGAGTATTA 1202
 QY 1281 GAGCCGACAAAGCTCTAGTAGTACAGAGAGTGGCCCGAGGACGACATCAAGCCGAGG 1340
 Db 1203 GAGCCGACAAAGCTCTAGTAGTACAGAGAGTGGCCCGAGGACGACATCAAGCCGAGG 1262
 QY 1341 CAGTCCACCAAAAGTCCAGAGAGTGGAGCTTCAACGACGAAACCGCTTCCGGCCCTC 1400
 Db 1263 CAGTCCACCAAAAGTCCAGAGAGTGGAGCTTCAACGACGAAACCGCTTCCGGCCCTC 1322
 QY 1401 GCTGGCCCTCAAAAGTCTCAGCCAAACGATGATGCTGACACAGCCCTTGGCAC 1460
 Db 1323 GCTGGCCCTCAAAAGTCTCAGCCAAACGATGATGCTGACACAGCCCTTGGCAC 1382
 QY 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 Db 1383 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
 QY 1521 ACCACTTAAACCTGATTCAGAGCTATCAGATATGATGATGATGATGATGATGATGATGAT 1580
 Db 1443 ACCACTTAAACCTGATTCAGAGCTATCAGATATGATGATGATGATGATGATGATGATGAT 1502
 QY 1581 GTTAAAGGAACATTAAGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 Db 1503 GTTAAAGGAACATTAAGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
 QY 1641 TCATCTGACATGTTGTGTAGATTAAGACCTTCAACACGCTGTGATCAAAATCTTGG 1700
 Db 1563 TCATCTGACATGTTGTGTAGATTAAGACCTTCAACACGCTGTGATCAAAATCTTGG 1622
 QY 1701 AAAAGGGCAATTCACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAATGAGAC 1760
 Db 1623 AAAAGGGCAATTCACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAATGAGAC 1682
 QY 1761 CACAGAGCATCTCAGTATGCTCGGTGCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1820
 Db 1683 CACAGAGCATCTCAGTATGCTCGGTGCGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1742
 QY 1821 AGAATCCAGCTGACAGTCCCTACTAGACATCTATACAGAGTCTTGGAAAGGCTCTGC 1880
 Db 1743 AGAATCCAGCTGACAGTCCCTACTAGACATCTATACAGAGTCTTGGAAAGGCTCTGC 1802
 QY 1881 CTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1940
 Db 1803 CTCAGCCCTGCTTGGCTTCAATTCAGATCCCACTTTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1862
 QY 1941 CTATCAAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
 Db 1863 CTATCAAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
 QY 2001 ATCCAGATCAACTAGTCCCAACATCTGAGAGGCTCCAGATCTTCTGAGCCCAATGA 2060
 Db 1923 ATCCAGATCAACTAGTCCCAACATCTGAGAGGCTCCAGATCTTCTGAGCCCAATGA 1982
 QY 2061 GTTCAAGTCCCAAGCTTCTAGCCGCTTAAAGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2120
 Db 1983 GTTCAAGTCCCAAGCTTCTAGCCGCTTAAAGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2042
 QY 2121 GCCAATTAAGCAAGGATGCTCAGAGTGGAGCCAGCCAGCAACCAATTCGCAACCAAT 2180
 Db 2043 GCCAATTAAGCAAGGATGCTCAGAGTGGAGCCAGCCAGCAACCAATTCGCAACCAAT 2102
 QY 2181 AATAGGCAACCAAGCCAGAGCCCAACCAATTAAGATGCTCAGCCAGC 2240

Db 2103 AATAAGGACCCAGCCAGCAGCCACCACTTACAGATCCACCTCTCTCCAGC 2162
 QY 2241 CATCAACATCTGCGCCAGGAGCAAACTGCAACCTTACAGGCTTACAGAAAG 2300
 Db 2163 CATCAAGCATCTGCCAGGCAAACTGCAACCTTACAGGCTTACAGAAAG 2222
 QY 2301 CATTTCTGACGACGACCTGCTTGTGCTCCAGGAAATGTCAGTTGACAGTC 2360
 Db 2223 CATTTCTGACGACGACCTGCTTGTGCTCCAGGAAATGTCAGTTGACAGTC 2282
 QY 2361 AATCTCACCAGGACGCTTCTATGAGAAAGCTTGAATGGAGAGAAACCTGTT 2420
 Db 2283 AATCTCACCAGGACGCTTCTATGAGAAAGCTTGAATGGAGAGAAACCTGTT 2342
 QY 2421 GTCTGTCTGCTCCATGGTGGCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACCTGAT 2480
 Db 2343 GTCTGTCTGCTCCATGGTGGCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACCTGAT 2402
 QY 2481 CAGGTGACCGAGGAGACTGATATATACAACTTTCAGGAGTACATCAAGTGGCTCCAGAGG 2540
 Db 2403 CAGGTGACCGAGGAGACTGATATATACAACTTTCAGGAGTACATCAAGTGGCTCCAGAGG 2462
 QY 2541 CAGCAAGATTTTATCCCAATGAGGAAATCCAAATTTTATTAAGTATGAAGAGT 2600
 Db 2463 CAGCAAGATTTTATCCCAATGAGGAAATCCAAATTTTATTAAGTATGAAGAGT 2522
 QY 2601 GGGTCCCGAAGAGACAGACAGACACTTTGATGCCAGCCAGCTGCCAGGAAAGC 2660
 Db 2523 GGGTCCCGAAGAGACAGACAGACACTTTGATGCCAGCCAGCTGCCAGGAAAGC 2582
 QY 2661 TGGCTTTGACATCACTCTCTAAGAGACTGGAAGTCAAGATCATCTCAGAGCATTTGTA 2720
 Db 2583 TGGCTTTGACATCACTCTCTAAGAGACTGGAAGTCAAGATCATCTCAGAGCATTTGTA 2642
 QY 2721 GGCAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAATGAAATTA 2772
 Db 2643 GGCAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAATGAAATTA 2694
 RESULT 6
 AAC64371
 ID AAC64371 standard; cDNA; 3718 BP.
 XX AAC64371;
 AC
 XX
 DT 07-FEB-2001 (first entry)
 DE
 XX
 DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
 XX
 KW Human; KCNQ5; KC6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardiocutaneous; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200061606-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000MO-US09587.
 XX
 PR 14-APR-1999; 99US-0129274.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Petrunkin K, Caskey CT, Li W, Metzker ML;
 XX
 DR WPI: 2000-647417/62.
 DR P-PSDB: AAB24241.

XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 PS Claim 3; Fig 2; 99p; English.
 XX
 CC The present sequence encodes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.
 CC
 SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
 Query Match 54.18; Score 1501; DB 21; Length 3718;
 Best Local Similarity 99.98; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1221 TCAGAGCTAAGTTTAAAGGAGCGAGTCCCATGCTAGCCCGAGGCGCAGATATTAA 1280
 Db 1127 TCAGAGCTAAGTTTAAAGGAGCGAGTCCCATGCTAGCCCGAGGCGCAGATATTAA 1186
 QY 1281 GAGCCGCAAGCCTCAGTAGGTGACAGAGAGTCCCGCAAGCCAGCATCAAGCCGAGG 1340
 Db 1187 GAGCCGCAAGCCTCAGTAGGTGACAGAGAGTCCCGCAAGCCAGCATCAAGCCGAGG 1246
 QY 1341 CAGTCCCAAGAAAGTGAGAGAGCTGAGCTTCAAGCAGCAAGCCGCTCCGCGCTC 1400
 Db 1247 CAGTCCCAAGAAAGTGAGAGAGCTGAGCTTCAAGCAGCAAGCCGCTCCGCGCTC 1306
 QY 1401 GCTGCGCCTCAAAAGTTCTCAGCCCAAAACAGTATAGATCTGACACAGCCCTTGAC 1460
 Db 1307 GCTGCGCCTCAAAAGTTCTCAGCCCAAAACAGTATAGATCTGACACAGCCCTTGAC 1366
 QY 1461 TGATGATGATATATATGAAAAAGATGCCAGTGTATGATGATGAGAGAGCTTACCCC 1520
 Db 1367 TGATGATGATATATATGAAAAAGATGCCAGTGTATGATGATGAGAGAGCTTACCCC 1426
 QY 1521 ACCACTTAAACCTGATGAGCTATCAGATTAATGAAATTTGATTTGCAAAACGGA 1580
 Db 1427 ACCACTTAAACCTGATGAGCTATCAGATTAATGAAATTTGATTTGCAAAACGGA 1486
 QY 1581 GTTTAAGGAAACATTACCTCATATGATGTAAGAGATGTCATTGAAACATATTCGCTGG 1640
 Db 1487 GTTTAAGGAAACATTACCTCATATGATGTAAGAGATGTCATTGAAACATATTCGCTGG 1546
 QY 1641 TCATCTGACATGTTGTGTAGATTAAGAGCTTCAAAACAGCTGTGATCAATTCCTGG 1700
 Db 1547 TCATCTGACATGTTGTGTAGATTAAGAGCTTCAAAACAGCTGTGATCAATTCCTGG 1606
 QY 1701 AAAAGGGCAATACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAAATGAGAG 1760
 Db 1607 AAAAGGGCAATACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAAATGAGAG 1666
 QY 1761 CACAGACATCTCAGATTAAGCTGCTGCGGTGCTCAAGTTGAAAAACAGTACAGTCAAT 1820
 Db 1667 CACAGACATCTCAGATTAAGCTGCTGCGGTGCTCAAGTTGAAAAACAGTACAGTCAAT 1726
 QY 1821 AGAATCAAGCTGAGCTCCTACTAGACATCTATCAACAGTCTCTCGGAAAGGCTCTGC 1880
 Db 1727 AGAATCAAGCTGAGCTCCTACTAGACATCTATCAACAGTCTCTCGGAAAGGCTCTGC 1786
 QY 1881 CTCAGCCCTCGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGCATCTGA 1940
 Db 1787 CTCAGCCCTCGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGCATCTGA 1846


```

OY 1941 CTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAACAGTGGCTCTT 2000
DB 1847 CTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGACAAACAGTGGCTCTT 1906
OY 2001 ATCCAGATCAACTAGTGTCCCAACATCTCGAGAGGCTCGAGTTTCATTTGAGCCCAATGA 2060
DB 1907 ATCCAGATCAACTAGTGTCCCAACATCTCGAGAGGCTCGAGTTTCATTTGAGCCCAATGA 1966
OY 2061 GTTCAGAGCCAGACTTCTAGAGGCTTAGGCTTACTATGACAGTCAAGCAACACAGGT 2120
DB 1967 GTTCAGAGCCAGACTTCTAGAGGCTTAGGCTTACTATGACAGTCAAGCAACACAGGT 2026
OY 2121 GCCAATTAGTCAAGCGATGCTCAGCAGTGGCAGCCACCAACACATTTGCAACCAAT 2180
DB 2027 GCCAATTAGTCAAGCGATGCTCAGCAGTGGCAGCCACCAACACATTTGCAACCAAT 2086
OY 2181 AAATAGGCGACCCCAAGCCAGACAGCCCAACAACTTTACAGATCCACCTCTCTCCAGC 2240
DB 2087 AAATAGGCGACCCCAAGCCAGACAGCCCAACAACTTTACAGATCCACCTCTCTCCAGC 2146
OY 2241 CATCAAGCATCTGCCAGAGCCAGAAACTCTGACCCCTAACCTTGAGGCTTACAGGAAG 2300
DB 2147 CATCAAGCATCTGCCAGAGCCAGAAACTCTGACCCCTAACCTTGAGGCTTACAGGAAG 2206
OY 2301 CATTTGACGTCAACCACTGCTGTTGCTCCCAAGGAAATGTTTCAGTTCAGCAGTGC 2360
DB 2207 CATTTGACGTCAACCACTGCTGTTGCTCCCAAGGAAATGTTTCAGTTCAGCAGTGC 2266
OY 2361 AAATTCACCAAGAGCCGTTCTATAGAGAAAGCTTTACATGGAGAGGAAACTCTGTT 2420
DB 2267 AAATTCACCAAGAGCCGTTCTATAGAGAAAGCTTTACATGGAGAGGAAACTCTGTT 2326
OY 2421 GTCTGTCTGTCCATGTTGCCAGAGACTTGGCAAACTTTGTGTGCAAAACCTGAT 2480
DB 2327 GTCTGTCTGTCCATGTTGCCAGAGACTTGGCAAACTTTGTGTGCAAAACCTGAT 2386
OY 2481 CAGGTGACCGAGAGAACTGAATATACAACTTTCAGGGAGTGAAGTGCCTCCAGAGG 2540
DB 2387 CAGGTGACCGAGAGAACTGAATATACAACTTTCAGGGAGTGAAGTGCCTCCAGAGG 2446
OY 2541 CAGCCAAAGTTTTTACCCCAATAGAGGAAATCCAAATGTTTAACTGATGAAGAGT 2600
DB 2447 CAGCCAAAGTTTTTACCCCAATAGAGGAAATCCAAATGTTTAACTGATGAAGAGT 2506
OY 2601 GGGTCCCGAAGAGACAGACACACTTTTGTATGCCGACCGACCTGCCAGGGAAGC 2660
DB 2507 GGGTCCCGAAGAGACAGACACACTTTTGTATGCCGACCGACCTGCCAGGGAAGC 2566
OY 2661 TGCCCTTTCATCAGACTCTTAAGAGACTGGAAGTCAAGTCAATCTCAGACATTTGTA 2720
DB 2567 TGCCCTTTCATCAGACTCTTAAGAGACTGGAAGTCAAGTCAATCTCAGACATTTGTA 2626
OY 2721 GGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2772
DB 2627 GGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2678

```

RESULT 7
 AAS14652
 ID AAS14652 standard; cDNA: 2694 BP.
 AC AAS14652;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.
 XX
 KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nontropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; splice variant.

```

XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 1..2994
XX FT /tag= a
XX FT /product= "hKCNQ5-1"
XX
XX MO200107059-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US09328.
XX
XX 21-MAR-2000; 2000US-190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI: 2001-611467/70.
XX
XX P-PSDB; AAU09020.
XX
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ alpha
XX subunits
XX
XX Claim 5; Page 62-63; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
XX alpha-subunit of a KCNQ potassium channel, with a subsequence having
XX 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
XX sequence and forms a KCNQ potassium channel having the characteristic of
XX voltage-gating with at least an additional KCNQ alpha-subunit. Also
XX included in the scope of the invention are the nucleic acids encoding
XX hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
XX expression vectors encoding them, antibodies against them, the use of
XX 3-dimensional computer modelling to identify molecules that bind to a
XX KCNQ containing potassium channel and modulate ion flux through the
XX channel. The KCNQ polypeptide is useful for identifying a compound that
XX increases or decreases ion flux through a potassium channel expressed in
XX an eukaryotic host cell or cell membrane. The compound (and the
XX KCNQ nucleic acid when used in gene therapy) is useful as
XX a pharmaceutical agent for treating diseases involving abnormal ion flux,
XX such as disorders of the central nervous system, such as epilepsy,
XX migraines, hearing and vision problems, psychotic disorders, seizures,
XX learning and memory disorders, stroke and pain. The antibodies are
XX useful for detecting a KCNQ5 polypeptide in a human tissue and the
XX use of a nucleotide sequence of KCNQ5 to search computer databases to
XX find variants of the sequence which are associated with disease states,
XX is useful for screening mutations of KCNQ5. The present sequence is
XX a splice variant of hKCNQ5 encoding hKCNQ5-1.
XX
XX Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;
XX
XX Query Match 52.3%; Score 1450; DB 22; Length 2694;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX OY 1221 TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCGATGAGCCCGAGGGCCAGATTTAA 1280
XX 1143 TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCGATGAGCCCGAGGGCCAGATTTAA 1202
XX
XX OY 1281 GAGCCGCAAGCCTCAGTAGTACAGAGAGTCCCAAGCACCGCATACAGCCGAGGG 1340
XX 1203 GAGCCGCAAGCCTCAGTAGTACAGAGAGTCCCAAGCACCGCATACAGCCGAGGG 1262
XX
XX OY 1341 CAGTCCACCAAGAGTACAGAGAGTGGAGCTTCAAGACCGAAGCCGCTTCCGGCCCTC 1400
XX 1263 CAGTCCACCAAGAGTACAGAGAGTGGAGCTTCAAGACCGAAGCCGCTTCCGGCCCTC 1322
XX
XX OY 1401 GCTGGCCCTCAAAAAGTTCTCAGCCAAAACAGTAGATGCTGACACAGCCCTTGGCAG 1460

```



```

|||||
Db 1323 GCTGGCCCTCAAAAAGTTCTCACCCAAAACAGATGATGTCGACACACCCCTTGGCAC 1382
Oy 1461 TGATGATGATATATGATGAAGAAAGATGCCAGTGTGATGATCATGTGGAACCTCACCCC 1520
Db 1383 TGATGATGATATGATGAAGAAAGATGCCAGTGTGATGATCATGTGGAACACCTCACCCC 1442
Oy 1521 ACCACTTAAAGTGTGATGTCGAGCTATCAGAAATTAAGAAATTTGATGTCGAAACGGAA 1580
Db 1443 ACCACTTAAAGTGTGATGTCGAGCTATCAGAAATTAAGAAATTTGATGTCGAAACGGAA 1502
Oy 1581 GTTTAAGGAACATTAAGTCCATATATGATGAAGAAAGATGATGAACAAATTTCTGCTGG 1640
Db 1503 GTTTAAGGAACATTAAGTCCATATATGATGAAGAAAGATGATGAACAAATTTCTGCTGG 1562
Oy 1641 TCATCTGACATGTTGTGATGAATTAAGAAAGCTTCAACACAGTGTGATCAAAATCTCTGG 1700
Db 1563 TCATCTGACATGTTGTGATGAATTAAGAAAGCTTCAACACAGTGTGATCAAAATCTCTGG 1622
Oy 1701 AAAAGGGCAAAATCAGATCAGATTAAGAAAGCCGAGAGAAAATACAGACAGATGAGAC 1760
Db 1623 AAAAGGGCAAAATCAGATCAGATTAAGAAAGCCGAGAGAAAATACAGACAGATGAGAC 1682
Oy 1761 CACAGACAGATCAGATGCTCGGTGGTGTGTCAGAGTTGAAAAACAGTATACATCCAT 1820
Db 1683 CACAGACAGATCAGATGCTCGGTGGTGTGTCAGAGTTGAAAAACAGTATACATCCAT 1742
Oy 1821 AGAATCCAAAGCTGAGTGCCTACTAGACATCTATCAACAGGTCTCTGGAAAGGCTCTGC 1880
Db 1743 AGAATCCAAAGCTGAGTGCCTACTAGACATCTATCAACAGGTCTCTGGAAAGGCTCTGC 1802
Oy 1881 CTGAGCCCTGCTTGGCTTCATCCAGATGCCACTTTGAAAGTGAACAGACATCTGA 1940
Db 1803 CTGAGCCCTGCTTGGCTTCATCCAGATGCCACTTTGAAAGTGAACAGACATCTGA 1862
Oy 1941 CTATCAAAAGCCCTGTGATGAGCAAGAATCTTCCGGGTTCCGACAAAACAGTGGCTGT 2000
Db 1863 CTATCAAAAGCCCTGTGATGAGCAAGAATCTTCCGGGTTCCGACAAAACAGTGGCTGT 1922
Oy 2001 ATCCAGATCAATAGTATGATGAGCAAGAGCCCTGACAGTTCAATTCGACCCCAATGA 2060
Db 1923 ATCCAGATCAATAGTATGATGAGCAAGAGCCCTGACAGTTCAATTCGACCCCAATGA 1982
Oy 2061 GTTCAGTCCCAAGCTTCTACGCGCTTACGCGCTTACATGACAGTCAAGCAACAGGT 2120
Db 1983 GTTCAGTCCCAAGCTTCTACGCGCTTACGCGCTTACATGACAGTCAAGCAACAGGT 2042
Oy 2121 GCCAATTAAGTCAAGCGATGCTGAGCAGTGGCAGCCACCAACACATTCGAAACCAAT 2180
Db 2043 GCCAATTAAGTCAAGCGATGCTGAGCAGTGGCAGCCACCAACACATTCGAAACCAAT 2102
Oy 2181 AAATAGGCGCACCAAGCCAGCAGACGCCCAACAACATTTACAGATCCCACTCTCTCCAGC 2240
Db 2103 AAATAGGCGCACCAAGCCAGCAGACGCCCAACAACATTTACAGATCCCACTCTCTCCAGC 2162
Oy 2241 CATCAAGATGCTGCCAGGCGCAGAAAGTGTGACCTTAACCTGACAGGTTACAGGAAG 2300
Db 2163 CATCAAGATGCTGCCAGGCGCAGAAAGTGTGACCTTAACCTGACAGGTTACAGGAAG 2222
Oy 2301 CATTTCTGACGTCACCACTGCTGCTTGTGCTCACAAGAAAATGTTCAAGTTGACAGTC 2360
Db 2223 CATTTCTGACGTCACCACTGCTGCTTGTGCTCACAAGAAAATGTTCAAGTTGACAGTC 2282
Oy 2361 AAATCTCACAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGGAGAAACCTGTT 2420
Db 2283 AAATCTCACAAGACCGTTCTATAGAGAAAAGCTTTGACATGGAGGAGAAACCTGTT 2342
Oy 2421 GTCCTGTGTCGCATGATGTCGAGAGACTTGGGCAAAATCTTTGCTGTGCAAAAACCTGAT 2480
Db 2343 GTCCTGTGTCGCATGATGTCGAGAGACTTGGGCAAAATCTTTGCTGTGCAAAAACCTGAT 2402
Oy 2481 CAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAAGTCAAGTGGCTTCAGAGG 2540
|||||

```

```

Db 2403 CAGGTGACCGAGAGAACTGAATATACAACTTTCAGGAGTGAAGTGGCTCCAGAGG 2462
Oy 2541 CAGCCAAATTTTACCCCAATTGAGAGGAATCCAAATGTTATATACATGATGAAGAGT 2600
Db 2463 CAGCCAAATTTTACCCCAATTGAGAGGAATCCAAATGTTATATACATGATGAAGAGT 2522
Oy 2601 GGGTCCCGAGAGACAGACAGACACTTTGATGCGGACCGCAGCCCTGCCAGGAGAGC 2660
Db 2523 GGGTCCCGAGAGACAGACAGACACTTTGATGCGGACCGCAGCCCTGCCAGGAGAGC 2582
Oy 2661 TGCCCTTGATCAGACTCTTAAGAGACTGGAAGTCAAGATCATCTCAGAGCATTTGTAA 2720
Db 2583 TGCCCTTGATCAGACTCTTAAGAGACTGGAAGTCAAGATCATCTCAGAGCATTTGTAA 2642
Oy 2721 GGCAGAGAGAAATACAGATGAGCCCTCAGCTTGCCTCATGTCAACTGAAATTA 2772
Db 2643 GGCAGAGAGAAATACAGATGAGCCCTCAGCTTGCCTCATGTCAACTGAAATTA 2694

```

RESULT 8

AAD27192
ID AAD27192 standard; cDNA; 2694 BP.

XX AAD27192;
XX 09-APR-2002 (first entry)

DE Human potassium channel polypeptide, KCNQ5 cDNA.

XX Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
XX dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
XX ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
XX anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
XX addiction; myokymia; Alzheimer's disease; age-associated memory loss;
XX learning deficiency; cognitive disorder; motor disease; neuron disease;
XX neurophysiological disorder; neuropsychological disorder; asthma;
XX neuron cell death; brain tumour; gene therapy; antisense therapy;
XX synaptic transmission; electrical excitability; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..2694
FT CDS /tag= a
FT /product= "Human KCNQ5 protein"

PN W020019256-A1.

XX 06-DEC-2001.

XX 24-MAY-2001; 2001WO-US17314.

XX 26-MAY-2000; 2000US-207389P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;
XX Gribkoff VK;

XX WPI; 2002-122069/16.

XX P-PSDB; AAE16599.

XX Novel potassium channel polypeptide, KCNQ5 and poly nucleotide encoding
XX it, for diagnosing, treating and identifying modulators useful in
XX treating neurological, neuropsychological and neuropsychological
XX diseases

XX Claim 3; Fig 1; 128pp; English.

XX The invention relates to potassium channel polypeptides referred to
XX as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
XX polypeptides are useful for identifying compounds that modulate their
XX biological activity. The compounds identified and KCNQ5 polynucleotides

CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amniotic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for treating neuropsychological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCMOS polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease
 CC tissues or cells. The present sequence is human KCMOS cDNA.

XX Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 52.3%; Score 1450; DB 24; Length 2694;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1221 TCAGACCTAGTATTTAAGAGCAGTGGCGATGGCTACCCAGGGGCGAGATATTA 1280
 1143 TCAGACCTAGTATTTAAGAGCAGTGGCGATGGCTACCCAGGGGCGAGATATTA 1202
 1281 GAGCCGACAGCCTCAGTACGAGAGGTCCCAACGACGACATCAGACCCGAGG 1340
 1203 GAGCCGACAGCCTCAGTACGAGAGGTCCCAACGACGACATCAGACCCGAGG 1262
 1341 CAGTCCACCAAGCTGAGAGAGTGGAGTTCACACGACCCGCTCCGCGCTC 1400
 1263 CAGTCCACCAAGCTGAGAGAGTGGAGTTCACACGACCCGCTCCGCGCTC 1322
 1401 GCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGAC 1460
 1323 GCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGAC 1382
 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 1383 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
 1521 ACCACTTAAACCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1580
 1443 ACCACTTAAACCTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1502
 1581 GTTTAAGGAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGAT 1640
 1503 GTTTAAGGAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGAT 1562
 1641 TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1700
 1563 TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
 1701 AAAAGGGCAATTCATCAGATTAAGAGCCGAGAGAAATTAACAGAGAAATGAGAC 1760
 1623 AAAAGGGCAATTCATCAGATTAAGAGCCGAGAGAAATTAACAGAGAAATGAGAC 1682
 1761 CACAGAGCATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1820
 1683 CACAGAGCATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1742
 1821 AGAATCCAAAGTGAAGTGGCTTACATCAGATCAGATCAGATCAGATCAGATCAGAT 1880
 1743 AGAATCCAAAGTGAAGTGGCTTACATCAGATCAGATCAGATCAGATCAGATCAGAT 1802
 1881 CTCACCCCTCGCTTGGCTTCAATTCAGATCAGATCAGATCAGATCAGATCAGATCAG 1940
 1803 CTCACCCCTCGCTTGGCTTCAATTCAGATCAGATCAGATCAGATCAGATCAGATCAG 1862
 1941 CTATCAAAAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
 1863 CTATCAAAAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922

QY 2001 ATCCAGATCACTAGTCCCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAAATGA 2060
 DB 1923 ATCCAGATCACTAGTCCCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAAATGA 1982
 QY 2061 GTTCACATGCCCACTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACAGGT 2120
 DB 1983 GTTCACATGCCCACTTCTACGCGCTTACGCGCTTACTATGACAGTCAAGCAACAGGT 2042
 QY 2121 GCCAATTAAGCAAGGATGGCTCAGCAGTGGAGCCGACCAACCATTTGCAACCAAT 2180
 DB 2043 GCCAATTAAGCAAGGATGGCTCAGCAGTGGAGCCGACCAACCATTTGCAACCAAT 2102
 QY 2181 AATATGAGCAACCAAGCAGCAGCCCAACACTTACAGATCCACCTCTCTCCAGC 2240
 DB 2103 AATATGAGCAACCAAGCAGCAGCCCAACACTTACAGATCCACCTCTCTCCAGC 2162
 QY 2241 CATCAAGCATCTGCGCCAGGCGCAGAACTCTGCACCCCTACCCCTGACAGGCTTACAGAAAG 2300
 DB 2163 CATCAAGCATCTGCGCCAGGCGCAGAACTCTGCACCCCTACCCCTGACAGGCTTACAGAAAG 2222
 QY 2301 CATTTCTGACGTACACCACTGCTTGTGCTCCCAAGAAATGTTGAGTTGACAGATC 2360
 DB 2223 CATTTCTGACGTACACCACTGCTTGTGCTCCCAAGAAATGTTGAGTTGACAGATC 2282
 QY 2361 AATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGACATGGAGAGAACTCTGTT 2420
 DB 2283 AATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGACATGGAGAGAACTCTGTT 2342
 QY 2421 GTCTGTCTGTCCTCATGCTGCTCCGAGAGCTTGGCAATCTTTGCTGCAAAACCTGAT 2480
 DB 2343 GTCTGTCTGTCCTCATGCTGCTCCGAGAGCTTGGCAATCTTTGCTGCAAAACCTGAT 2402
 QY 2481 CAGGTCCAGCCGAGCACTATATATCACTTTGAGGAGTGAAGTCAAGTGGCTCCAGAG 2540
 DB 2403 CAGGTCCAGCCGAGCACTATATATCACTTTGAGGAGTGAAGTCAAGTGGCTCCAGAG 2462
 QY 2541 CAGCCAAAGATTTTACCCCAATGAGAGGAAATGCAATGTTTATATCTATGAGAGGT 2600
 DB 2463 CAGCCAAAGATTTTACCCCAATGAGAGGAAATGCAATGTTTATATCTATGAGAGGT 2522
 QY 2601 GGGTCCGAAAGAGACAGACAGACACTTTGATGCGCAGCCGACCTGCGAGGAGG 2660
 DB 2523 GGGTCCGAAAGAGACAGACAGACACTTTGATGCGCAGCCGACCTGCGAGGAGG 2582
 QY 2661 TGCTTTGATCAGACCTGCTTAAGAGCTGGAAGGTACAGATCATCTCAAGCAATTGTA 2720
 DB 2583 TGCTTTGATCAGACCTGCTTAAGAGCTGGAAGGTACAGATCATCTCAAGCAATTGTA 2642
 QY 2721 GGCAGAGAAAGTACAGATGCGCTGAGCTTGCCTCATGTCMAAAGTGAATA 2772
 DB 2643 GGCAGAGAAAGTACAGATGCGCTGAGCTTGCCTCATGTCMAAAGTGAATA 2694

RESULT 9

AS14651
 ID AS14651 standard; cDNA; 3071 BP.

AS14651:

18-DEC-2001 (first entry)

Human cDNA for voltage gated potassium channel hKvMOS.

Human; ss; voltage-gated potassium channel; hKvMOS; motropic;

central nervous system disorder; analgesic; vision disorder;

psychotic disorder; seizure; learning disorder; memory disorder;

stroke; pain; gene therapy.

Homo sapiens.
 WO200170759-A1.

PD 27-SEP-2001.
XX 20-MAR-2001; 2001WO-US09328.
PF 21-MAR-2000; 2000US-190954P.
PR (ICAG-) ICAGEN INC.
XX Jegla TJ;
XX WPI: 2001-611467/70.
DR Polyptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits
PS Claim 5; page 61-62; 78pp; English.
XX The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a representative cDNA for hKCNQ5.
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other:
Query Match 52.3%; Score 1450; DB 22; Length 3071;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1221 TCAGAGCTAGCTTTAGAGGCGAGTGGCTAGGCTGAGGCGGCGAGAGTATTTAA 1280
DB 1152 TCAGAGCTAGCTTTAGAGGCGAGTGGCTAGGCTGAGGCGGCGAGAGTATTTAA 1211
QY 1281 GAGCGAGCAAGCTCAGTAGTGACAGAGAGTCCCAAGCAGCAGATCAGAGCCGAGG 1340
DB 1212 GAGCGAGCAAGCTCAGTAGTGACAGAGAGTCCCAAGCAGCAGATCAGAGCCGAGG 1271
QY 1341 CAGTCCCAAGAGTGCAGAGAGTGCAGAGTCCCAAGCAGCAGATCAGAGCCGAGG 1400
DB 1272 CAGTCCCAAGAGTGCAGAGAGTGCAGAGTCCCAAGCAGCAGATCAGAGCCGAGG 1331
QY 1401 GCTGGCGCTCAAAAGTCTCAGCCCAAAAGCAGTATGATGCTGACAGACCCCTGGCAC 1460
DB 1332 GCTGGCGCTCAAAAGTCTCAGCCCAAAAGCAGTATGATGCTGACAGACCCCTGGCAC 1391
QY 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
DB 1392 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1451
QY 1521 ACCAGCTTAAAGTGCATGAGCTATCAGATTAATTAATTAATTAATTAATTAATTAAT 1580
DB 1452 ACCAGCTTAAAGTGCATGAGCTATCAGATTAATTAATTAATTAATTAATTAATTAAT 1511

QY 1581 GTTTAAGAAACATTAGCTCCATATGATGATGATGATGATGATGATGATGATGATGATG 1640
DB 1512 GTTTAAGAAACATTAGCTCCATATGATGATGATGATGATGATGATGATGATGATGATG 1571
QY 1641 TCATCTGACATGTTGTGTAGAAATTTAAAGCCTTCAACACGCTGTGATCAATTCCTGG 1700
DB 1572 TCATCTGACATGTTGTGTAGAAATTTAAAGCCTTCAACACGCTGTGATCAATTCCTGG 1631
QY 1701 AAAAGGCAATTCATCATGATTAAGAGAGGCGAGGAAATTAACAGCAATGAGAG 1760
DB 1632 AAAAGGCAATTCATCATGATTAAGAGAGGCGAGGAAATTAACAGCAATGAGAG 1691
QY 1761 CACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1820
DB 1692 CACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1751
QY 1821 AGAATCCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1880
DB 1752 AGAATCCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1811
QY 1881 CTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1940
DB 1812 CTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1871
QY 1941 CTATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2000
DB 1872 CTATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1931
QY 2001 ATCCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2060
DB 1932 ATCCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991
QY 2061 GTTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2120
DB 1992 GTTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2051
QY 2121 GCCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2180
DB 2052 GCCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
QY 2181 AAATAGGCGACCCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 2240
DB 2112 AAATAGGCGACCCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 2171
QY 2241 CATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2300
DB 2172 CATCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2231
QY 2301 CATTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2360
DB 2232 CATTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2291
QY 2361 AAATCTCAGCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 2420
DB 2292 AAATCTCAGCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 2351
QY 2421 GTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2480
DB 2352 GTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2411
QY 2481 CAGGTGCGACGAGAGCAATGATATACAACTTTGAGGAGTGAAGTGAAGTGAAGTGAAGT 2540
DB 2412 CAGGTGCGACGAGAGCAATGATATACAACTTTGAGGAGTGAAGTGAAGTGAAGTGAAGT 2471
QY 2541 CAGGCAAGATTTTACCCCAATGAGAGGAAATGAAATGAAATGAAATGAAATGAAATG 2600
DB 2472 CAGGCAAGATTTTACCCCAATGAGAGGAAATGAAATGAAATGAAATGAAATGAAATG 2531
QY 2601 GGGTCCGAG 2660
DB 2532 GGGTCCGAG 2591
QY 2661 TGCTTTGCAATGAGACTCTTAAGAGCTGGAAGTCAAGATCATCTCAAGAGCATTTGTA 2720

CC diseases, and may have cell proliferation or differentiation, cytokine, immunomodulatory, haematopoiesis regulating, tissue growth, inhibin or CC activin, chemotactic or chemokinetic, haemostatic or thrombolytic CC and/or antiinflammatory activities. The present sequence is one of the CC ORF coding sequences of the invention.

XX Sequence 548 BP; 83 A; 152 C; 194 G; 119 T; 0 other;

Query Match 9.7%; Score 270; DB 24; Length 548;

Best Local Similarity 100.0%; Pred. No. 1.4e-119; Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 158 CCAAGGGGAGAGCGCTCTACTGCTGGGACCCCGCGGCGACCTCGATGGGCGCGC 217
 95 CCAGGGGGAGAGCGCTCTACTGCTGGGACCCCGCGGCGACCTCGATGGGCGCGC 154
 OY 218 GTGGCTGAGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 277
 DB 155 GTGGCTGAGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 214
 OY 278 CGCTCTCTTACACGAGTAGACGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 337
 DB 215 CGCTCTCTTACACGAGTAGACGAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 274
 OY 338 ACTACCTGTACACGAGTAGACGAGAGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGG 397
 DB 275 ACTACCTGTACACGAGTAGACGAGAGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGG 334
 OY 398 TTTTCTCTCTGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 427
 DB 335 TTTTCTCTCTGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 364

RESULT 13

ABN35212 standard; DNA: 60 BP.

ABN35212:

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:7960.

Human: mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

MO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001MO-IB01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which

selectively hybridize to mRNAs transcribed from a transcription unit of

a genome, useful for detecting tissue-, pathology-, and

developmental-specific genes

Example 1; SEQ ID 7960; 47pp; English.

The present invention describes oligonucleotide libraries for detecting

messenger RNAs that populate a (sub-)transcriptome, where the

(sub-)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition: to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPRO
 CC at ftp.wipro.int/pub/published_pct_sequences.

Sequence 60 BP; 17 A; 16 C; 14 G; 13 T; 0 other;

Query Match 2.2%; Score 60; DB 24; Length 60;

Best Local Similarity 100.0%; Pred. No. 2.3e-18; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 CACGATCATCTCAGACATTTGTAAGGACAGAGAACTACAGATCCCTCAGCTTGCCTC 2755
 DB 1 CACGATCATCTCAGACATTTGTAAGGACAGAGAACTACAGATCCCTCAGCTTGCCTC 60

RESULT 14

AA26588 standard; DNA: 2169 BP.

AA26588:

16-JUN-1999 (first entry)

Nucleotide sequence of murine KCNQ2 (formerly known as (KvLR1).

KCNQ protein; nervous system-specific potassium channel;

neuronal excitability; neurotransmitter release; KCNQ modulator;

ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;

age-associated memory loss; learning deficiency; motor neuron disease;

epilepsy; stroke; ss.

Mus sp.

Key CDS

1.2169

Location/Qualifiers

/*tag= a

W09907832-A1.

18-FEB-1999.

26-JUN-1998; 98WO-US13276.

12-AUG-1997; 97US-0055599.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Blancat MA, Dworetzky S, Gribkoff VK, Levesque PC;

Little WA, Neubauer MG, Yang W;

WPI; 1999-190047/16.

P-Psdb; AAY01530.

New potassium channels, KCNQ2 and KCNQ3 - may be involved in

neurotransmission and neuroprotection, used to treat, e.g. ataxia

XX Claim 7; Fig 10A-D; 64pp; English.

XX The present sequence encodes murine KCNQ2/Kv1.1. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.

XX Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 other;

Query Match 1.0%; Score 29; DB 20; Length 2169;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGGCTTCATCTACACGC 392

DB 262 CCCCCGGGCTGGGCTTCATCTACACGC 290

Result 15

AAC64379/c

XX AAC64379 standard; DNA; 28 BP.

AC AAC64379;

XX 07-FEB-2001 (first entry)

DE Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:16.

XX Human: KCNQ5; KCNQ6; chromosome 6; voltage-gated potassium channel;

KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;

KW Salla disease; ophthalmological; auditory; central nervous system;

KW cardioactive; anticonvulsant; gastrointestinal; muscular active;

KW age-related macular degeneration; macular degeneration; deafness;

KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;

KW gastrointestinal disorder; PCR primer; ss.

XX Homo sapiens.

OS WO200061606-A1.

XX 19-OCT-2000.

PD 10-APR-2000; 2000WO-US09587.

XX 14-APR-1999; 99US-0129274.

PR (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

PI WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying

PT inhibitors and activators which can treat e.g. Stargardt-like macular

PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -

XX Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCNQ6)

XX protein, which is a voltage-gated potassium channel protein. Human

XX KCNQ5 has ophthalmological, auditory, central nervous system (CNS),

XX cardioactive, anticonvulsant, gastrointestinal and muscular active

XX activities. Sequences and methods from the present invention are useful

XX for identifying activators or inhibitors of KCNQ5 protein. These

XX activators and inhibitors are useful for treating Stargardt-like macular

XX dystrophy, cone-rod dystrophy, Salla disease, age-related macular

XX degeneration, other forms of macular degeneration, deafness, epilepsy,

XX and different forms of neuropsychiatric, heart, gastrointestinal, and

CC muscle disorders. Stargardt-like macular dystrophy and cone-rod

CC dystrophies are located at chromosome 6q. The present sequence represents

CC a PCR primer for human KCNQ5, which is used in an example from the

CC present invention.

XX Sequence 28 BP; 6 A; 4 C; 9 G; 9 T; 0 other;

QY 439 TCTACCATCCTGAGCAGACAAATTTGG 466

DB 28 TCTACCATCCTGAGCAGACAAATTTGG 1

Result 16

AAC64381

XX AAC64381 standard; DNA; 26 BP.

AC AAC64381;

XX 07-FEB-2001 (first entry)

DE Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:18.

XX Human: KCNQ5; KCNQ6; chromosome 6; voltage-gated potassium channel;

KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;

KW Salla disease; ophthalmological; auditory; central nervous system;

KW cardioactive; anticonvulsant; gastrointestinal; muscular active;

KW age-related macular degeneration; macular degeneration; deafness;

KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;

KW gastrointestinal disorder; PCR primer; ss.

XX Homo sapiens.

OS WO200061606-A1.

XX 19-OCT-2000.

PD 10-APR-2000; 2000WO-US09587.

XX 14-APR-1999; 99US-0129274.

PR (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

PI WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying

PT inhibitors and activators which can treat e.g. Stargardt-like macular

PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -

XX Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCNQ6)

XX protein, which is a voltage-gated potassium channel protein. Human

XX KCNQ5 has ophthalmological, auditory, central nervous system (CNS),

XX cardioactive, anticonvulsant, gastrointestinal and muscular active

XX activities. Sequences and methods from the present invention are useful

XX for identifying activators or inhibitors of KCNQ5 protein. These

XX activators and inhibitors are useful for treating Stargardt-like macular

XX dystrophies are located at chromosome 6q. The present sequence represents

XX a PCR primer for human KCNQ5, which is used in an example from the

XX present invention.

XX Sequence 26 BP; 11 A; 0 C; 8 G; 7 T; 0 other;

Db 26 GSTACAGTCCATAGAAATCCAGCTGG 1

RESULT 19

AAS14656

ID AAS14656 standard; cDNA; 26 BP.

AC AAS14656;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human voltage-gated potassium channel hKCNQ5 PCR primer #3.

XX

KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder;

KW stroke; pain; gene therapy; PCR primer.

OS Homo sapiens.

XX

PN WO200170759-A1.

XX

PD 27-SEP-2001.

XX

PF 20-MAR-2001; 2001WO-0509328.

XX

PR 21-MAR-2000; 2000US-190954P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ;

XX

DR WPI: 2001-611467/70.

XX

PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

PT identifying a compound modulating ion flux in eukaryotic cell or cell

PT membrane expressing the protein, comprises KCNQ alpha

PT subunits

PS

XX

PS Claim 6; Page 65; 78pp; English.

XX

CC The invention relates to an isolated polypeptide comprising an

CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid

CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha-subunit. Also

CC included in the scope of the invention are the nucleic acids encoding

CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),

CC expression vectors encoding them, antibodies against them, the use of

CC 3-dimensional computer modelling to identify molecules that bind to a

CC KCNQ containing potassium channel and modulate ion flux through the

CC channel. The KCNQ polypeptide is useful for identifying a compound that

CC increases or decreases ion flux through a potassium channel expressed in

CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy) is useful as

CC a pharmaceutical agent for treating diseases involving abnormal ion flux,

CC such as disorders of the central nervous system, such as epilepsy,

CC migraines, hearing and vision problems, psychotic disorders, seizures,

CC learning and memory disorders, stroke and pain. The antibodies are

CC useful for detecting a KCNQ5 polypeptide in a human tissue and the

CC use of a nucleotide sequence of KCNQ5 to search computer databases to

CC find variants of the sequence which are associated with disease states,

CC is useful for screening mutations of KCNQ5. The present sequence is

CC a PCR primer used to amplify a 1.2kb cDNA clone containing the 3'

CC region of hKCNQ5.

XX

XX

SQ Sequence 26 BP; 13 A; 4 C; 8 G; 1 T; 0 other;

Query Match 0.9%; Score 26; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1725 GAAGAGCCGAGAGAAATATACGACG 1750

Db 1 GAAGAGCCGAGAGAAATATACGACG 26

RESULT 20

AAS14657

ID AAS14657 standard; cDNA; 26 BP.

AC AAS14657;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human voltage-gated potassium channel hKCNQ5 PCR primer #4.

XX

KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder;

KW stroke; pain; gene therapy; PCR primer.

OS Homo sapiens.

XX

PN WO200170759-A1.

XX

PD 27-SEP-2001.

XX

PF 20-MAR-2001; 2001WO-0509328.

XX

PR 21-MAR-2000; 2000US-190954P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ;

XX

DR WPI: 2001-611467/70.

XX

PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

PT identifying a compound modulating ion flux in eukaryotic cell or cell

PT membrane expressing the protein, comprises KCNQ alpha

PT subunits

PS

XX

PS Claim 6; Page 65; 78pp; English.

XX

CC The invention relates to an isolated polypeptide comprising an

CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid

CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha-subunit. Also

CC included in the scope of the invention are the nucleic acids encoding

CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),

CC expression vectors encoding them, antibodies against them, the use of

CC 3-dimensional computer modelling to identify molecules that bind to a

CC KCNQ containing potassium channel and modulate ion flux through the

CC channel. The KCNQ polypeptide is useful for identifying a compound that

CC increases or decreases ion flux through a potassium channel expressed in

CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy) is useful as

CC a pharmaceutical agent for treating diseases involving abnormal ion flux,

CC such as disorders of the central nervous system, such as epilepsy,

CC migraines, hearing and vision problems, psychotic disorders, seizures,

CC learning and memory disorders, stroke and pain. The antibodies are

CC useful for detecting a KCNQ5 polypeptide in a human tissue and the

CC use of a nucleotide sequence of KCNQ5 to search computer databases to

CC find variants of the sequence which are associated with disease states,

CC is useful for screening mutations of KCNQ5. The present sequence is

CC a PCR primer used to amplify a 1.2kb cDNA clone containing the 3'

CC region of hKCNQ5.

XX

XX

SQ Sequence 26 BP; 6 A; 6 C; 7 G; 7 T; 0 other;

Query Match 0.9%; Score 26; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1949 GCCCTGTGATAGCAAGATCTTGC 1974
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 1 GCCCTGTGATAGCAAGATCTTGC 26

RESULT 21
AAT85964
ID AAT85964 standard; cDNA: 1182 BP.
XX
AC AAT85964;

DT 09-JAN-1998 (first entry)

XX Human K+ channel gene coding sequence.

KW Human; neuroblastoma; K+ channel; glioma; probe; diagnosis; detection;
XX tumour; ds.
XX

OS Homo sapiens.

XX JP09191882-A.

XX 29-JUL-1997.

XX 16-JAN-1996; 96JP-0004726.

XX 16-JAN-1996; 96JP-0004726.

XX (NISR) JAPAN TOBACCO INC.

XX WPI: 1997-429182/40.

XX P-PSDB; AAW14282.

XX DNA encoding new human K+ channel protein - useful for detecting
PT glioma(s) and tumours

PS Claim 3; Page 10-12; 14pp; Japanese.

XX This is the nucleotide sequence encoding a novel human K+ channel
XX protein which is expressed on human glioma cells. The gene was isolated
XX from a 3' directed cDNA library prepared from human neuroblastoma cell
XX line CHP134. The screen isolated a clone designated GS008740 whose
XX insert contained the coding sequence (presented here) and the 5' and 3'
XX sequences of the gene (AAT85965-6 respectively). Expression of the gene
XX was detected in neuroblastoma cell lines. Oligonucleotides derived from
XX the sequence of the K+ channel gene can be used as probes for diagnosing
XX human gliomas, and in the detection of new tumours.

XX Sequence 1182 BP; 201 A; 372 C; 364 G; 245 T; 0 other;

Query Match 0.9%; Score 26; DB 18; Length 1182;

Best Local Similarity 100.0%; Pred. No. 0.058; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTCATCTACACGC 392
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 265 CGCGGCTGGCGCTCATCTACACGC 290

RESULT 22
ABK64418
ID ABK64418 standard; DNA: 1425 BP.
XX
AC ABK64418;

DT 18-JUN-2002 (first entry)

XX Human benign prostatic hyperplasia gene #313.

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX

OS Homo sapiens.

XX WO200212440-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US24708.

XX 07-AUG-2000; 2000US-223323P.

XX 05-JUN-2001; 2001US-0873319.

XX (GENE-) GENE LOGIC INC.
XX (NISR) JAPAN TOBACCO INC.

XX Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;

XX WPI: 2002-257476/30.

XX Identifying drugs for and diagnosing benign prostatic hyperplasia, by
XX detecting expression levels of one or more genes in prostate cells from
XX patient that are differentially regulated compared to normal prostate
XX cells -

XX Disclosure; Page 188; 444pp; English.

XX The invention relates to a method of diagnosing (I) the onset or
XX progression of benign prostatic hyperplasia (BPH), or screening (II) for
XX or identifying an agent that modulates the onset or progression of BPH.
XX The method is based on changes in gene expression in BPH tissue isolated
XX from patients exhibiting different clinical states of prostate
XX hyperplasia as compared to normal prostate tissue. (I) comprises
XX detecting the expression levels of one or more genes in prostate cells
XX from the subject that are differentially regulated compared to normal
XX prostate cells. (II) comprises preparing a first gene expression profile
XX of BPH cells or BPH-like cell population, exposing the cells to the
XX agent, preparing a second gene expression profile of the agent exposed
XX cells, and comparing the first and second gene expression profiles.
XX (I) is useful for diagnosing the onset or progression of BPH. (II) is
XX useful for identifying an agent that modulates the onset or progression
XX of BPH. The methods are useful to present information identifying
XX the expression level in a tissue or cells, by comparing the expression
XX level of genes given in the specification in the tissue or cells to the
XX level of expression of gene in the database, and displaying the
XX expression levels of at least one gene in the tissue or cell sample
XX compared to the expression level in BPH. Agents using (II) are useful for
XX treating BPH or prostate cancer. ABK64106-ABK64860 represent human
XX benign prostatic hyperplasia gene sequences of the invention.

XX Sequence 1425 BP; 231 A; 462 C; 439 G; 293 T; 0 other;

Query Match 0.9%; Score 26; DB 24; Length 1425;

Best Local Similarity 100.0%; Pred. No. 0.058; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTCATCTACACGC 392
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 442 CGCGGCTGGCGCTCATCTACACGC 467

RESULT 23
AAK81548
ID AAK81548 standard; DNA: 2565 BP.
XX
AC AAK81548;

DT 25-AUG-1999 (first entry)

XX Human brain-derived potassium channel DNA structural DNA.

KW Human; brain-derived potassium channel; neurophysiology;
KW cognitive disorder; behavioural disorder; psychiatric disorder;
KW neurodegenerative disorder; developmental disorder; mental retardation;
KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
XX

KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 OS Homo sapiens.
 PN MO9931232-A1.
 XX
 XX
 PD 24-JUN-1999.
 XX
 XX
 PF 11-DEC-1998; 98WO-GH03720.
 XX
 XX
 PR 13-DEC-1997; 97GB-0026339.
 XX
 XX
 PA (ZENE) ZENECA LTD.
 XX
 XX
 PI Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 XX
 XX
 DR WPI; 1999-395178/33.
 XX
 XX
 PT New isolated potassium channel polypeptide
 PS Claim 2; Fig 2; 151pp; English.
 XX
 XX
 CC The present sequence represents brain-derived potassium channel DNA.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 SO Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other;
 QY
 QY 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
 Db 265 CGCGGCTGGCGCTTCATCTACCAAGC 290
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 0.9%; Score 26; DB 20; Length 2565;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 RESULT 24
 AAX81547
 ID AAX81547 standard; cDNA; 3029 BP.
 XX
 XX
 AC AAX81547;
 DT 25-AUG-1999 (first entry)
 XX
 XX
 DE Human brain-derived potassium channel cDNA.
 XX
 XX
 KW Human; brain-derived potassium channel; neurophysiology;

KW cognitive disorder; behavioural disorder; psychiatric disorder;
 KW neurodegenerative disorder; developmental disorder; mental retardation;
 KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
 KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 OS Homo sapiens.
 PN MO9931232-A1.
 XX
 XX
 PD 24-JUN-1999.
 XX
 XX
 PF 11-DEC-1998; 98WO-GH03720.
 XX
 XX
 PR 13-DEC-1997; 97GB-0026339.
 XX
 XX
 PA (ZENE) ZENECA LTD.
 XX
 XX
 PI Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 XX
 XX
 DR WPI; 1999-395178/33.
 XX
 XX
 DR P-PSDB; AAY23215.
 XX
 XX
 PT New isolated potassium channel polypeptide
 PS Example 1; Fig 1; 151pp; English.
 XX
 XX
 CC The present sequence encodes a human brain-derived potassium channel.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 SO Sequence 3029 BP; 546 A; 972 C; 1004 G; 507 T; 0 other;
 QY
 QY 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
 Db 275 CGCGGCTGGCGCTTCATCTACCAAGC 300
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 0.9%; Score 26; DB 20; Length 3029;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 RESULT 25
 AAS74831
 ID AAS74831 standard; cDNA; 3195 BP.
 XX
 XX
 AC AAS74831;
 DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #10635.
 XX XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PE
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR P-PSDB; ABG10644.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 10635; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3195 BP; 559 A; 1048 C; 1068 G; 520 T; 0 other;
 XX
 XX Query Match 0.9%; Score 26; DB 23; Length 3195;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 367 CGCGGCTGGCGCTTCATCTACACGCG 392
 Db 440 CGCGGCTGGCGCTTCATCTACACGCG 465
 XX
 XX RESULT 26
 XX ID AAS7057 standard; DNA; 3232 BP.
 XX AC AAS7057;
 XX XX
 XX 22-JUL-1999 (first entry)
 XX DE Human KCNQ2 cDNA.

XX KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
 KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 128..2746
 FT /*tag= a
 FT /product= "KCNQ2"
 XX
 PN MO9921875-A1.
 PD 06-MAY-1999.
 XX
 XX 23-OCT-1998; 98WO-US22375.
 PF
 XX 24-OCT-1997; 97US-0063147.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 XX Charlier C, Leppert MF, Singh NA;
 PI WPI; 1999-312938/26.
 DR P-PSDB; AAY08341.
 XX
 XX Nucleic acid encoding potassium channels KCNQ2 and 3
 PT
 XX
 PS Claim 1; Page 117-122; 195pp; English.
 XX
 CC This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 XX
 SQ Sequence 3232 BP; 577 A; 1054 C; 1061 G; 533 T; 7 other;
 XX
 XX Query Match 0.9%; Score 26; DB 20; Length 3232;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 367 CGCGGCTGGCGCTTCATCTACACGCG 392
 Db 392 CGCGGCTGGCGCTTCATCTACACGCG 417
 XX
 XX RESULT 27
 XX ID AAS74830 standard; cDNA; 3232 BP.
 XX AC AAS74830;
 XX XX
 XX 13-FEB-2002 (first entry)
 XX DE DNA encoding novel human diagnostic protein #10634.
 XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001: 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Dmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR P-PSDB; ABG10643.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 1: SEQ ID NO 10634; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3232 BP; 576 A; 1054 C; 1061 G; 533 T; 8 other;
 XX
 XX Query Match 0.9%; Score 26; DB 23; Length 3232;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 367 CGCGGCTGGGCGTTTCATTCACACGC 392
 DB 392 CGCGGCTGGGCGTTTCATTCACACGC 417

RESULT 28
 AAX57145
 ID AAX57145 standard; DNA: 3237 BP.
 XX AC AAX57145;
 XX DT 22-JUL-1999 (first entry)
 XX DE Human mutant KCNQ2 cDNA.
 XX KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BPNE; juvenile myoclonic epilepsy;
 KW JME; Rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; ss.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key
 XX FT CDS Location/Qualifiers
 FT CDS 128..2920
 FT /tag= a
 FT /product= "KCNQ2"
 XX
 XX PN WO9921875-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98WO-US22375.
 XX PR 24-OCT-1997; 97US-0063147.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Charlier C, Leppert MF, Singh NA;
 XX DR WPI: 1999-312938/26.
 XX DR P-PSDB; AAY08347.
 XX PT Nucleic acid encoding potassium channels KCNQ2 and 3
 PS Claim 1: Page 168-172; 195pp; English.

XX CC This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BPNE), juvenile myoclonic
 CC epilepsy (JME) or Rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.

XX SQ Sequence 3237 BP; 577 A; 1056 C; 1064 G; 533 T; 7 other;
 XX
 XX Query Match 0.9%; Score 26; DB 20; Length 3237;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 367 CGCGGCTGGGCGTTTCATTCACACGC 392
 DB 392 CGCGGCTGGGCGTTTCATTCACACGC 417

RESULT 29
 AAX26587
 ID AAX26587 standard; DNA: 3287 BP.
 XX AC AAX26587;
 XX DT 16-JUN-1999 (first entry)
 XX DE Nucleotide sequence of human KCNQ2 (formerly known as KVLRL1).
 XX KW Human; KCNQ protein; nervous system-specific potassium channel;
 KW neuronal excitability; neurotransmitter release; KCNQ modulator;
 KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KW age-associated memory loss; learning deficiency; motor neuron disease;
 KW epilepsy; stroke; ss.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 61..2676
 FT /*tag= a
 XX
 XX MO9907832-A1.
 XX
 XX 18-FEB-1999.
 XX
 XX
 XX 26-JUN-1998; 98MO-US13276.
 XX
 XX 12-AUG-1997; 97US-0055599.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Blauar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 XX Little WA, Neubauer MG, Yang W;
 XX WPI; 1999-190047/16.
 XX P-PSDB; AAY01529.
 XX
 XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
 XX
 XX Claim 5; Fig 2; 64pp; English.
 XX
 XX The present sequence encodes human KCNQ2/KvLRI. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.
 XX
 XX Sequence 3287 BP; 587 A; 1062 C; 1083 G; 555 T; 0 other.
 SO
 Query Match 0.9%; Score 26; DB 20; Length 3287;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
 DB 325 CGCGGCTGGGCGTTCATCTACACGC 350
 XX
 XX RESULT 30
 XX AAS74832
 XX ID AAS74832 standard; CDNA; 7413 BP.
 XX
 XX AAS74832;
 XX
 XX 13-FEB-2002 (first entry)
 XX
 XX DNA encoding novel human diagnostic protein #10636.
 DE
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW
 OS Homo sapiens.
 XX
 XX MO200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001MO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG10645.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 XX Claim 1; SEQ ID No 10636; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPRO
 CC at ftp.wipro.int/pub/published_pct_sequences.
 XX
 XX Sequence 7413 BP; 1354 A; 2331 C; 2353 G; 1368 T; 7 other;
 SO
 Query Match 0.9%; Score 26; DB 23; Length 7413;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
 DB 311 CGCGGCTGGGCGTTCATCTACACGC 336
 XX
 XX RESULT 31
 XX AAC64374
 XX ID AAC64374 standard; DNA; 25 BP.
 XX
 XX AAC64374;
 XX
 XX 07-FEB-2001 (first entry)
 XX
 XX Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:11.
 DE
 KW Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardiocactive; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; PCR primer; ss.
 KW
 OS Homo sapiens.
 XX
 XX MO200061606-A1.
 XX
 XX 19-OCT-2000.
 XX
 XX 10-APR-2000; 2000MO-US09587.
 XX
 XX 14-APR-1999; 99US-0129274.
 XX

PA (MERL) MERCK & CO INC.
 XX
 PI Petrukhin K, Caskey CT, Li W, Metzker ML;
 XX
 DR WPI: 2000-647417/62.
 XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Example 1; Page 32; 99pp; English.
 XX
 CC The present invention describes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardiovascular, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q. The present sequence represents
 CC a PCR primer for human KCNQ5, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 0 A; 5 C; 5 G; 15 T; 0 other;
 XX
 Query Match 0.9%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 399 TTTTCTCTGCTGCTTGTGCTGCTG 423
 Db 1 TTTTCTCTGCTGCTTGTGCTGCTG 25
 XX
 RESULT 32
 AAS14658/C
 ID AAS14658 standard; cDNA: 25 BP.
 XX
 AC AAS14658;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human voltage-gated potassium channel hKCNQ5 PCR primer #5.
 XX
 DE Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI: 2001-611467/70.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha

PT subunits -
 XX
 PS Claim 6; Page 65; 78pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a PCR primer used to amplify a 650bp cDNA clone containing the 5'
 CC region of hKCNQ5.
 XX
 SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 other;
 XX
 Query Match 0.9%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 765 GGGTTACAGTGTATGCTCAGC 789
 Db 25 GGGTTACAGTGTATGCTCAGC 1
 XX
 RESULT 33
 AAS14659/C
 ID AAS14659 standard; cDNA: 25 BP.
 XX
 AC AAS14659;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human voltage-gated potassium channel hKCNQ5 PCR primer #6.
 XX
 DE Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI: 2001-611467/70.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

Identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ alpha subunits

Claim 6; Page 65; 78pp; English.

The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a PCR primer used to amplify a 650bp cDNA clone containing the 5' region of hKCNQ5.

Sequence 25 BP; 5 A; 8 C; 8 G; 4 T; 0 other;

Query Match 0.9%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

712 CAGATCCCGCCGATGTCGCGCATGG 736
|||||
25 CAGATCCCGCCGATGTCGCGCATGG 1

RESULT 34

AAC64384
ID AAC64384 standard; DNA; 24 BP.

AC AAC64384;

07-FEB-2001 (first entry)

Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:21.

Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
Stargardt-like macular dystrophy; cone-rod macular dystrophy;
Salla disease; ophthalmological; auditory; central nervous system;
cardioactive; anticonvulsant; gastrointestinal; muscular active;
age-related macular degeneration; macular degeneration; deafness;
epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
gastrointestinal disorder; PCR primer; ss.

Homo sapiens.

MO200061606-A1.

19-OCT-2000.

10-APR-2000; 2000MO-US09587.

14-APR-1999; 99US-0129274.

(MERI) MERCK & CO INC.

Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
XX
PS Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCN6q)
CC protein, which is a voltage-gated potassium channel protein. Human
CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
CC cardioactive, anticonvulsant, gastrointestinal and muscular active
CC activities. Sequences and methods from the present invention are useful
CC for identifying activators or inhibitors of KCNQ5 protein. These
CC activators and inhibitors are useful for treating Stargardt-like macular
CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
CC degeneration, other forms of macular degeneration, deafness, epilepsy,
CC and different forms of neuropsychiatric heart, gastrointestinal, and
CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
CC dystrophies are located at chromosome 6q. The present sequence represents
CC a PCR primer for human KCNQ5, which is used in an example from the
XX present invention.

Sequence 24 BP; 9 A; 2 C; 4 G; 9 T; 0 other;

Query Match 0.9%; Score 24; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1549 AGAATTATGAATTTGATGTTGCA 1572
|||||
DB 1 AGAATTATGAATTTGATGTTGCA 24

Search completed: June 19, 2003, 13:42:23
Job time : 602 secs

|||||
Db 541 TCTCGGGTTCCTGTTGCGATATAGAGATGCGAAGAACTGAGCTTGCTCGAAG 600
QY 601 CCCTTCGTGTATATAGATACATGTTGTTCTTATCGCTTCAATACAGTTGTTTCGCAAA 660
Db 601 CCCTTCGTGTATATAGATACATGTTGTTCTTATCGCTTCAATACAGTTGTTTCGCAAA 660
QY 661 ACTCAGGGAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGTTTCTTACAGATCTC 720
Db 661 ACTCAGGGAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGTTTCTTACAGATCTC 720
QY 721 CGCATGTGGCGATGAGACCGAAGGGGAGGCACTTGGAAATTTACTGGGTTCACTGTTAT 780
Db 721 CGCATGTGGCGATGAGACCGAAGGGGAGGCACTTGGAAATTTACTGGGTTCACTGTTAT 780
QY 781 GCTCAGACGAAGAAATATATCAGACTTGTACATAGATTTTGGTCTTATTTTTCG 840
Db 781 GCTCAGACGAAGAAATATATCAGACTTGTACATAGATTTTGGTCTTATTTTTCG 840
QY 841 TCTTTCTGTCTATCTGTGAGAAAAGATGCCAATTAAGAGTTTCTACATATGAGAT 900
Db 841 TCTTTCTGTCTATCTGTGAGAAAAGATGCCAATTAAGAGTTTCTACATATGAGAT 900
QY 901 GCTCTCTGTGTGGGACAAATTCATTTGATGACACTATTTGCTATGAGACAAACTCCCTA 960
Db 901 GCTCTCTGTGTGGGACAAATTCATTTGATGACACTATTTGCTATGAGACAAACTCCCTA 960
QY 961 ACTTGGCTGGAAATTTCTTCTGACAGCTTGTGACCTTGGCACTTCTTCTTTCGA 1020
Db 961 ACTTGGCTGGAAATTTCTTCTGACAGCTTGTGACCTTGGCACTTCTTCTTTCGA 1020
QY 1021 CTTCCTCCCGGCAATTTCTTGTGCTCAGGTTTGGCATTAAGATTAAGAACACCGGCGAG 1080
Db 1021 CTTCCTCCCGGCAATTTCTTGTGCTCAGGTTTGGCATTAAGATTAAGAACACCGGCGAG 1080
QY 1081 AAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTTATCAGTGTGTTGGCTAGT 1140
Db 1081 AAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTTATCAGTGTGTTGGCTAGT 1140
QY 1141 TACGCACTGATGAGAAATCTGTTTCCATTGTGCACTGGAAGCCACACTTGAAGGCTTG 1200
Db 1141 TACGCACTGATGAGAAATCTGTTTCCATTGTGCACTGGAAGCCACACTTGAAGGCTTG 1200
QY 1201 CACACCTGCAAGCCTTACCATCAGAACTAGTTTAAAGAGCAGTGGCATGCTTAC 1260
Db 1201 CACACCTGCAAGCCTTACCATCAGAACTAGTTTAAAGAGCAGTGGCATGCTTAC 1260
QY 1261 CCCAGGGGCCAGATTTAAGAGCCGACAGAGCTAGTAGTGACAGAGGTCGCCAAGC 1320
Db 1261 CCCAGGGGCCAGATTTAAGAGCCGACAGAGCTAGTAGTGACAGAGGTCGCCAAGC 1320
QY 1321 ACCGACATCAGAGCGAGGAGGATCCACAAAGTGCAAGAGAGTGAGGCTTCAACGAG 1380
Db 1321 ACCGACATCAGAGCGAGGAGGATCCACAAAGTGCAAGAGAGTGAGGCTTCAACGAG 1380
QY 1381 CGAAGCCGCTTCCGGCCCTGCTGCTGCTCAAAAGTTCTCAGCCAAAACCACTGATAGAT 1440
Db 1381 CGAAGCCGCTTCCGGCCCTGCTGCTGCTCAAAAGTTCTCAGCCAAAACCACTGATAGAT 1440
QY 1441 GCTGACACAGCCCTTGGCAGTATGATGATGAAAAAGATGCGCAGTGTGATG 1500
Db 1441 GCTGACACAGCCCTTGGCAGTATGATGATGAAAAAGATGCGCAGTGTGATG 1500
QY 1501 TCACTGGAAGACCTTACCCACACTTAAACTGTCATTTGAGTATGAGATTTTATGAAA 1560
Db 1501 TCACTGGAAGACCTTACCCACACTTAAACTGTCATTTGAGTATGAGATTTTATGAAA 1560
QY 1561 TTTTCACTGGAAGACCTTAAAGAAATTTAGGAAATTTAGTCCATGATGATGAAAAGATGTC 1620
Db 1561 TTTTCACTGGAAGACCTTAAAGAAATTTAGGAAATTTAGTCCATGATGATGAAAAGATGTC 1620
QY 1621 ATTGAACAATATTTCTGCTGATCTGACATGTTGTAGAAATTAAGCCCTTCAACA 1680
Db 1621 ATTGAACAATATTTCTGCTGATCTGACATGTTGTAGAAATTAAGCCCTTCAACA 1680

Db 1621 ATTGAACAATATTTCTGCTGATCTGACATGTTGTAGAAATTAAGCCCTTCAACA 1680
QY 1681 CGTGTGATCAATTTCTGGAAAAGGCAATACATCAGATTAAGAGCCGAGAGAA 1740
Db 1681 CGTGTGATCAATTTCTGGAAAAGGCAATACATCAGATTAAGAGCCGAGAGAA 1740
QY 1741 ATACAGCAAGACATGAGACACAGAGATCTCAGTATGCTGCGGTGGTCAAGGTT 1800
Db 1741 ATACAGCAAGACATGAGACACAGAGATCTCAGTATGCTGCGGTGGTCAAGGTT 1800
QY 1801 GAAAAACAGATACAGTCCATAGATCCAACTGAGTCCCTACTAGACATCTATCAACAG 1860
Db 1801 GAAAAACAGATACAGTCCATAGATCCAACTGAGTCCCTACTAGACATCTATCAACAG 1860
QY 1861 GTCCTTGGAAAGGCTGCTCAGAGCCCTGCTTGGCTTATTCATTCAGATCCACCTTT 1920
Db 1861 GTCCTTGGAAAGGCTGCTCAGAGCCCTGCTTGGCTTATTCATTCAGATCCACCTTT 1920
QY 1921 GAATGTGAACAGACATCTGATATCAAAAGCCCTGTGATAGCAAGATCTTTCGGTTCC 1980
Db 1921 GAATGTGAACAGACATCTGATATCAAAAGCCCTGTGATAGCAAGATCTTTCGGTTCC 1980
QY 1981 GCACAAACAGTGGCTGCTTATTCAGATCAATAGTCCAAACATCTGAGAGGCTGAG 2040
Db 1981 GCACAAACAGTGGCTGCTTATTCAGATCAATAGTCCAAACATCTGAGAGGCTGAG 2040
QY 2041 TTTATTTGAGGCGCAATAGTTTCACTGAGTCCCACTTTCAGGCGTTAGCCCTATAG 2100
Db 2041 TTTATTTGAGGCGCAATAGTTTCACTGAGTCCCACTTTCAGGCGTTAGCCCTATAG 2100
QY 2101 CACAGTCAAGCAACAGAGTGGCCAAATTTAGCAAAAGGATGGCTCAGCAGTGGGCAACC 2160
Db 2101 CACAGTCAAGCAACAGAGTGGCCAAATTTAGCAAAAGGATGGCTCAGCAGTGGGCAACC 2160
QY 2161 AACACATTTGCAAAACCAATTAATATGCGGACCCAGCAGCAGCCCAACACTTTACAG 2220
Db 2161 AACACATTTGCAAAACCAATTAATATGCGGACCCAGCAGCAGCCCAACACTTTACAG 2220
QY 2221 ATCCGACCTCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAAATCTGACCTTAC 2280
Db 2221 ATCCGACCTCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAAATCTGACCTTAC 2280
QY 2281 CCTGCAAGCTTACAGAAAAGCAATTTCTGACGTCACCACTGCTTGTGCTCCAAAGAA 2340
Db 2281 CCTGCAAGCTTACAGAAAAGCAATTTCTGACGTCACCACTGCTTGTGCTCCAAAGAA 2340
QY 2341 AATGTTCAAGTTGCAAGTCAATCTACCAAGAGGCTTCTATGAGAAAAGCTTGCAC 2400
Db 2341 AATGTTCAAGTTGCAAGTCAATCTACCAAGAGGCTTCTATGAGAAAAGCTTGCAC 2400
QY 2401 ATGGAGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2401 ATGGAGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2461 TTTGCTGTGCAAAACCTGATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
Db 2461 TTTGCTGTGCAAAACCTGATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
QY 2521 GAGTCAAGTGGCTCCAGAGGCGCAAGTTTACCACAAATGAGGGAATCCAAATTTG 2580
Db 2521 GAGTCAAGTGGCTCCAGAGGCGCAAGTTTACCACAAATGAGGGAATCCAAATTTG 2580
QY 2581 TTTATTAAGTGAAGAGGTGGTCCGAAAGAGACAGACAGACACTTTTGAATGCGCGA 2640
Db 2581 TTTATTAAGTGAAGAGGTGGTCCGAAAGAGACAGACAGACACTTTTGAATGCGCGA 2640
QY 2641 CCGCAGCTGCCAGGGAAGCTGCTTGTGATCAGACTCTCTAAGACTGGAAGTCAAGA 2700
Db 2641 CCGCAGCTGCCAGGGAAGCTGCTTGTGATCAGACTCTCTAAGACTGGAAGTCAAGA 2700
QY 2701 TCACTCTGAGACATTTTGAAGCAGAGAAATTAACAGATGSCCTCAGCTTGCATGTC 2760
Db 2701 TCACTCTGAGACATTTTGAAGCAGAGAAATTAACAGATGSCCTCAGCTTGCATGTC 2760

QY 2761 AACTGAATAA 2772
Db 2761 AACTGAATAA 2772

RESULT 2

US-09-825-147-3
Sequence 3, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael C.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
FILE REFERENCE: LEX-0160-USA
CURRENT APPLICATION NUMBER: US/09/825,147
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,255
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
US-09-825-147-3

Query Match 100.0%; Score 2772; DB 10; Length 3111;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGACACACGCGGAGAGAGAGAGGCGCGCGCGCTGTGGTGAAGAGC 60
Db 60 ATGCCCCGACACACGCGGAGAGAGAGAGGCGCGCGCGCTGTGGTGAAGAGC 119
QY 61 GGGCGACGCGGCGGCGGCGGCGGCGGCGCTGTGGTGAAGAGTGTGGAG 120
Db 120 GGGCGACGCGGCGGCGGCGGCGGCGGCGCTGTGGTGAAGAGTGTGGAG 179
QY 121 TCGGCGCGGCGACGCTGTGCTGTAACCTCGGACGCGCGAGGGGCGACGCGCTACTG 180
Db 180 TCGGCGCGGCGACGCTGTGCTGTAACCTCGGACGCGCGAGGGGCGACGCGCTACTG 239
QY 181 CTGGGCGACCGCGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAGAGCGCGG 240
Db 240 CTGGGCGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAGAGCGCGG 299
QY 241 GGGAGAGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAGAGCGCGG 300
Db 300 GGGAGAGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAGAGCGCGG 359
QY 301 AGCTGCGCGGCGACGCTCAAGTACCGGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAG 360
Db 360 AGCTGCGCGGCGACGCTCAAGTACCGGCGGCGGCGGCGGCGGCGGCGGCTGTGGTGAAGAG 419
QY 361 AGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 420 AGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479
QY 421 TTGATTTTGTGAGGTTTGTACACCTGCTGAGCGACACAAATGGCCCTCAAGTGTGCTC 480
Db 480 TTGATTTTGTGAGGTTTGTACACCTGCTGAGCGACACAAATGGCCCTCAAGTGTGCTC 539
QY 481 TTGATCTGAGAGTGTGATGATGATGCTGCTTTGGTTGGATTCATTCATTCGAATCTGG 540
Db 540 TTGATCTGAGAGTGTGATGATGATGCTGCTTTGGTTGGATTCATTCATTCGAATCTGG 599

QY 541 TCTGCGGTTGCTGTGTGATATAGAGATGCGAAGAGAGAGTGTGCTGGAAG 600
Db 600 TCTGCGGTTGCTGTGTGATATAGAGATGCGAAGAGAGAGTGTGCTGGAAG 659
QY 601 CCCCTGTGTATATAGATACATTTCTTATGCGCTTCAATAGCATGTTTCTGCAAA 660
Db 660 CCCCTGTGTATATAGATACATTTCTTATGCGCTTCAATAGCATGTTTCTGCAAA 719
QY 661 ACTGAGGTAATATTTTGGCAGCTGTGCACTGAGAGTCTCCGTTTCTTACAGATCTTC 720
Db 720 ACTGAGGTAATATTTTGGCAGCTGTGCACTGAGAGTCTCCGTTTCTTACAGATCTTC 779
QY 721 CGCATGTGCGCATGAGACCGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 780 CGCATGTGCGCATGAGACCGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 839
QY 781 GCTACAGCAAGGAATTAATACAGCTTGTGATAGAGATTTTGGTTCTTATTTTTCG 840
Db 840 GCTACAGCAAGGAATTAATACAGCTTGTGATAGAGATTTTGGTTCTTATTTTTCG 899
QY 841 TCTTCTGTGTCTATCTGTGTGGAAGAGATGCCAATAAGATTTTCTTACATATGAGAT 900
Db 900 TCTTCTGTGTCTATCTGTGTGGAAGAGATGCCAATAAGATTTTCTTACATATGAGAT 959
QY 901 GCTCTGTGCGGCGCAATTAATACATTAATGCACTTGTGCTGTGAGACAAACCTCCCTA 960
Db 960 GCTCTGTGCGGCGCAATTAATACATTAATGCACTTGTGCTGTGAGACAAACCTCCCTA 1019
QY 961 ACTTGTGCGGGAAGATTTGCTTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 1020
Db 1020 ACTTGTGCGGGAAGATTTGCTTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 1079
QY 1021 CTTCCTGCGGCGGCTTGTGCTGAGGCTTGTGATTAAGATGCAAGAACACCGCGCAG 1080
Db 1080 CTTCCTGCGGCGGCTTGTGCTGAGGCTTGTGATTAAGATGCAAGAACACCGCGCAG 1139
QY 1081 AACAATTTGAGAAAG 1140
Db 1140 AACAATTTGAGAAAG 1199
QY 1141 TAGGAGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCCACACTTGAAGGCTTG 1200
Db 1200 TAGGAGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCCACACTTGAAGGCTTG 1259
QY 1201 CACACCTGAGGCGCTCAATCAATGAGAGCTAAGTTTAAAGAGCGAGGCGGAGTGGCTAGC 1260
Db 1260 CACACCTGAGGCGCTCAATCAATGAGAGCTAAGTTTAAAGAGCGAGGCGGAGTGGCTAGC 1319
QY 1261 CCCAGGCGCAGAGATTAATTAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1320 CCCAGGCGCAGAGATTAATTAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
QY 1321 ACCGACATACAGCGGAGGAG 1380
Db 1380 ACCGACATACAGCGGAGGAG 1439
QY 1381 CGAACCGGCTGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440
Db 1440 CGAACCGGCTGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1499
QY 1441 GCTGACAGAGCCCTTGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1500 GCTGACAGAGCCCTTGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1559
QY 1501 TCAGTGAAGAGAGCTACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1560 TCAGTGAAGAGAGCTACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619
QY 1561 TTTCAATGTTGCAAAAGGAGGTTTAAAGAAACCTTACGATATGATGATGATGATGAT 1620
Db 1620 TTTCAATGTTGCAAAAGGAGGTTTAAAGAAACCTTACGATATGATGATGATGATGAT 1679
QY 1621 ATTGAACAATATTTGCTGTGCTATGACATGTTGTGATGAAATTAAGAGCTTCAACA 1680

```

Db      1680 ATTGACAAATATTCTGCTGTCATCTGGACATGTTGTAGATAAAGCCCTTCAACA 1739
QY      1681 CGTGTGATCAAAATTTCTGGAAAAGGCAATTCACATAGATAGACAGCCGAGAGAA 1740
Db      1740 CGTGTGATCAAAATTTCTGGAAAAGGCAATTCACATAGATAGACAGCCGAGAGAA 1799
QY      1741 ATPACAGCAGACATGAGACACAGACGATCTCAGTATGTCGGGTGGTTCAGAGTT 1800
Db      1800 ATPACAGCAGACATGAGACACAGACGATCTCAGTATGTCGGGTGGTTCAGAGTT 1859
QY      1801 GAAAAACAGGTACAGTCCATAGATCAAGCTGAGCTGCTTACTATGACATCTATCAACAG 1860
Db      1860 GAAAAACAGGTACAGTCCATAGATCAAGCTGAGCTGCTTACTATGACATCTATCAACAG 1919
QY      1861 GTCTCTGGAAAAGGCTTGGCTGAGCCCTGCTTGGCTTCAATTCAGATCCGACTTTT 1920
Db      1920 GTCTCTGGAAAAGGCTTGGCTGAGCCCTGCTTGGCTTCAATTCAGATCCGACTTTT 1979
QY      1921 GAATGTGACAGACATCTGACTATCAAGCCCTGAGTACAGAGATCTTTCGGGTTC 1980
Db      1980 GAATGTGACAGACATCTGACTATCAAGCCCTGAGTACAGAGATCTTTCGGGTTC 2039
QY      1981 GCACAAAACAGTGGCTCTTATCCAGATCAACTAGTCCACATCTCGAGAGGCTTCAG 2040
Db      2040 GCACAAAACAGTGGCTCTTATCCAGATCAACTAGTCCACATCTCGAGAGGCTTCAG 2099
QY      2041 TTGATTTGAGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Db      2100 TTGATTTGAGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2159
QY      2101 CACAGTCAACACACAGTGCCTTATGATCAAGCGATGATGATGATGATGATGATGATG 2160
Db      2160 CACAGTCAACACACAGTGCCTTATGATCAAGCGATGATGATGATGATGATGATGATG 2219
QY      2161 AACACATTGCAACCAATTAATACGCGACCCCAAGCAGCCCAACCAATTTACAG 2220
Db      2220 AACACATTGCAACCAATTAATACGCGACCCCAAGCAGCCCAACCAATTTACAG 2279
QY      2221 ATCCCACTCTCTCCAGACCATCAAGCATCTGCCAGGCGCAAAATCTGACCCCTAC 2280
Db      2280 ATCCCACTCTCTCCAGACCATCAAGCATCTGCCAGGCGCAAAATCTGACCCCTAC 2339
QY      2281 CCTGACAGCTTACAGAAAGCATTTCTGACGTCACACCTGCTTGTTCCTTCAAGAA 2340
Db      2340 CCTGACAGCTTACAGAAAGCATTTCTGACGTCACACCTGCTTGTTCCTTCAAGAA 2399
QY      2341 AATGTTAGCTTGCACAGTCAATCTCACCAAGACCGTTCTATGAGAAAAGCTTTGAC 2400
Db      2400 AATGTTAGCTTGCACAGTCAATCTCACCAAGACCGTTCTATGAGAAAAGCTTTGAC 2459
QY      2401 ATGGGAGAGAAATCTGTTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2460
Db      2460 ATGGGAGAGAAATCTGTTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2519
QY      2461 TTGCTGTGCAAAAACCTGATCAGTGCAGCCGAGAACTGAATATACAACTTTCAGGAGT 2520
Db      2520 TTGCTGTGCAAAAACCTGATCAGTGCAGCCGAGAACTGAATATACAACTTTCAGGAGT 2579
QY      2521 GAGTCAAGTGGCTTCAAGAGCAGCAAGATTTTACCCCAATGAGGGAATTCAAATTTG 2580
Db      2580 GAGTCAAGTGGCTTCAAGAGCAGCAAGATTTTACCCCAATGAGGGAATTCAAATTTG 2639
QY      2581 TTTTAACTGATGAAGAGTGGGTCGCAAGAGACAGACAGACCTTTTGTGCGCA 2640
Db      2640 TTTTAACTGATGAAGAGTGGGTCGCAAGAGACAGACAGACCTTTTGTGCGCA 2699
QY      2641 CCGCAGCTGCGCAGAGAGTGCCTTTGATCAGATCAGATCTCTAAGAGCTGGAAGGTCAG 2700
Db      2700 CCGCAGCTGCGCAGAGAGTGCCTTTGATCAGATCAGATCTCTAAGAGCTGGAAGGTCAG 2759
QY      2701 TCATCTGAGACATTTTGAAGGAGAGAAAGTACAGATGCCCTGAGCTTGGCTCATGTC 2760

```

```

Db      2760 TCATCTGAGACATTTTGAAGGAGAGAAAGTACAGATGCCCTGAGCTTGCCTCATGTC 2819
QY      2761 AAACGAAATAA 2772
Db      2820 AAACGAAATAA 2831

RESULT 3
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentl Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match          90.7%: Score 2514; DB 10; Length 2667;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      106 ATGAAGATGTGAGATCGGGCGGGGCAAGGATGCTGTAATTCGCGAGCGCGAGGGC 165
Db      1 ATGAAGATGTGAGATCGGGCGGGGCAAGGATGCTGTAATTCGCGAGCGCGAGGGC 60
QY      166 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCGACGCTGCTGCTGCTGCTGCTGCTGCTG 225
Db      61 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCGACGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY      226 AGGGAGAGCGCGGGGCAAGAGAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCT 285
Db      121 AGGGAGAGCGCGGGGCAAGAGAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCT 180
QY      286 TACACGATGACAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGACAGAACTACCTG 345
Db      181 TACACGATGACAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGACAGAACTACCTG 240
QY      346 TACACGATGACAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGACAGAACTACCTG 405
Db      241 TACACGATGACAGAGCTGCCGCGCAACGTCAGTACCGCGGGGTGACAGAACTACCTG 300
QY      406 CTGCTGTTGTTGCTGATTTTGTTCAGTGTCTTACCAATCCCTGAGCACACAAATTTG 465
Db      301 CTGCTGTTGTTGCTGATTTTGTTCAGTGTCTTACCAATCCCTGAGCACACAAATTTG 360
QY      466 GCTTCAGTGTGCTTGTGATCTGAGTTCGATGATGATGATGATGATGATGATGATGATG 525
Db      361 GCTTCAGTGTGCTTGTGATCTGAGTTCGATGATGATGATGATGATGATGATGATGATG 420
QY      526 ATCATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
Db      421 ATCATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY      586 AGGTTGCTGCAAGAGCCCTTCTGTTATGATACATGTTCTTATCGCTTCAATATTA 645
Db      481 AGGTTGCTGCAAGAGCCCTTCTGTTATGATACATGTTCTTATCGCTTCAATATTA 540

```

QY	646	GTGTGTTTCGCAAAAACCTGAGGGTAAATATTTTGGCAGCCTGACCTCAGAGTCTCCGT	705
Db	541	GTGTGTTTCGCAAAAACCTGAGGGTAAATATTTTGGCAGCCTGACCTCAGAGTCTCCGT	600
QY	706	TTCCTACAGATCCTCCGCAATGTGTGCGCATGAGCCGAAAGGGGAGGACCTTGGAAATTA	765
Db	601	TTCCTACAGATCCTCCGCAATGTGTGCGCATGAGCCGAAAGGGGAGGACCTTGGAAATTA	660
QY	766	GGTTCCAGTGGTTATATGCTCAGACAGCAAGGAATTAAATCAGCCTTGGTACATAGGATTTT	825
Db	661	GGTTCCAGTGGTTATATGCTCAGACAGCAAGGAATTAAATCAGCCTTGGTACATAGGATTTT	720
QY	826	GTTCCTATATTTTTCGTCCTTCCCTTGTCTATCTGTGTTGGAAAGAGATCCCAATAAGAGTT	885
Db	721	GTTCCTATATTTTTCGTCCTTCCCTTGTCTATCTGTGTTGGAAAGAGATCCCAATAAGAGTT	780
QY	886	TCTACATATGCAAGATGCTCTGTGGTGGGCGCAATTAATGCAACTATTTGGCTATGGA	945
Db	781	TCTACATATGCAAGATGCTCTGTGGTGGGCGCAATTAATGCAACTATTTGGCTATGGA	840
QY	946	GACAAACCTCCCTTAACCTTGGCTGGGAAAGATTCCTTCTGACAGCTTGGACCTCTGGC	1005
Db	841	GACAAACCTCCCTTAACCTTGGCTGGGAAAGATTCCTTCTGACAGCTTGGACCTCTGGC	900
QY	1006	ATTTCTTTCTTTGCACTTCCTGCGCGGCAATTCCTTGGCTCAGGTTTGGCATTTAAAGTACA	1065
Db	901	ATTTCTTTCTTTGCACTTCCTGCGCGGCAATTCCTTGGCTCAGGTTTGGCATTTAAAGTACA	960
QY	1066	GAACAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGGCAACCTCATTTAG	1125
Db	961	GAACAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGGCAACCTCATTTAG	1020
QY	1126	TGTTGTTTGGGCTAGTTACGACGAGTGATGAGAAATCTGTTTCATTTGCAACTGGAAGCCA	1185
Db	1021	TGTTGTTTGGGCTAGTTACGACGAGTGATGAGAAATCTGTTTCATTTGCAACTGGAAGCCA	1080
QY	1186	CACTTTGAAGGCTTTGCAACACCTGCAAGCCCTTACCAATAGAAAGCTAAAGTTTAAAGAGCCA	1245
Db	1081	CACTTTGAAGGCTTTGCAACACCTGCAAGCCCTTACCAATAGAAAGCTAAAGTTTAAAGAGCCA	1140
QY	1246	GTGGGCATGGCTTACCCCGAGGGGCGACAGTATTAAGAGCGACAGAGGCTCAGTAGTGAC	1305
Db	1141	GTGGGCATGGCTTACCCCGAGGGGCGACAGTATTAAGAGCGACAGAGGCTCAGTAGTGAC	1200
QY	1306	AGAGAGTCCCAAGCACCGACATCAAGCCGAGGGGAGTCCCAACAAAGTGCAGAGAGC	1365
Db	1201	AGAGAGTCCCAAGCACCGACATCAAGCCGAGGGGAGTCCCAACAAAGTGCAGAGAGC	1260
QY	1366	TGGAGCTTCAACAGACCGAACCCTTCCGCGCTCCGCTGCGGCTCAAAAGTTCACGCCA	1425
Db	1261	TGGAGCTTCAACAGACCGAACCCTTCCGCGCTCCGCTGCGGCTCAAAAGTTCACGCCA	1320
QY	1426	AAACGAGTATGATGCTGACACAGCCCTTGGCACTGATGATATGATGAAAAAGGA	1485
Db	1321	AAACGAGTATGATGCTGACACAGCCCTTGGCACTGATGATATGATGAAAAAGGA	1380
QY	1486	TGCCAGTGTGATGTATCAGTGGAAAGACTCAACCCACCACTTAAAACTGTCAATCGAGCT	1545
Db	1381	TGCCAGTGTGATGTATCAGTGGAAAGACTCAACCCACCACTTAAAACTGTCAATCGAGCT	1440
QY	1546	ATCAGAAATTATGAATTTTCATGTGGCAAAAGGAAATTAAAGAAACATTAAGCTCCATAT	1605
Db	1441	ATCAGAAATTATGAATTTTCATGTGGCAAAAGGAAATTAAAGAAACATTAAGCTCCATAT	1500
QY	1606	GATGTAAAAAGATGTCATTTGAACAATATTTCTGCTGCTCATCTGGACATGTTGTGTAAGATT	1665
Db	1501	GATGTAAAAAGATGTCATTTGAACAATATTTCTGCTGCTCATCTGGACATGTTGTGTAAGATT	1560
QY	1666	AAAAGCCTTCAAAACAGCTGTTGATCAAAATTTCTGGAAAAAGGCAAAATACATCAGATTAAG	1725
Db	1561	AAAAGCCTTCAAAACAGCTGTTGATCAAAATTTCTGGAAAAAGGCAAAATACATCAGATTAAG	1620

Qy	1726	NAGAGCCGAGAGAAAATTAACAGAGAAATGAGAGCCAGACGAAATTCAGATAGCTCGGT	1785
Db	1621	AAGAGCCGAGAGAAAATTAACAGAGAAATGAGAGCCAGACGAAATTCAGATAGCTCGGT	1680
Qy	1786	CGAGGTGTCAGAGTTGAAAAACAGGTACAGTCCATAGAAATCCAACTGGAGCTGCCTACTA	1845
Db	1681	CGAGGTGTCAGAGTTGAAAAACAGGTACAGTCCATAGAGTCCAACTGGAGCTGCCTACTA	1740
Qy	1846	GACATCTATACACAGGTCTTTCGGAAAGGCTCTGCTCCAGCCCTGGCTTGGCTTCATTC	1905
Db	1741	GACATCTATACACAGGTCTTTCGGAAAGGCTCTGCTCCAGCCCTGGCTTGGCTTCATTC	1800
Qy	1906	CAGATCCCACTTTTGAATGTGAACAGACATCTAGATCTCAAAAGCCCTGTGGATAGCAAA	1965
Db	1801	CAGATCCCACTTTTGAATGTGAACAGACATCTAGATCTCAAAAGCCCTGTGGATAGCAAA	1860
Qy	1966	GATCTTTGGGGTTCCGCACAAACACAGTGGCTGCTTATCCAGATCAACTATAGTCCAAATTC	2025
Db	1861	GATCTTTGGGGTTCCGCACAAACACAGTGGCTGCTTATCCAGATCAACTATAGTCCAAATTC	1920
Qy	2026	TCGAGAGGCGCTGCAGTTCATTCCTGACGCAATGAGTTGAGTGGCCAGACTTTTCTACGGG	2085
Db	1921	TCGAGAGGCGCTGCAGTTCATTCCTGACGCAATGAGTTGAGTGGCCAGACTTTTCTACGGG	1980
Qy	2086	CTTAGCCCTACTATGACAGTCAAGCAACACAGTGGCCAAATTATGTCAAAGCGATGGCTCA	2145
Db	1981	CTTAGCCCTACTATGACAGTCAAGCAACACAGTGGCCAAATTATGTCAAAGCGATGGCTCA	2040
Qy	2146	GCATGGGCACGCCACCAACACCATTTGCAAAACCAATTAATATAGCGACGCCAAGCCAGCAGCC	2205
Db	2041	GCATGGGCACGCCACCAACACCATTTGCAAAACCAATTAATATAGCGACGCCAAGCCAGCAGCC	2100
Qy	2206	CCAAACAACCTTTACAGATCCCACTCTCTCTCCAGCCATCAAGACTCTGCCAGGCCAGAA	2265
Db	2101	CCAAACAACCTTTACAGATCCCACTCTCTCTCCAGCCATCAAGACTCTGCCAGGCCAGAA	2160
Qy	2266	ACTCTGACCCCTAACCCCTGCAGGCTTAAAGGAAACCATTTTCGAGGTCCACACCTCGCTT	2325
Db	2161	ACTCTGACCCCTAACCCCTGCAGGCTTAAAGGAAACCATTTTCGAGGTCCACACCTCGCTT	2220
Qy	2326	GTTGGCCCTCAAGAAAAATGTTGAGGTTGCACAGTCAAAATCTACCAAGNACCGTTCTATG	2385
Db	2221	GTTGGCCCTCAAGAAAAATGTTGAGGTTGCACAGTCAAAATCTACCAAGNACCGTTCTATG	2280
Qy	2386	AGGAAAAAGCTTTGACATGGAAGAGAGAAACCTGTTGTCTGTCTGCCATGGTGGCCGAG	2445
Db	2281	AGGAAAAAGCTTTGACATGGAAGAGAGAAACCTGTTGTCTGTCTGCCATGGTGGCCGAG	2340
Qy	2446	GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCAGCCGAGAACTGGAATATA	2505
Db	2341	GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCAGCCGAGAACTGGAATATA	2400
Qy	2506	CAACTTTCAGGAGATGAGTCAAGTGGCTCCAGAGGCGAGCCAGATTTTTTACCCCAATYG	2565
Db	2401	CAACTTTCAGGAGATGAGTCAAGTGGCTCCAGAGGCGAGCCAGATTTTTTACCCCAATYG	2460
Qy	2566	AGGGAATCCAAATTTTATATAACTGATGAAGAGGTGGGTCCGAAAGAGACAGAGACGAC	2625
Db	2461	AGGGAATCCAAATTTTATATAACTGATGAAGAGGTGGGTCCGAAAGAGACAGAGACGAC	2520
Qy	2626	ACTTTTGAATGGCGCACCGGAGCTGCAGAGGAAAGCTGCTTTGCATCAGACTCTCTAAG	2685
Db	2521	ACTTTTGAATGGCGCACCGGAGCTGCAGAGGAAAGCTGCTTTGCATCAGACTCTCTAAG	2580
Qy	2686	ACTGGAAGTCAAGATCATCTGAGAGCAATTTGTAAGCGAGAGAAAGTACAGATGCCCTC	2745
Db	2581	ACTGGAAGTCAAGATCATCTGAGAGCAATTTGTAAGCGAGAGAAAGTACAGATGCCCTC	2640
Qy	2746	AGCTTGCCTCATGTCAAACTGAAATATA 2772	
Db	2641	AGCTTGCCTCATGTCAAACTGAAATATA 2667	

;; CURRENT FILING DATE: 2001-10-12
;; PRIOR APPLICATION NUMBER: US 60/190,954
;; PRIOR FILING DATE: 2000-03-21
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 2694
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PEPTIDE:
;; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
;; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
;; NAME/KEY: CDS
;; LOCATION: (1)-(2694)
;; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 52.3%; Score 1450; DB 10; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1221	TCAGAGCTAAGTTTAAGGAGGAGTGGCATGGCTAGGCCCGGAGGCGCAGATTATTA	1280
DB	1143	TCAGAACTAAGTTTAAGGAGGAGTGGCATGGCTAGGCCCGGAGGCGCAGATTATTA	1202
QY	1281	GAGCCGACAGCCTCAGTAGTGACAGAGAGTCCCAAGACCGACATCACAGCCGAGG	1340
DB	1203	GAGCCGACAGCCTCAGTAGTGACAGAGAGTCCCAAGACCGACATCACAGCCGAGG	1262
QY	1341	CAGTCCACCAAGTGCAGAGAGCTGGAGCTTCACAGCCGAACCGCTCCGAGCCTC	1400
DB	1263	CAGTCCACCAAGTGCAGAGAGCTGGAGCTTCACAGCCGAACCGCTCCGAGCCTC	1322
QY	1401	GGTGGCCTCAAAAGTTCTGAGCCAAACAGATGATGATGATGATGATGATGATGATG	1460
DB	1323	GGTGGCCTCAAAAGTTCTGAGCCAAACAGATGATGATGATGATGATGATGATGATG	1382
QY	1461	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1520
DB	1383	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1442
QY	1521	ACCACCTTAAACCTGCTATGAGCTATCAGATTTATGAAATTTATGTTGCAAAACGAA	1580
DB	1443	ACCACCTTAAACCTGCTATGAGCTATCAGATTTATGAAATTTATGTTGCAAAACGAA	1502
QY	1581	GTTTAAGGAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATG	1640
DB	1503	GTTTAAGGAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATG	1562
QY	1641	TCATCTGGACATGTTGTGTAGAAATTAAGCCTTCAACACAGTGTGATCAAAATTTCTGG	1700
DB	1563	TCATCTGGACATGTTGTGTAGAAATTAAGCCTTCAACACAGTGTGATCAAAATTTCTGG	1622
QY	1701	AAAAAGGCAATACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGACATGAAC	1760
DB	1623	AAAAAGGCAATACATCAGATTAAGAAAGCCGAGAGAAATTAACAGCAGACATGAAC	1682
QY	1761	CACAGAGATCTAGTATGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1820
DB	1683	CACAGAGATCTAGTATGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1742
QY	1821	AGATCCAGAGCTGAGCTCTACTAGACATCTATCAACAGGTCTCTCGAAAGGCTCTGC	1880
DB	1743	AGATCCAGAGCTGAGCTCTACTAGACATCTATCAACAGGTCTCTCGAAAGGCTCTGC	1802
QY	1881	CTCAGCCCTGCTTGGCTTCTATCCAGATCCACCTTTTGAATGTGAACAGACTCTGA	1940
DB	1803	CTCAGCCCTGCTTGGCTTCTATCCAGATCCACCTTTTGAATGTGAACAGACTCTGA	1862
QY	1941	CTATCAAGCCCTGTGTGATGCAAAAGATCTTTGGGTTTCGACAAACAGTGGTGGT	2000
DB	1863	CTATCAAGCCCTGTGTGATGCAAAAGATCTTTGGGTTTCGACAAACAGTGGTGGT	1922

QY	2001	ATCCAGATCACTAGTGGCCAGACATCTCGAGAGCCCTGAGTTCATCTGAGCCCAATGA	2060
DB	1923	ATCCAGATCACTAGTGGCCAGACATCTCGAGAGCCCTGAGTTCATCTGAGCCCAATGA	1982
QY	2061	GTTTCCAGTCCGAGACTTTTACGCGCTTACGCTTACCTACTATGACAGTCAAGCAACAGT	2120
DB	1983	GTTTCCAGTCCGAGACTTTTACGCGCTTACGCTTACCTACTATGACAGTCAAGCAACAGT	2042
QY	2121	GCCAAATTAAGTCAAAAGGATGGCTCAGCAGTGGGAGGAGCCACCAACCATTTCAACCAAT	2180
DB	2043	GCCAAATTAAGTCAAAAGGATGGCTCAGCAGTGGGAGGAGCCACCAACCATTTCAACCAAT	2102
QY	2181	AAATAGGACCCCAAGCCAGACAGCCCAACCAACTTACAGATCCACCTCTCCAGC	2240
DB	2103	AAATAGGACCCCAAGCCAGACAGCCCAACCAACTTACAGATCCACCTCTCCAGC	2162
QY	2241	CATCAAGCATCTGCGCCAGGCGCAAACTGTGACCTTAACCTCGAGGCTTACAGGAAG	2300
DB	2163	CATCAAGCATCTGCGCCAGGCGCAAACTGTGACCTTAACCTCGAGGCTTACAGGAAG	2222
QY	2301	CATTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2360
DB	2223	CATTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2282
QY	2361	AAATCTACCAAGAGACCGTTCTATGAGAAAGCTTTGACATGGAGAGAAACTCTGTT	2420
DB	2283	AAATCTACCAAGAGACCGTTCTATGAGAAAGCTTTGACATGGAGAGAAACTCTGTT	2342
QY	2421	GTCGTCTCTCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2480
DB	2343	GTCGTCTCTCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2402
QY	2481	CAGGTGACGAGGAGTCAATATACACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAG	2540
DB	2403	CAGGTGACGAGGAGTCAATATACACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAG	2462
QY	2541	CAGCCAAATTTTATCCCAATGAGAGGAAATCCAAATTTTATTAATCTGATGAAGGT	2600
DB	2463	CAGCCAAATTTTATCCCAATGAGAGGAAATCCAAATTTTATTAATCTGATGAAGGT	2522
QY	2601	GGTCCCGAAGAGACAGACAGACACTTTGATGGCCGACCGAGCTCGCAGAGAGC	2660
DB	2523	GGTCCCGAAGAGACAGACAGACACTTTGATGGCCGACCGAGCTCGCAGAGAGC	2582
QY	2661	TGCTTTGATGACATCTCTCTTAAGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGAA	2720
DB	2583	TGCTTTGATGACATCTCTCTTAAGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGAA	2642
QY	2721	GGCAGGAGAAATGACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA	2772
DB	2643	GGCAGGAGAAATGACAGATGCTCAGCTTGCCTCATGTCAAACTGAATTA	2694

RESULT 6
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeda, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

OTHER INFORMATION: human outwardly rectifying, voltage-gated
 ;
 ;
 ; NAME/KEY: CDS
 ; LOCATION: (10)..(2703)
 ;
 ; OTHER INFORMATION: KCNQ5-1
 ; US-09-810-796-1

Query Match 52.3%; Score 1450; DB 10; Length 3071;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1221 TCAGAAAGCTAAGTTTAAAGAGGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1280
DB 1152 TCAGAAAGCTAAGTTTAAAGAGGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1211
QY 1281 GAGCCGACAAAGCTCAGTAGTACAGAGAGTCCCAAGCAGCATCACAGCCGAGAGG 1340
DB 1212 GAGCCGACAAAGCTCAGTAGTACAGAGAGTCCCAAGCAGCATCACAGCCGAGAGG 1271
QY 1341 CAGTCCACCAAGTGCAGAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1400
DB 1272 CAGTCCACCAAGTGCAGAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1331
QY 1401 GCTGGCCCTCAAAAGTTTCAGCCAAACAGTAGATGCTGACACAGCCCTTGCGAC 1460
DB 1332 GCTGGCCCTCAAAAGTTTCAGCCAAACAGTAGATGCTGACACAGCCCTTGCGAC 1391
QY 1461 TGATGATGATATGATGAAAAAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1520
DB 1392 TGATGATGATATGATGAAAAAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1451
QY 1521 ACCACTTAAAGTGTATTCAGAGCTTACAGAAATTAAGAAATTCATGTTGCAAAACGGA 1580
DB 1452 ACCACTTAAAGTGTATTCAGAGCTTACAGAAATTAAGAAATTCATGTTGCAAAACGGA 1511
QY 1581 GTTTAAGGAAATTAAGTGCATATGATGAAAAAGATGATTAACAAATTTCTGCTGG 1640
DB 1512 GTTTAAGGAAATTAAGTGCATATGATGAAAAAGATGATTAACAAATTTCTGCTGG 1571
QY 1641 TCATCTGACATGTTGTTAGAAATTAAGGCTTCAACAGAGTGTGATCAAAATTTCTGG 1700
DB 1572 TCATCTGACATGTTGTTAGAAATTAAGGCTTCAACAGAGTGTGATCAAAATTTCTGG 1631
QY 1701 AAAAGGCAATCAGATCAGATAGAGAGCCGAGAGAAAAATTAACAGACAGATGAGAC 1760
DB 1632 AAAAGGCAATCAGATCAGATAGAGAGCCGAGAGAAAAATTAACAGACAGATGAGAC 1691
QY 1761 CACAGAGATCTCAGTATGCTGCTGGTGGTGCAGAGTTGAAAAAGAGTACAGTCCAT 1820
DB 1692 CACAGAGATCTCAGTATGCTGCTGGTGGTGCAGAGTTGAAAAAGAGTACAGTCCAT 1751
QY 1821 AGAATCCAGCTGAGTGCCTACTAGACATCTATCAACAGAGTCTTGGAAAAAGCTCTGC 1880
DB 1752 AGAATCCAGCTGAGTGCCTACTAGACATCTATCAACAGAGTCTTGGAAAAAGCTCTGC 1811
QY 1881 CTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTGAATGTGACAGACATCTGA 1940
DB 1812 CTCAGCCCTGCTTGGCTTCAATTCAGATCCACCTTTGAATGTGACAGACATCTGA 1871
QY 1941 CTATCAAGCCCTGAGATAGAGAAAGATCTTTCGGTTCGCAAAAGAGTGGCTGCT 2000
DB 1872 CTATCAAGCCCTGAGATAGAGAAAGATCTTTCGGTTCGCAAAAGAGTGGCTGCT 1931
QY 2001 ATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGAGTATCTTGACGCCAATGA 2060
DB 1932 ATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGAGTATCTTGACGCCAATGA 1991
QY 2061 GTTCAAGTCCAGACTTTCACGCGCTTAGCCCTACTATGACAGTCAACACAGAGT 2120
DB 1992 GTTCAAGTCCAGACTTTCACGCGCTTAGCCCTACTATGACAGTCAACACAGAGT 2051
QY 2121 GCCAATTAGTCAAGCGAATGGTGCAGAGTGCAGCAGCAGCAGCAGCAGCAGCAGT 2180

```

```

DB 2052 GCCAATTAGTCAAGCGAATGGTGCAGAGTGCAGCAGCAGCAGCAGCAGCAGT 2111
QY 2181 AATACGCGACCCAGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2240
DB 2112 AATACGCGACCCAGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2171
QY 2241 CATCAACATCTGCGCGAGCGGAGAGAACTCTGACACCTTAACCTGACAGCTTACAGAAAG 2300
DB 2172 CATCAACATCTGCGCGAGCGGAGAGAACTCTGACACCTTAACCTGACAGCTTACAGAAAG 2231
QY 2301 CATTTCTGAGCTACACACCTGCTTGTGCTCCAGAGAAATTTTACAGTTGACAGTAC 2360
DB 2232 CATTTCTGAGCTACACACCTGCTTGTGCTCCAGAGAAATTTTACAGTTGACAGTAC 2291
QY 2361 AATCTCAGCAGAGAGCAGCTTCTATGAGAGAAAGCTTTCAGATGAGAGAGAACTCTGTT 2420
DB 2292 AATCTCAGCAGAGAGCAGCTTCTATGAGAGAAAGCTTTCAGATGAGAGAGAACTCTGTT 2351
QY 2421 GTCTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2480
DB 2352 GTCTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2411
QY 2481 CAGTGCAGCAGAGAGAGTGAATATACACTTTCAGAGAGTGAAGTGCCTCCAGAG 2540
DB 2412 CAGTGCAGCAGAGAGAGTGAATATACACTTTCAGAGAGTGAAGTGCCTCCAGAG 2471
QY 2541 CAGCCAGAGTTTATACCCCAATGAGAGAAATCCAAATTTGTTATATGATGAGAGAGT 2600
DB 2472 CAGCCAGAGTTTATACCCCAATGAGAGAAATCCAAATTTGTTATATGATGAGAGAGT 2531
QY 2601 GGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2660
DB 2532 GGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2591
QY 2661 TGCCTTTGATTCAGAGCTCTCTAAGAGCTGAGAGTCAAGATCATCTCAGAGCATTTGTA 2720
DB 2592 TGCCTTTGATTCAGAGCTCTCTAAGAGCTGAGAGTCAAGATCATCTCAGAGCATTTGTA 2651
QY 2721 GGCAGGAGAAAGTACAGATGCCCTCAGCTGCTCATGTCGAAGTGAATAA 2772
DB 2652 GGCAGGAGAAAGTACAGATGCCCTCAGCTGCTCATGTCGAAGTGAATAA 2703

```

RESULT 7
 US-10-128-870-5
 ; Sequence 5, Application US/10128870
 ; Patent No. US20020168724A1
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Blonar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ;
 ; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58adiV
 ; CURRENT APPLICATION NUMBER: US/10/128, 870
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ;
 ; SEQ ID NO 5
 ; LENGTH: 900
 ; TYPE: DNA
 ; ORGANISM: MOUSE
 ; FEATURE:
 ; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
 ; US-10-128-870-5

Query Match 1.0%; Score 29; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGCGTTCATCTACACGC 392
DB 82 CCCCCGGGCTGGCGTTCATCTACACGC 110

RESULT 8

US-10-131-685-5
; Sequence 5, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-131-685-5

Query Match 1.0%; Score 29; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGCGTTCATCTACACGC 392
DB 82 CCCCCGGGCTGGCGTTCATCTACACGC 110

RESULT 9

US-10-128-870-22
; Sequence 22, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoif, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58BDIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: MOUSE
US-10-128-870-22

Query Match 1.0%; Score 29; DB 9; Length 2169;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGCGTTCATCTACACGC 392
DB 262 CCCCCGGGCTGGCGTTCATCTACACGC 290

RESULT 10

US-10-131-685-22
; Sequence 22, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: MOUSE
US-10-131-685-22

Query Match 1.0%; Score 29; DB 9; Length 2169;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGCGTTCATCTACACGC 392
DB 262 CCCCCGGGCTGGCGTTCATCTACACGC 290

RESULT 11

US-09-810-796-7/c
; Sequence 7, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-00501005
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense
; OTHER INFORMATION: primer (2)
US-09-810-796-7

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1809 GGTACAGTCCATAGAAATCCAGCTGG 1834
|||||
Db 26 GGTACAGTCCATAGAAATCCAGCTGG 1

RESULT 12
US-09-810-796-8
; Sequence 8, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: standard 3'
US-09-810-796-8

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1725 GAAGAGCCGAGAGAAATATACAGCAG 1750
|||||
Db 1 GAAGAGCCGAGAGAAATATACAGCAG 26

RESULT 13
US-09-810-796-9
; Sequence 9, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: reamplification
US-09-810-796-9

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1949 GCGCTGTGATGCAAGATCTTTCG 1974
|||||
Db 1 GCGCTGTGATGCAAGATCTTTCG 26

RESULT 14
US-10-128-870-3

; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neuhauer, Michael G.
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/035,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

Query Match 0.9%; Score 26; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
|||||
Db 85 CGCGGCTGGGCGTTCATCTACACGC 110

RESULT 15
US-10-131-685-3
; Sequence 3, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neuhauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-131-685-3

Query Match 0.9%; Score 26; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
|||||
Db 85 CGCGGCTGGGCGTTCATCTACACGC 110

```
RESULT 16
US-10-128-870-19
; Sequence 19, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Dvoretzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC588d1y
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-870-19

Query Match
Best Local Similarity 100.0%; Score 26; DB 9; Length 3287;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGCGCTTCATCTACACGC 392
Db 325 CGCGGCTGGCGCTTCATCTACACGC 350

RESULT 17
US-10-131-685-19
; Sequence 19, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC588aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-685-19

Query Match
Best Local Similarity 100.0%; Score 26; DB 9; Length 3287;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGCGCTTCATCTACACGC 392
Db 325 CGCGGCTGGCGCTTCATCTACACGC 350
```

```
RESULT 18
US-09-810-796-10/C
; Sequence 10, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICGen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:nested standard
US-09-810-796-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 10; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 GGGTTCAGTGGTTATGCTCACAGC 789
Db 25 GGGTTCAGTGGTTATGCTCACAGC 1

RESULT 19
US-09-810-796-11/C
; Sequence 11, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICGen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:nested standard
US-09-810-796-11

Query Match
Best Local Similarity 100.0%; Score 25; DB 10; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 CAGATCCTCCGATGATGCGCATGG 736
Db 25 CAGATCCTCCGATGATGCGCATGG 1

Search completed: June 19, 2003, 18:46:29
Job time : 380 secs
```


CURRENT FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

CURRENT
PRIOR
PRIOR

TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 96
LENGTH: 930
TYPE: PRT
ORGANISM: Homo sapiens
US-09-177-650-96

Query Match 37.8%; Score 1789.5; DB 4; Length 930;
Best Local Similarity 43.9%; Pred. No. 2.5e-150;
Matches 433; Conservative 109; Mismatches 246; Indels 199; Gaps 26;

QY 21 GAAAGGGRGSGMKDYESGRVLLNSAARGDGLLLGTRAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLVGFVGDPGA-----PDSTRDGLLITAGSEAPK---RGSILSKPRA 59
QY 81 GKGARMSLLGKPLSYTSSQSCRNNVYRVQNYLYNVLPRGWAFIYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAYRKLQNLVLYNVLPRGWAFIYHAFVLLVFGC 106
QY 141 LILSVFTPEHTKGLASSCLLLEFVNVVFGLEFIIRWSAGCCCRVGGWGRURFARK 200
DB 107 LVLVSFTIKEYEKSEBEGALYILEIVTVFVGEYFVRIWAAGCCCRVGGWGRURFARK 166
QY 201 PCVIDITVLIASIVASVAKTQGNIFATSLRSRLRFLQILRMVRMDRGGTWKLLGSVY 260
DB 167 PCVIDITVLIASIVASVAKTQGNIFATSLRSRLRFLQILRMVRMDRGGTWKLLGSVY 226
QY 261 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFEFSTYADALWMTITLITIGYDGTPL 320
DB 227 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFEFSTYADALWMTITLITIGYDGTPL 286
QY 321 TWGRLLSAGFALLIGISFFALPAGILSGFGFALKVQEOHQHFKRRNPANLIQCVWRS 380
DB 287 TWGRLLAATFTLIGVFFALPAGILSGFGFALKVQEOHQHFKRRNPANLIQCVWRS 346
QY 381 YAAD-----EKSYSIATWK-----PHLKALHT----- 402
DB 347 YATNLSRTDLHSTWQYERTVTPVMSYQOTYQASRLIPPLNQLLELNLKSKSLAFR 406
QY 403 -----CSP--TNQKLSFKRVRMASPRGOSIKSRQASVGD--RR 437
DB 407 KDPPEPSPKSGPCRGPLCGCCPCGRSSQKVSLLKDRV-FSSPRGVAAGKGSPOAQTVRR 465
QY 438 SPSTDTAEGSPKVKQSWNDRTFRPSRLKSSQPKPVDADTALGTDVDDKGCQ 497
DB 466 SPADQSLSDSPKVPKSWFSDRSRQAFRIKGAASQNSE-EASLPGEDIVDDKSCP 524
QY 498 CDVSVEDLTPKLVIRAIRMKFVAKKFKETLPDYDVQVIEQYSAGHLDMLCRIKS 557
DB 525 CEFVTEDLTPGLKVSIRAVCMRFLVSKRKFESLRPDYDMVDIEQYSAGHLDMLSRIKS 584
QY 558 LOTRVDQILGGOITSDKRSREKITAETHETDOLSLMGRVVKVQVQSTESKLDCLLDI 617
DB 585 LQSRVDQILVGRPAITD-KDRTKGPAAELPEDPSNMGRGLKVEKQVLSKEKLDLFLVNI 643
QY 618 YQVLRKGSASALASAFQIPPEF-----EQTSYQSPVDSKDLGSAQNSGCLS 668
DB 644 YMQ--RMG-----IPPTETAYFGAKEPEPAPPVPHSPEDSRE---HVDHGGCIV 687
QY 669 RSTSANISRGLOFILTNEFSAGTFFALSPTMHSQATQVPISSDGSNAVAATNTIANQIN 728
DB 688 KIVRSSSTG----- 700
QY 729 TAPKPAATLQIPPL-----PAIKHLPRPETLH-----PNPAGLOESISDVITCL 775

701 FSAPPAAP-PVQCPSTSWQPSHPROGHGTSFVGDHGSLSVRIPPPAHERLSAYGGGN 759
776 VASKENVQAQSNLTK--DRSMRKSFDMGGETLLSCVMPVPRKDLAKSLSVQNLIRSTEEL 833
760 RASMEFLRQEDTPCCRPEGNLRDS-----DTSISIPSVVDEELERSFSGFSISQSKENL 814
834 NIOLSGSESSGSGSQDFYFKWRRESKLFITDEEV-----GP-----EETETDTDAAPQ 882
815 DALNSCYAAVAPCAKVRPIYAEGBSD---TSDSLCTPCGPPPSRATGEGPFVGVWAGPG 871
883 PAREAAAFASDLRTGRSSOSICKAG 909
872 PGSEALG---QWTRPRSSARCLRG 894

RESULT 3
US-09-105-058C-20
Sequence 20, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blamar, Michael A.
APPLICANT: Doretzky, Steven
APPLICANT: Gridneff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauber, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
US-09-105-058C-20

Query Match 37.8%; Score 1788.5; DB 4; Length 871;
Best Local Similarity 46.8%; Pred. No. 2.8e-150;
Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAGGGRGSGMKDYESGRVLLNSAARGDGLLLGTRAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLVGFVGDPGA-----PDSTRDGLLITAGSEAPK---RGSILSKPRA 59
QY 81 GKGARMSLLGKPLSYTSSQSCRNNVYRVQNYLYNVLPRGWAFIYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAYRKLQNLVLYNVLPRGWAFIYHAFVLLVFGC 106
QY 141 LILSVFTPEHTKGLASSCLLLEFVNVVFGLEFIIRWSAGCCCRVGGWGRURFARK 200
DB 107 LVLVSFTIKEYEKSEBEGALYILEIVTVFVGEYFVRIWAAGCCCRVGGWGRURFARK 166
QY 201 PCVIDITVLIASIVASVAKTQGNIFATSLRSRLRFLQILRMVRMDRGGTWKLLGSVY 260
DB 167 PCVIDITVLIASIVASVAKTQGNIFATSLRSRLRFLQILRMVRMDRGGTWKLLGSVY 226
QY 261 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFEFSTYADALWMTITLITIGYDGTPL 320
DB 227 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFEFSTYADALWMTITLITIGYDGTPL 286
QY 321 TWGRLLSAGFALLIGISFFALPAGILSGFGFALKVQEOHQHFKRRNPANLIQCVWRS 380
DB 287 TWGRLLAATFTLIGVFFALPAGILSGFGFALKVQEOHQHFKRRNPANLIQCVWRS 346
QY 381 YAAD-----EKSYSIATWK-----PHLKALHT----- 402
DB 347 YATNLSRTDLHSTWQYERTVTPVMSYQOTYQASRLIPPLNQLLELNLKSKSLAFR 406

QY 403 -----CSP--TNQKLSFKERVMA SPRGOSIKSROASVGD--RR 437
Db 407 KDPPEPSPSKSPGCGPCGRSSQKVSRLKDRV-FSSPRGVAAGKGSPOAQTVRR 465
QY 438 SPSTDTAEGSPKVKOSWFSNDRFRPSRLKSSOPKPIDADTALGTDDVDYDEKGCQ 497
Db 466 SPSAQSLSDSPSKVPKSWFSNDRFRPSRLKSSOPKPIDADTALGTDDVDYDEKGCQ 523
QY 498 CDVSVEDLTPPLKTVIRAIMKHFHAKRKFETLRPYDVYDKVDIEQYSAGHLDMLCRIKS 557
Db 524 CEFVTEDELTPGLKVSIRAVCMRFLVSKRKFESLRPYDVYDMVDIEQYSAGHLDMLSRKS 583
QY 558 LQTRVDQILGKGQITSDKKSREKITAETHETDLSMLGRVVKVKEQVOSIESKLDCLDI 617
Db 584 LQSRVDQIVGRGPAITD-KDRTKGPAEAELEPDSMMGRGLGKVEQVLSMEKKLDFLVNI 642
QY 618 YQOVLKSGSASALALASFQIPPEFC-----EQTSDYQSPVDSKDLGSAQNSGCLS 668
Db 643 YMQ--RMG-----IPPTETAYFGAKEPEPAPPYHSPEDSRE---HVDRHGCIV 686
QY 669 RSTSANISRLQFILTNPNEFSQAQTFYALSPTHSQAQTVPIQS-----DGSVAAT 720
Db 687 KIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSWQPSHPROGHGTSVP 732
QY 721 NTIANQINTAPKPAAPTTLQI-----PP-----PLPAI 748
Db 733 GDHGLSVRIPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPEGLRDSPTSISPSV 792
QY 749 KHLRPETHLPNAPAGLQESISDVTTCLVASKENVOVAQS 787
Db 793 DH-----EELERSFSGF--SISQ-----SKENLDALNS 818

RESULT 4

US-09-177-650-2
; Sequence 2, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 872
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-650-2

Query Match 37.7%; Score 1784; DB 4; Length 872;
Best Local Similarity 46.8%; Pred. No. 7e-150;
Matches 41; Conservative 92; Mismatches 196; Indels 180; Gaps 25;
QY 21 GAAAGAGGGRGSGMKDVSGRGVLLNSAARGDGLLLGTRATIGGGGGGLESRR 80
Db 9 GVTGPGSGEKKLVGVGLDPGA-----PSTREDGALLIAGEAPK---RGSILSKPA 59
QY 81 GKOGARMSLLGKPLSYTSOSSCRNVKRYRQVNYLVLEPRGWFAYIHAYVFLVFC 140
Db 60 GGAGA-----GKP-----PKNARYKQLNLYLVLEPRGWFAYIHAYVFLVFC 106
141 LILSVFSTPEHTKGLASSCLLLEFVMVVGLEFIIRWSAGCCCRVGRWGLRFAK 200
VLSVSTPEHTKGLASSCLLLEFVMVVGLEFIIRWSAGCCCRVGRWGLRFAK 200
VLSVSTPEHTKGLASSCLLLEFVMVVGLEFIIRWSAGCCCRVGRWGLRFAK 200

QY 201 PFCVIDRIVLIASIAVSAKTOGNIFATSAKLSRLFLQLRMVMDRRGGTWKLLGSVY 260
Db 167 PFCVIDRIVLIASIAVSAKTOGNIFATSAKLSRLFLQLRMVMDRRGGTWKLLGSVY 226
QY 261 AHSKELITAWYIGFLVLFSSFLVYLVKEDANKEESTYADALWNGTITLITIGYDKTPL 320
Db 227 AHSKELITAWYIGFLVLFSSFLVYLVKEDANKEESTYADALWNGTITLITIGYDKTPL 286
QY 321 TWGRLLSAGFALLIGISFFALPAGILSGFALKVQEQHQRKHFERRRNPAAALIOCVWRS 380
Db 287 TWGRLLSAGFALLIGISFFALPAGILSGFALKVQEQHQRKHFERRRNPAAALIOCVWRS 346
QY 381 YAAD-----EKSYSIATWK-----PHLKALHT-----402
Db 347 YATNLSRDLHSTWQYERTVTPMYSQOTYTGASRLIPPLNQLLELRNLKSKSLAFLR 406
QY 403 -----CSP--TNQKLSFKERVMA SPRGOSIKSROASVGD--RR 437
Db 407 KDPPEPSPSKSPGCGPCGRSSQKVSRLKDRV-FSSPRGVAAGKGSPOAQTVRR 465
QY 438 SPSTDTAEGSPKVKOSWFSNDRFRPSRLKSSOPKPIDADTALGTDDVDYDEKGCQ 497
Db 466 SPSAQSLSDSPSKVPKSWFSNDRFRPSRLKSSOPKPIDADTALGTDDVDYDEKGCQ 524
QY 498 CDVSVEDLTPPLKTVIRAIMKHFHAKRKFETLRPYDVYDKVDIEQYSAGHLDMLCRIKS 557
Db 524 CEFVTEDELTPGLKVSIRAVCMRFLVSKRKFESLRPYDVYDMVDIEQYSAGHLDMLSRKS 584
QY 558 LQTRVDQILGKGQITSDKKSREKITAETHETDLSMLGRVVKVKEQVOSIESKLDCLDI 617
Db 584 LQSRVDQIVGRGPAITD-KDRTKGPAEAELEPDSMMGRGLGKVEQVLSMEKKLDFLVNI 643
QY 618 YQOVLKSGSASALALASFQIPPEFC-----EQTSDYQSPVDSKDLGSAQNSGCLS 668
Db 643 YMQ--RMG-----IPPTETAYFGAKEPEPAPPYHSPEDSRE---HVDRHGCIV 687
QY 669 RSTSANISRLQFILTNPNEFSQAQTFYALSPTHSQAQTVPIQS-----DGSVAAT 720
Db 688 KIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSWQPSHPROGHGTSVP 733
QY 721 NTIANQINTAPKPAAPTTLQI-----PP-----PLPAI 748
Db 734 GDHGLSVRIPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPEGLRDSPTSISPSV 793
QY 749 KHLRPETHLPNAPAGLQESISDVTTCLVASKENVOVAQS 787
Db 794 DH-----EELERSFSGF--SISQ-----SKENLDALNS 819

RESULT 5

US-09-177-650-89
; Sequence 89, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-650-89

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 13:26:41 ; Search time 156 Seconds
(without alignments)
5449,410 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772
Sequence: 1 atgcgccgcgcacacgcg99.....ctcatgtcaactgaataa 2772

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 24

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCURS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	1.0	900	4	US-09-105-058C-5
2	29	1.0	2169	4	US-09-105-058C-22
3	26	0.9	900	4	US-09-105-058C-3
4	26	0.9	3232	4	US-09-177-650-1
5	26	0.9	3237	4	US-09-177-650-95
6	26	0.9	3287	4	US-09-105-058C-19

ALIGNMENTS

RESULT 1
US-09-105-058C-5
Sequence 5, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubaer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 900
TYPE: DNA
ORGANISM: mouse
FEATURE:
OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

Query Match 1.0%; Score 29; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCGCGGCTGGGCGTTCATCTACACGC 392
DB 82 CCCCGCGGCTGGGCGTTCATCTACACGC 110

RESULT 2
US-09-105-058C-22
Sequence 22, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubaer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 2169
TYPE: DNA
ORGANISM: mouse
US-09-105-058C-22

Query Match 1.0%; Score 29; DB 4; Length 2169;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCGCGGCTGGGCGTTCATCTACACGC 392
DB 262 CCCCGCGGCTGGGCGTTCATCTACACGC 290

RESULT 3
US-09-105-058C-3
Sequence 3, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubaer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599

```
;; PRIOR FILING DATE: 1997-08-12
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 900
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-09-105-058C-3

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 900;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGGCGTTCATCTACACGCG 392
DB 85 CGCGGCTGGGCGTTCATCTACACGCG 110

RESULT 4
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred K1504.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1691)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1846)
```

```
;; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
;; OTHER INFORMATION: the control population.
;; FEATURE:
;; NAME/KEY: mutation
;; LOCATION: (1469)
;; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
;; OTHER INFORMATION: K1525.
;; FEATURE:
;; NAME/KEY: mutation
;; LOCATION: (1094)
;; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
;; OTHER INFORMATION: K4443.
;; FEATURE:
;; NAME/KEY: mutation
;; LOCATION: (1125)
;; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
;; OTHER INFORMATION: K4516.
;; FEATURE:
;; NAME/KEY: mutation
;; LOCATION: (2736)..(2737)
;; OTHER INFORMATION: There is an insertion of GGGCC between these two
;; OTHER INFORMATION: nucleotides in K3963.
US-09-177-650-1
```

```
Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 3232;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 367 CGCGGCTGGGCGTTCATCTACACGCG 392
DB 392 CGCGGCTGGGCGTTCATCTACACGCG 417
```

```
RESULT 5
US-09-177-650-95
; Sequence 95, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 95
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2917)
US-09-177-650-95
```

```
Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 3237;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 367 CGCGGCTGGGCGTTCATCTACACGCG 392
DB 392 CGCGGCTGGGCGTTCATCTACACGCG 417
```

```
RESULT 6
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
```

```

; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

```

```

Query Match      0.9%; Score 26; DB 4; Length 3287;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 367 CGCGGCTGGCGGCTTCATCTACCCAGC 392
Db 325 CGCGGCTGGCGGCTTCATCTACCCAGC 350

```

Search completed: June 19, 2003, 16:39:11
 Job time : 166 secs

